Annex to: Update of the risk assessment of inorganic arsenic in food.
doi:10.2903/j.efsa.2024.8488

Annex E1 Benchmark dose modelling reports

Relative increase of the background incidence after adjustment for confounders by 5%[1]

Annex E1 provides a comprehensive overview of the benchmark dose (BMD) analyses carried out for the critical studies, employing the model averaging technique. The BMD analyses were conducted in accordance with the EFSA BMD guidance (EFSA Scientific Committee, 2022).

E1.1 Selection of the BMR

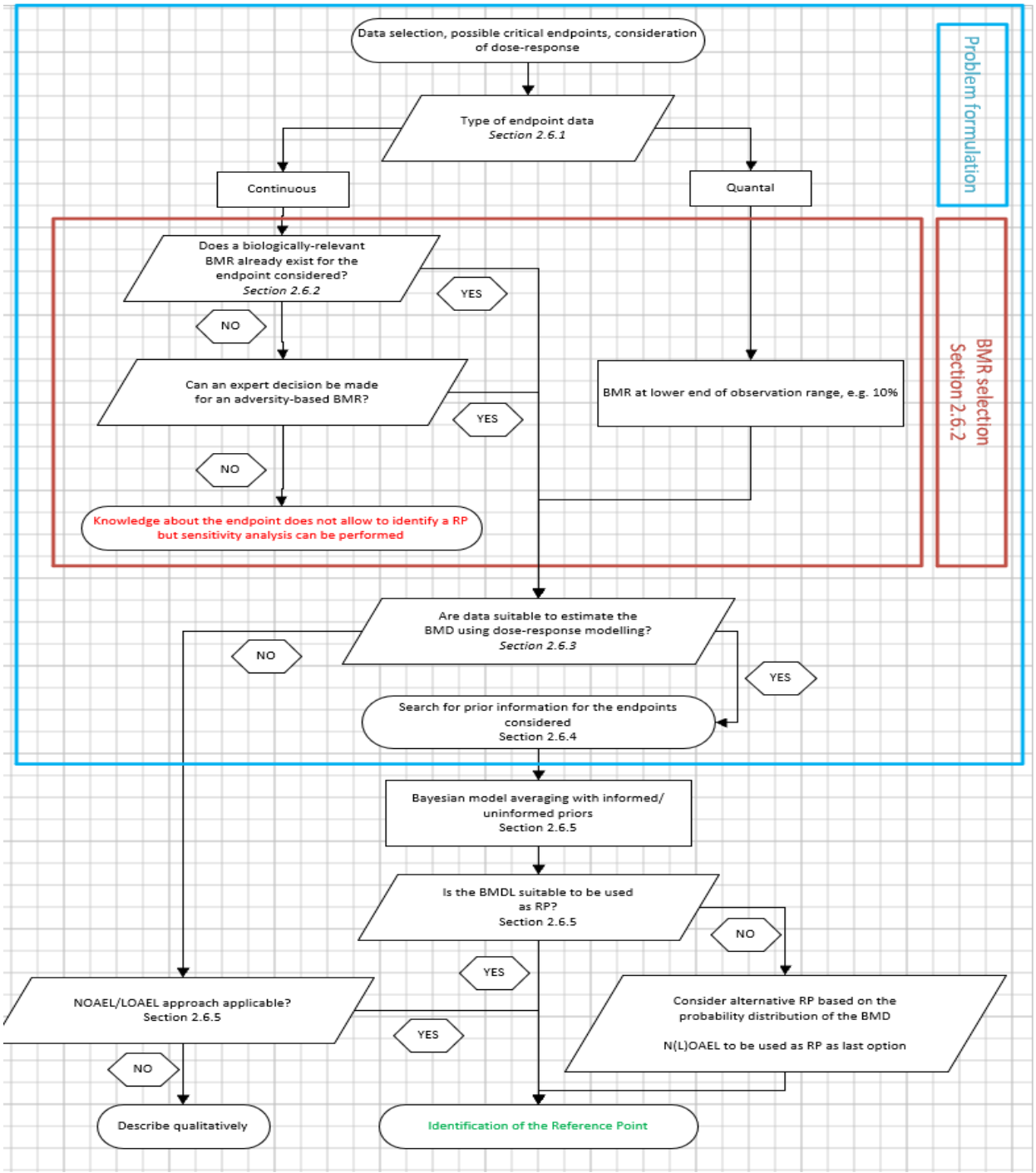
The BMD is identified as the specific dose that corresponds to the desired BMR level. To assess the uncertainty associated with the BMD, a 90% confidence interval is estimated, with the lower bound denoted as BMDL and the upper bound as BMDU. The BMDL and BMDU values help to quantify the range within which the true BMD value is expected to lie.

As BMR the CONTAM Panel decided to use a relative increase of the background incidence after adjustment for confounders by 5%[1].

E1.2 Software Used

Results are obtained using the EFSA web-tool for Bayesian BMD analysis, which uses the R-package [BMABMDR] version 0.0.0.9057/0.0.0.9060/0.0.0.9073 for the underlying calculations.

[1] Exceptions: For continuous endpoints including the studies of Parvez et al. (2013) on FEV1 and FVC, Siddique et al. (2020) on FEV1 and FEV6 and Vahter et al. (2020), an extra risk of 5% was applied.



Flowchart to derive a Reference Point (RP) from a dose-response dataset of a specified endpoint, using BMD analysis. Figure from EFSA BMD guidance (EFSA Scientific Committee, 2022).

E1.3 BMD modelling reports

Ahsan et al. (2006) skin lesions, relative BMR 5%

Data Description

The endpoint to be analyzed is: Adj.cases for skin lesions

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	N
1.22	51	2259
2.76	90	2122
5.60	143	2202
10.18	171	2185
19.64	239	2183

The 'Value for CES' is set to 0.00115489.

Extended dose range is applied.

Informative background prior: min: 0.02144754; the most likely: 0.02257636; max: 0.02370518. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 2.43e-03).

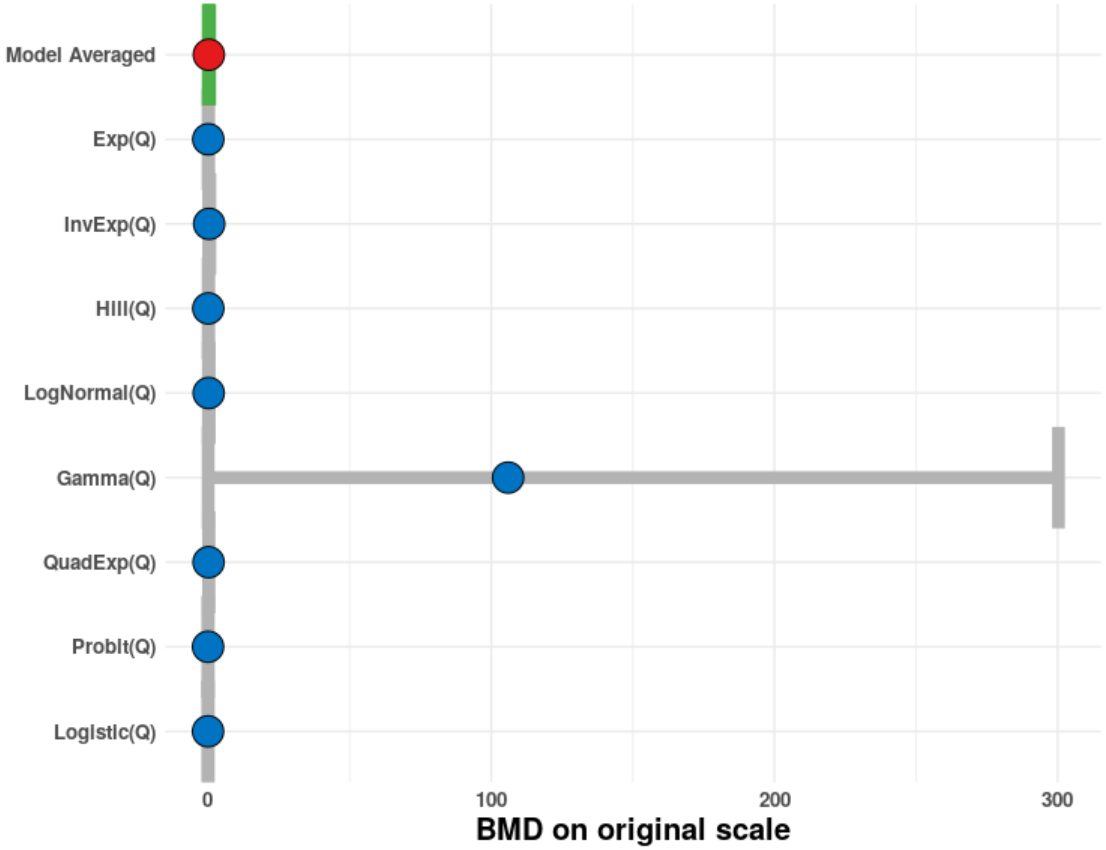
Model Averaged BMD

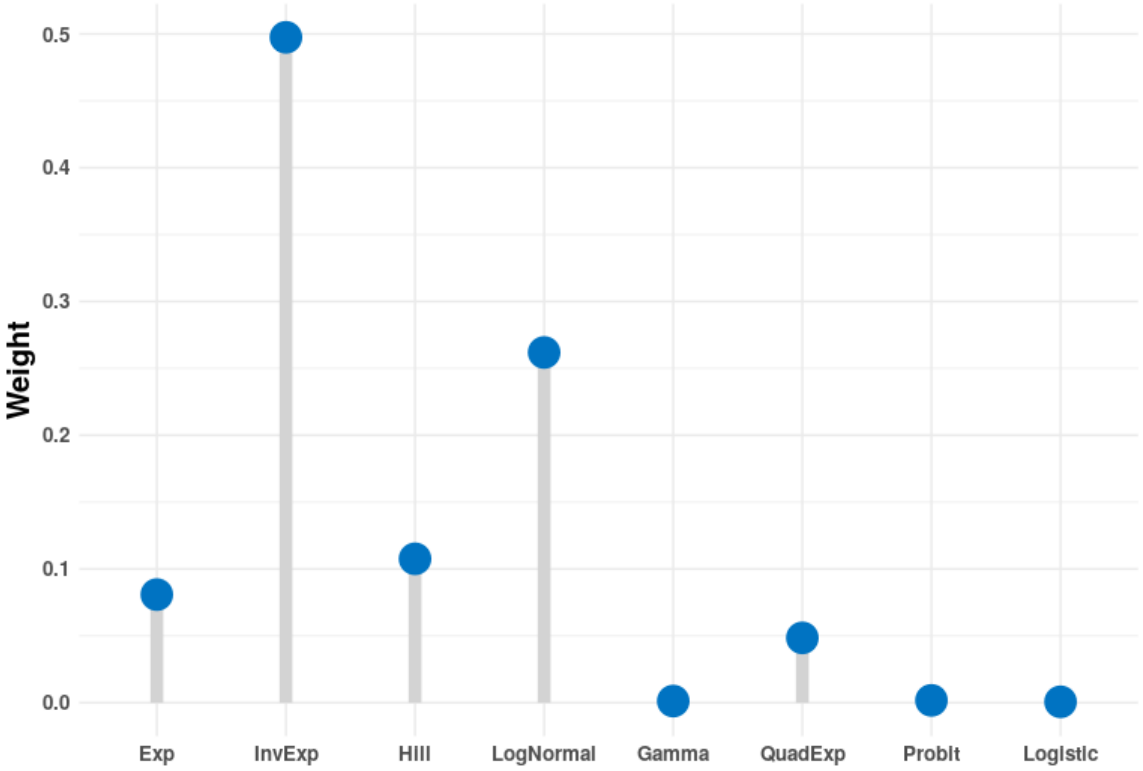
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.083	0.308	0.597

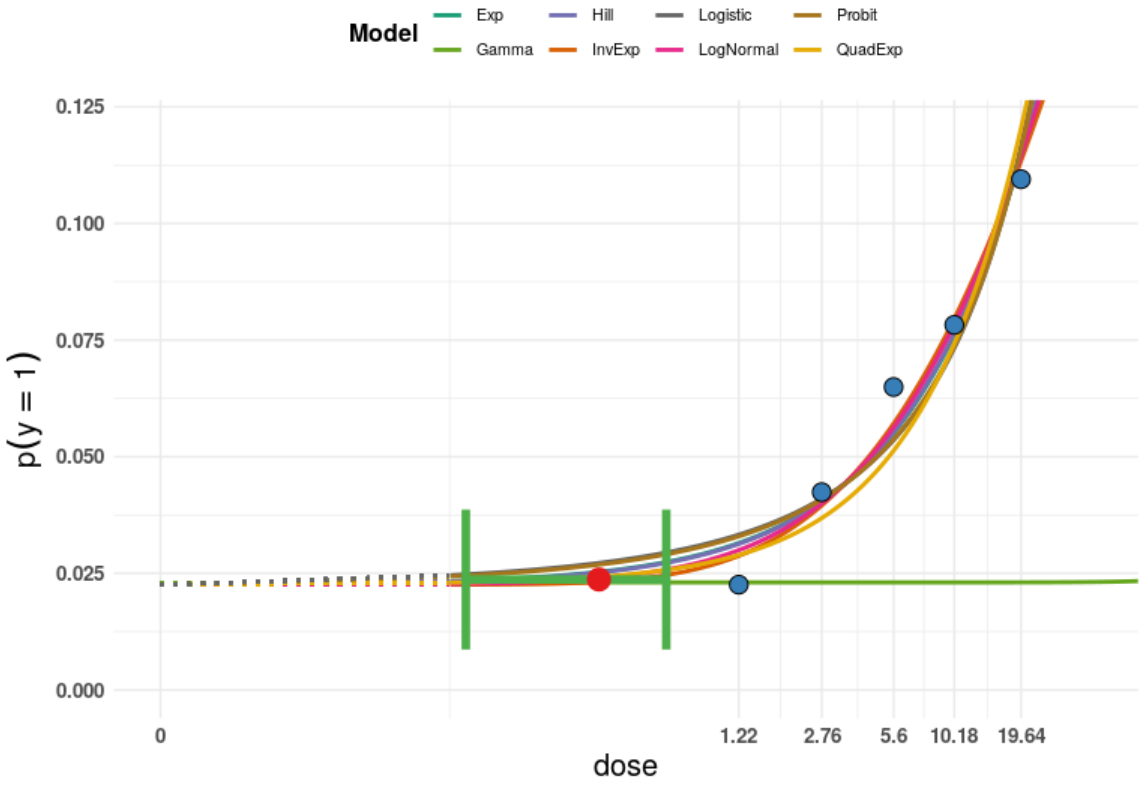
Estimated BMDs per model

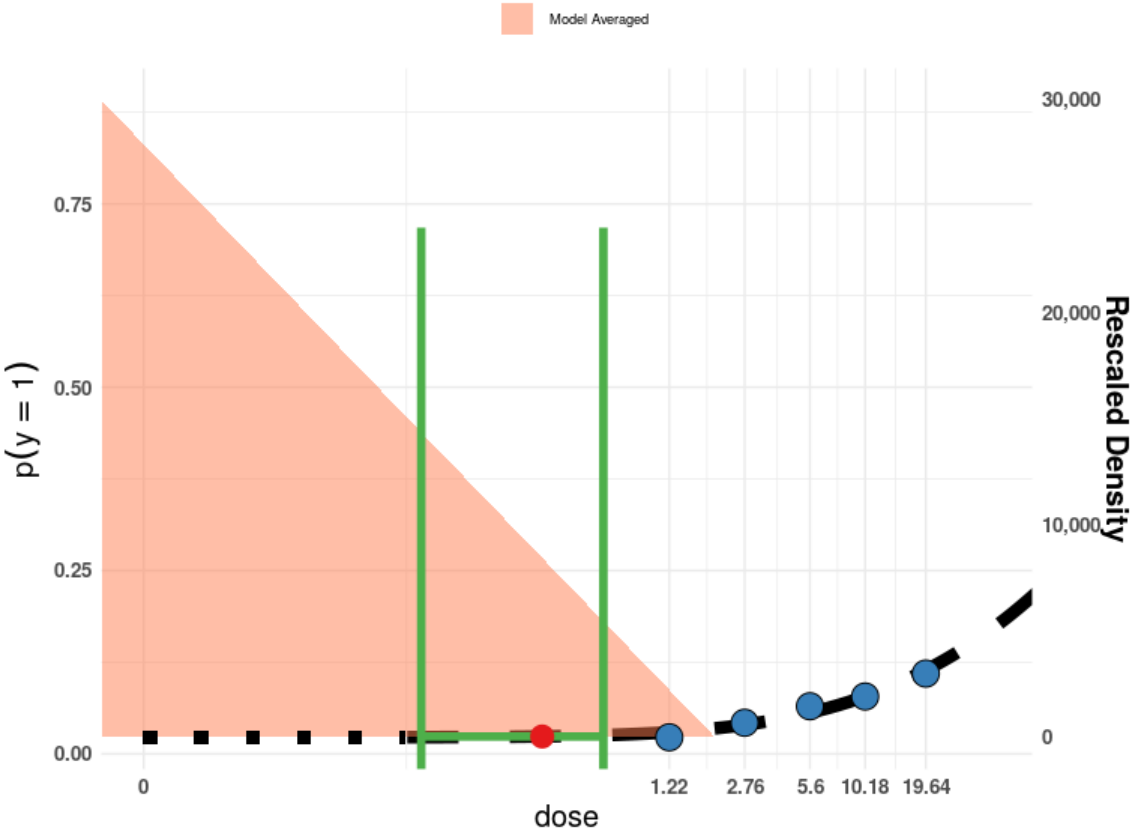
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.047	0.107	0.206	0.081	1
IE4_Q	0.252	0.419	0.652	0.497	1
H4_Q	0.055	0.117	0.225	0.108	1
LN4_Q	0.137	0.258	0.428	0.262	1
G4_Q	0.065	105.978	300.296	0.001	0
QE4_Q	0.198	0.218	0.247	0.048	1
P4_Q	0.011	0.033	0.075	0.002	1
L4_Q	0.008	0.024	0.058	0.001	1

Plots of Fitted Models




Weight
0.5
0.4
0.3
0.2
0.1
0.0
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
p(y = 1)
0.125
0.100
0.075
0.050
0.025
0.000
0
1.22
2.76
5.6
10.18
19.64
dose


Model Averaged
p(y = 1)
0.00
0.25
0.50
0.75
0
1.22
2.76
5.6
10.18
19.64
dose
Rescaled Density
0
10,000
20,000
30,000

Chen et al. (2010a) lung cancer, relative BMR 5%

Data Description

The endpoint to be analyzed is: Adj.cases for lung cancer

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	N
0.927	48	2288
2.288	48	2093
4.743	19	907
11.561	29	909
17.018	33	691

The 'Value for CES' is set to 0.00107143.

Extended dose range is not applied.

Informative background prior: min: 0.02076923; the most likely: 0.02097902; max: 0.02118881. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 1.93e-04).

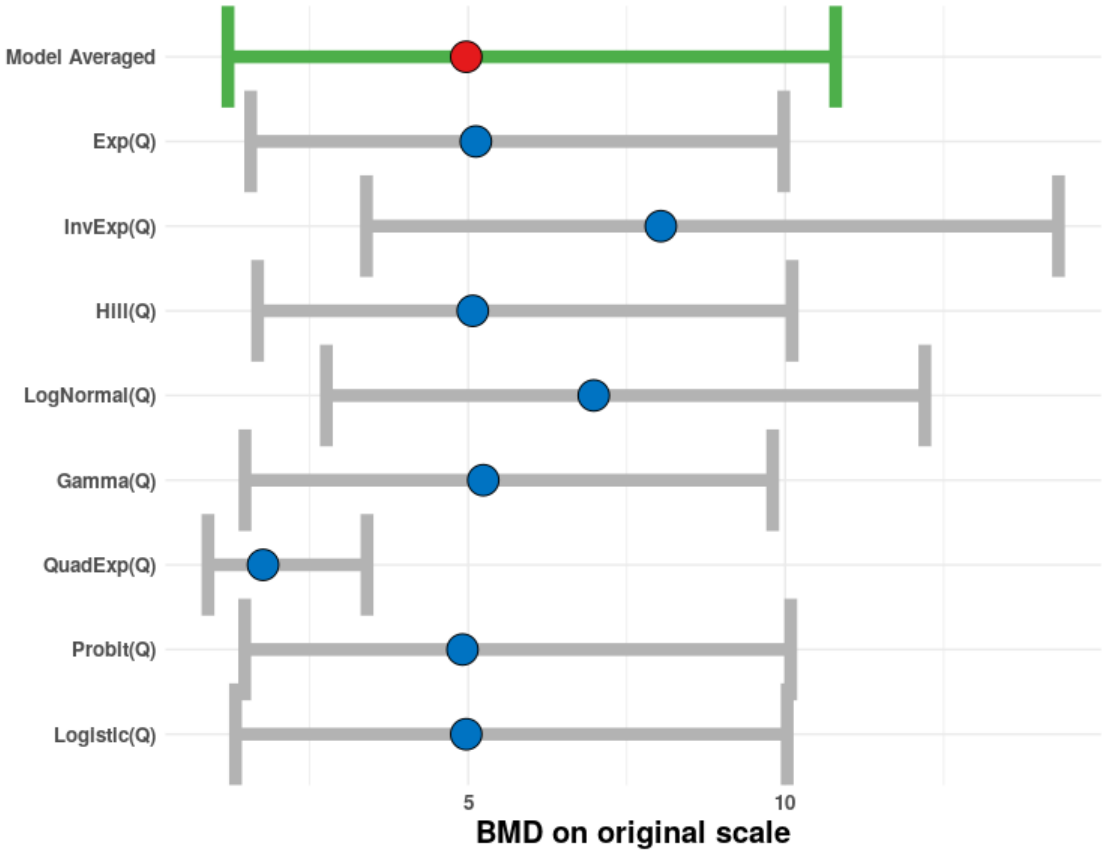
Model Averaged BMD

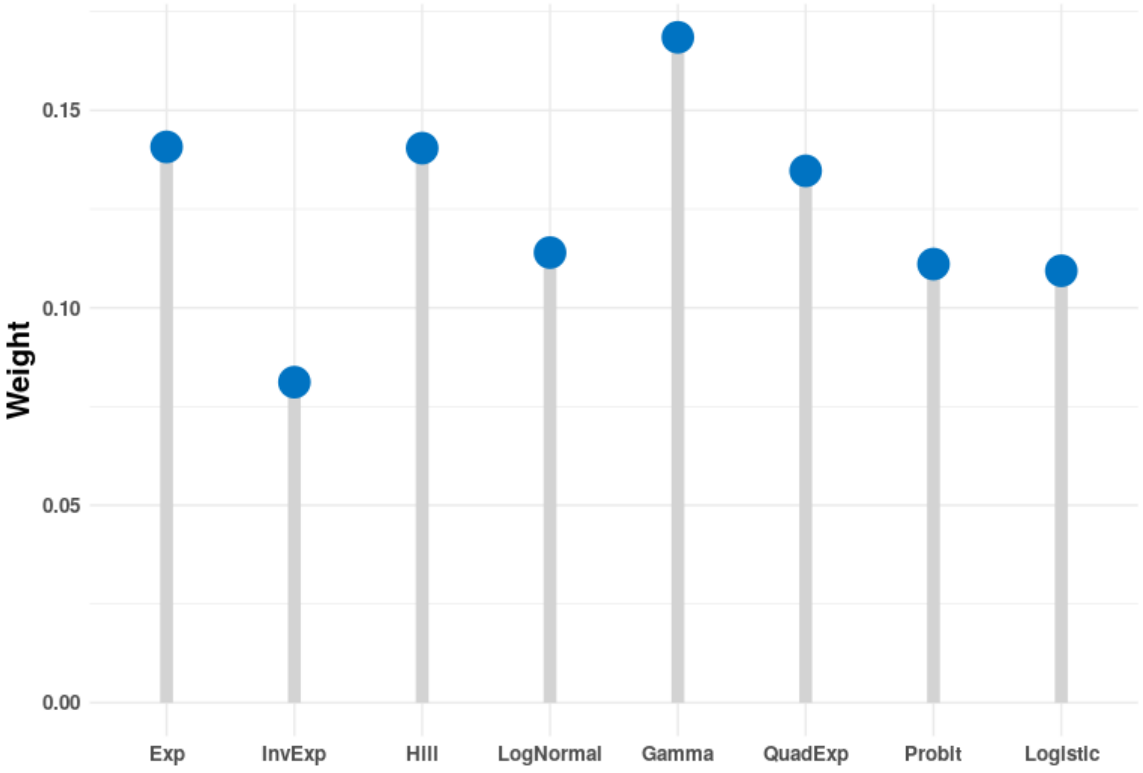
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	1.21	4.969	10.797

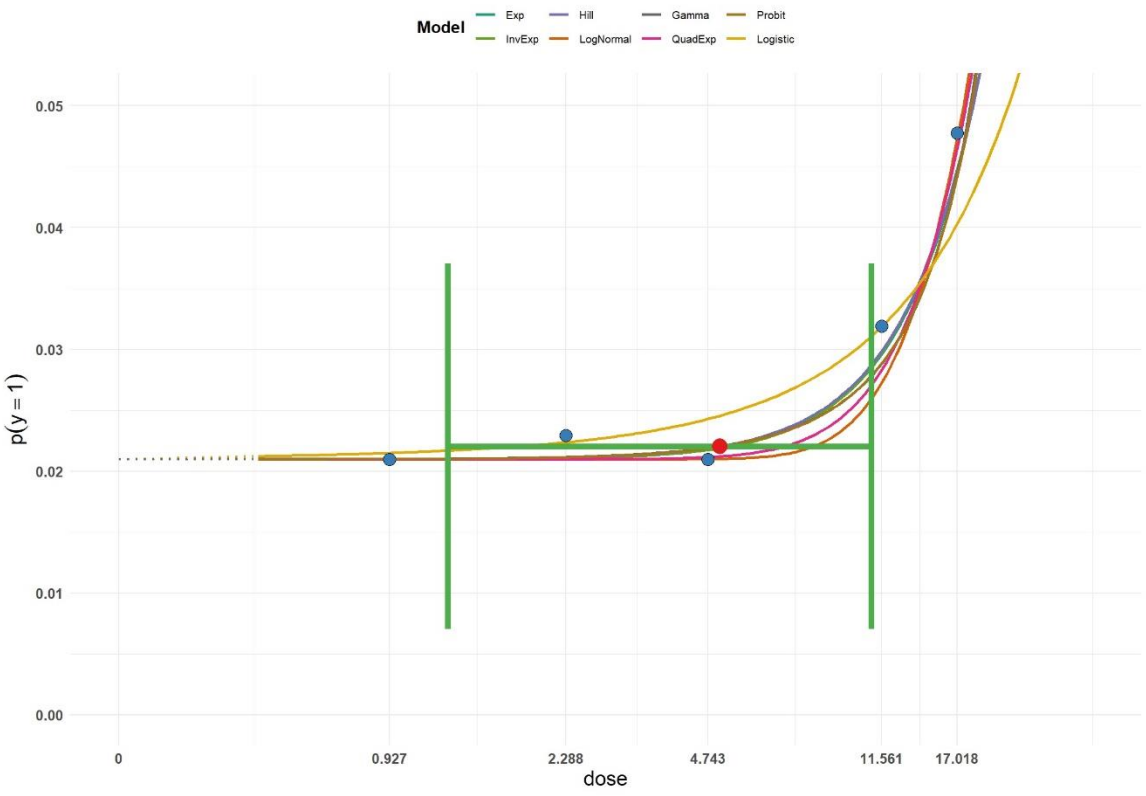
Estimated BMDs per model

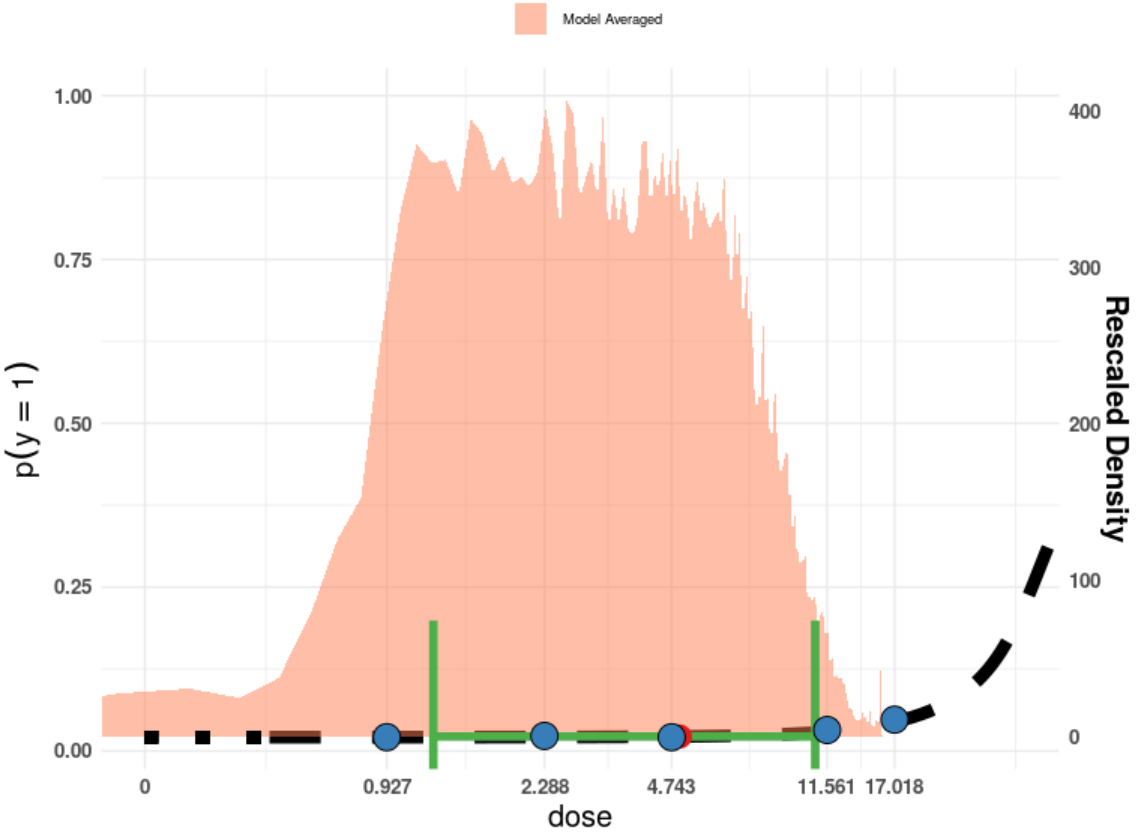
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	1.568	5.121	9.977	0.141	1
IE4_Q	3.395	8.038	14.312	0.081	1
H4_Q	1.678	5.072	10.110	0.140	1
LN4_Q	2.763	6.980	12.204	0.114	1
G4_Q	1.479	5.237	9.803	0.168	1
QE4_Q	0.895	1.764	3.404	0.135	1
P4_Q	1.474	4.910	10.088	0.111	1
L4_Q	1.329	4.969	10.032	0.109	1

Plots of Fitted Models




Weight
0.15
0.10
0.05
0.00
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic
p(y = 1)
0.05
0.04
0.03
0.02
0.01
0.00
0
0.927
2.288
4.743
11.561
17.018
dose


Model Averaged
1.00
0.75
0.50
0.25
0.00
p(y = 1)
400
300
200
100
0
Rescaled Density
0
0.927
2.288
4.743
11.561
17.018
dose

Chen et al. (2010b) bladder cancer, relative BMR 5%

Data Description

The endpoint to be analyzed is: Adj.cases for bladder cancer

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	N
0.927	3	2288
2.288	5	2093
4.743	3	907
11.561	7	909
17.018	11	691

The 'Value for CES' is set to 6.565e-05.

Extended dose range is not applied.

Informative background prior: min: 0.00111451; the most likely: 0.00131119; max: 0.00150787. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 2.59e-04).

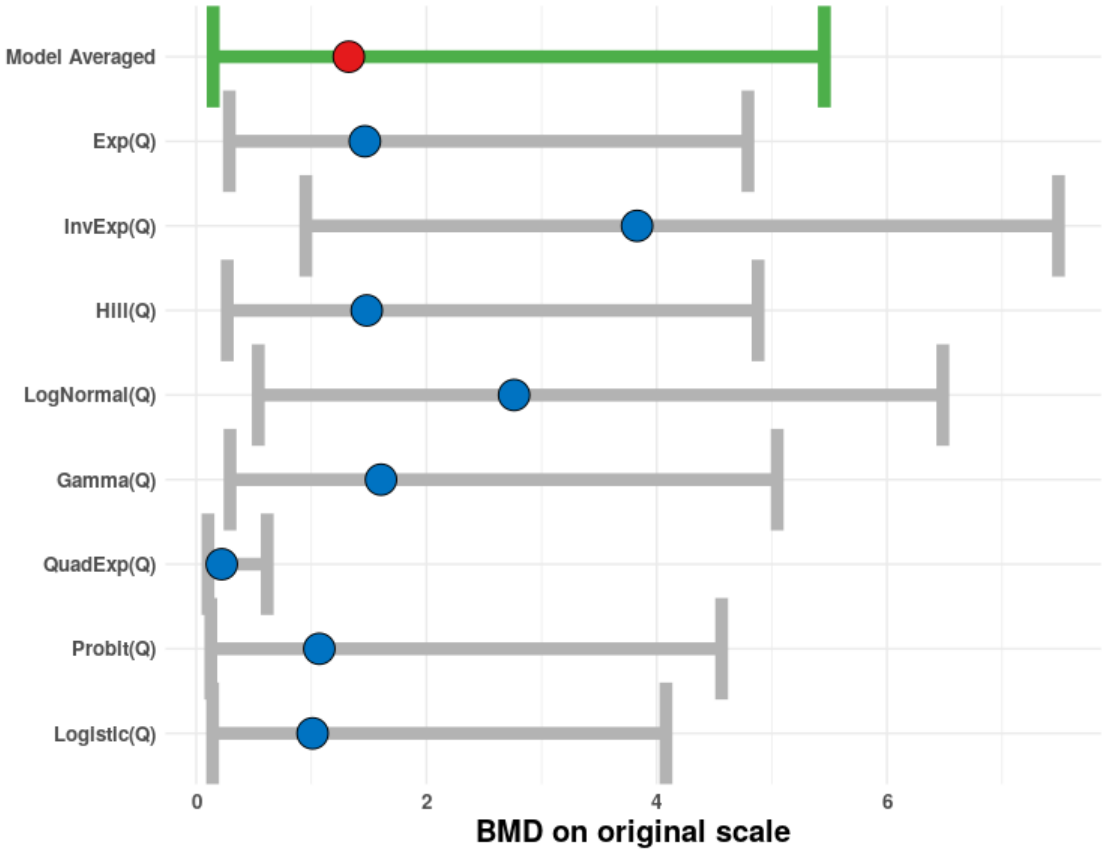
Model Averaged BMD

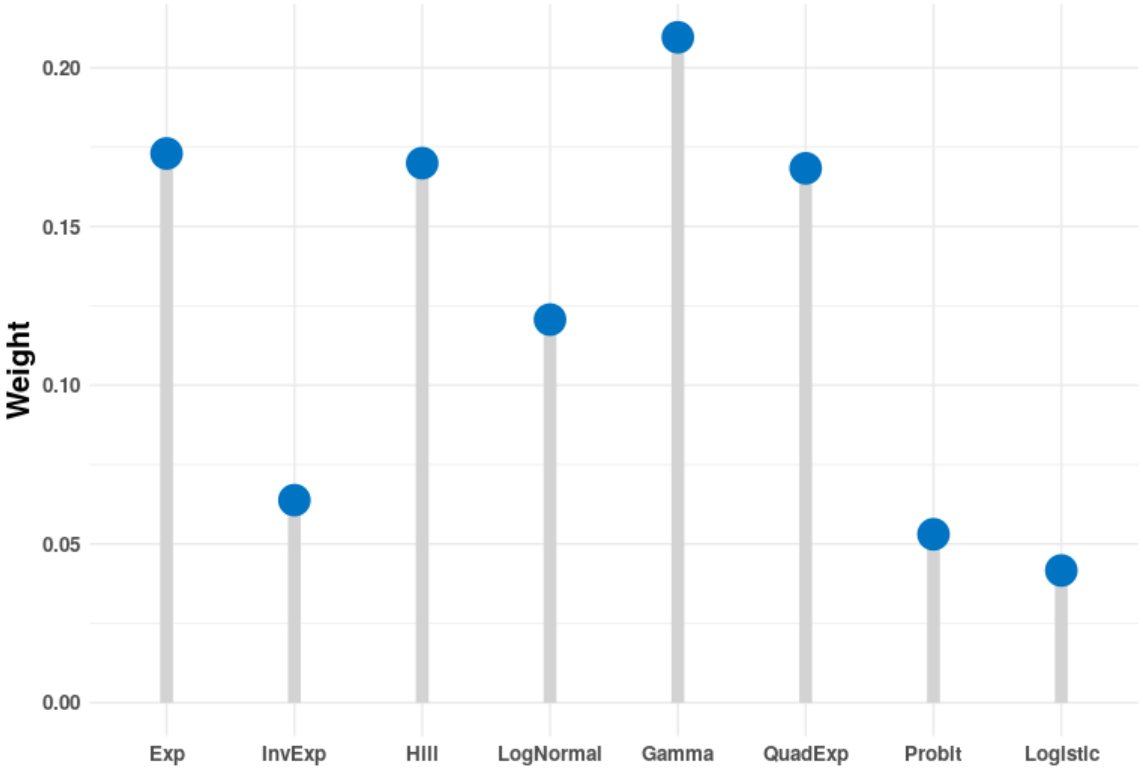
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.147	1.325	5.456

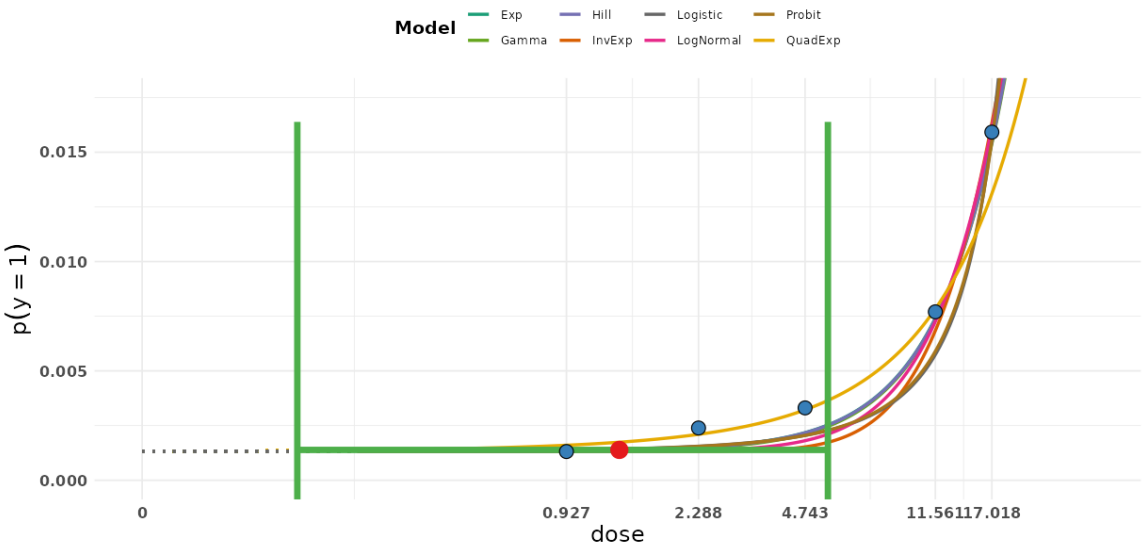
Estimated BMDs per model

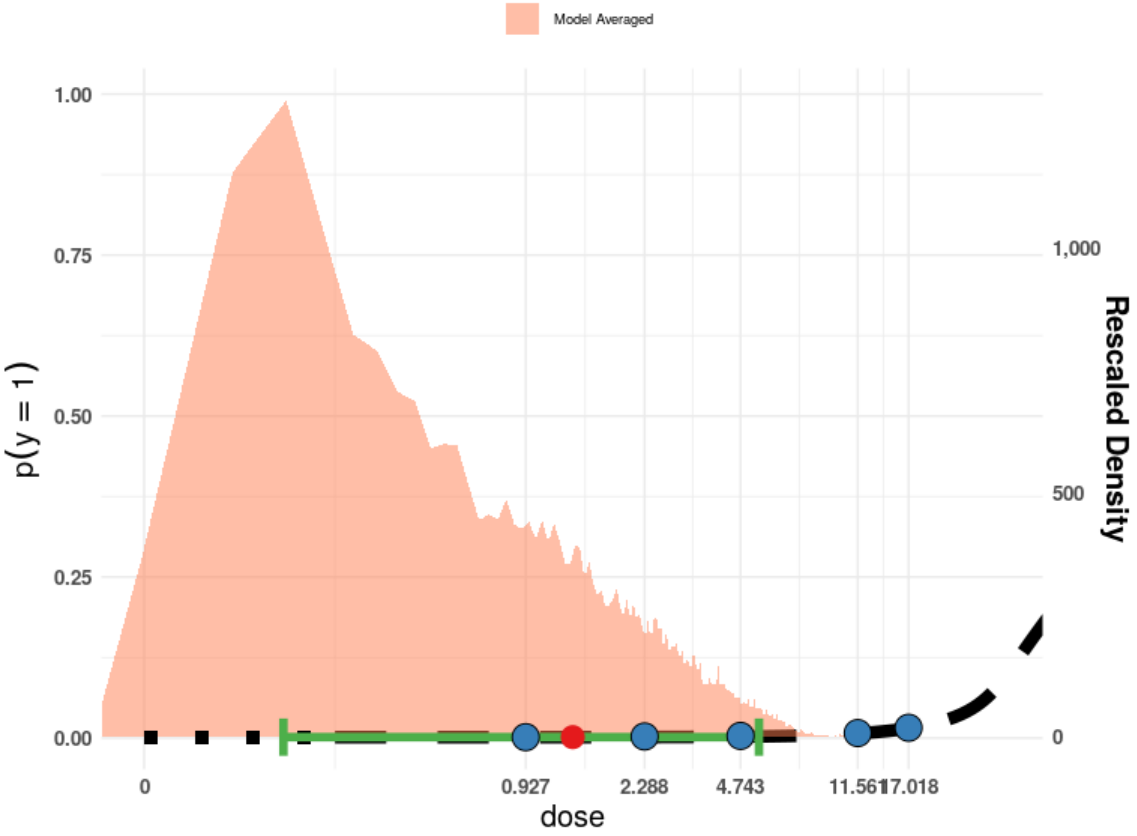
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.287	1.465	4.792	0.173	1
IE4_Q	0.952	3.829	7.490	0.064	1
H4_Q	0.270	1.481	4.881	0.170	1
LN4_Q	0.539	2.761	6.486	0.121	1
G4_Q	0.294	1.605	5.047	0.210	1
QE4_Q	0.102	0.221	0.617	0.168	1
P4_Q	0.127	1.069	4.564	0.053	1
L4_Q	0.142	1.011	4.080	0.042	1

Plots of Fitted Models




Weight
0.20
0.15
0.10
0.05
0.00
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
Gamma
Hill
InvExp
Logistic
LogNormal
Probit
QuadExp
p(y = 1)
0.015
0.010
0.005
0.000
0
0.927
2.288
4.743
11.561
17.018
dose


Model Averaged
1.00
0.75
0.50
0.25
0.00
p(y = 1)
1,000
500
0
Rescaled Density
0
0.927
2.288
4.743
11.561
17.018
dose

Chen et al. (2010b) bladder cancer, relative BMR 5%

Sensitivity analysis: The highest exposure point estimate doubled

Data Description

The endpoint to be analyzed is: Adj.cases for bladder cancer

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	N
0.927	3	2288
2.288	5	2093
4.743	3	907
11.561	7	909
33.382	11	691

The 'Value for CES' is set to 6.565e-05.

Extended dose range is not applied.

Informative background prior: min: 0.00111451; the most likely: 0.00131119; max: 0.00150787. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 2.24e-04).

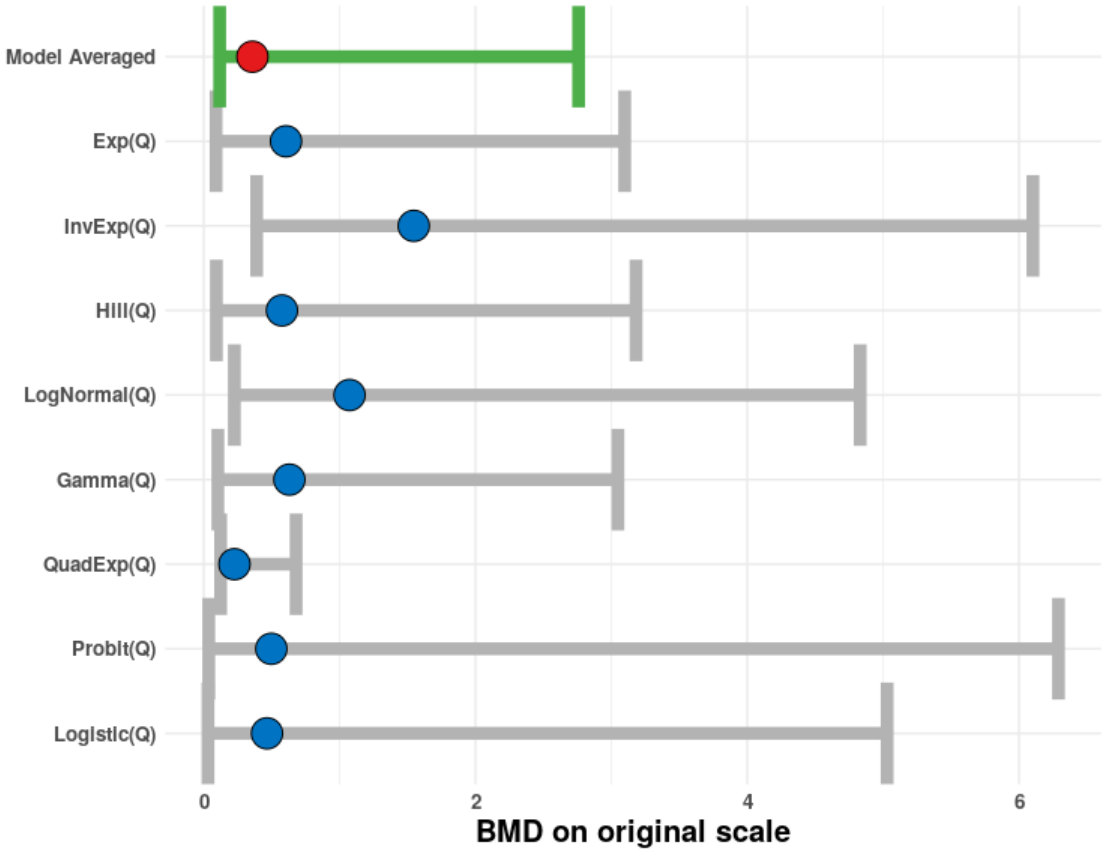
Model Averaged BMD

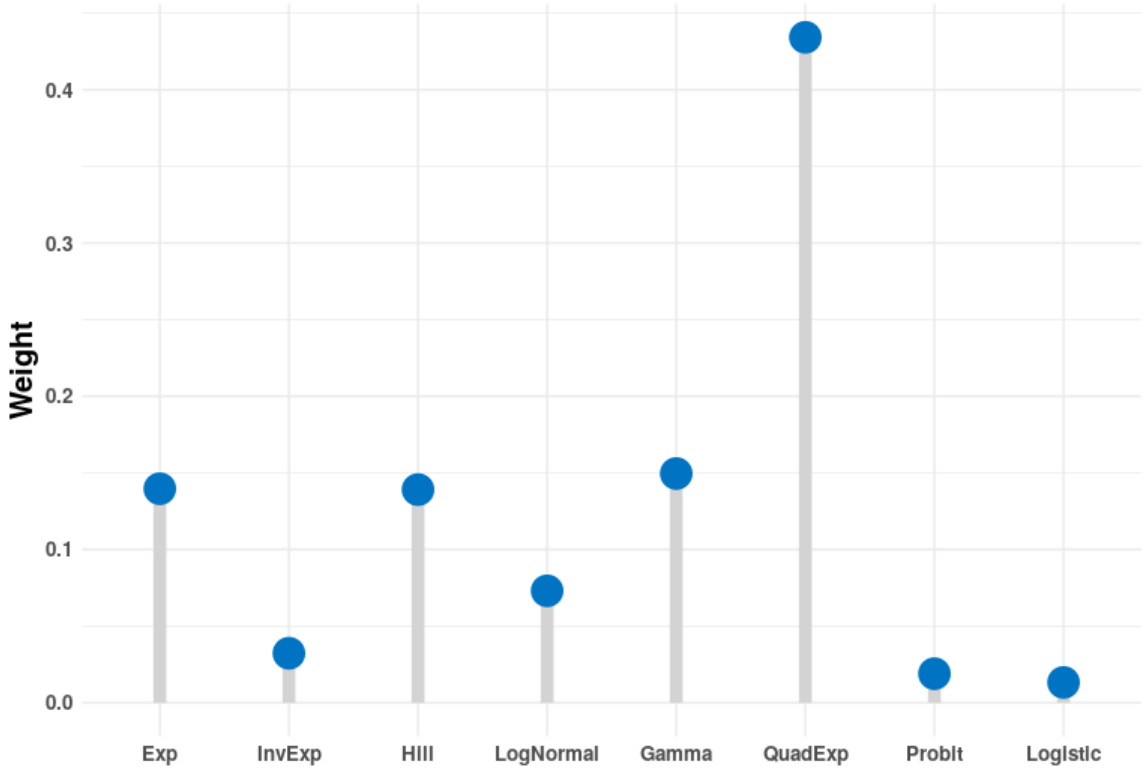
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.117	0.358	2.759

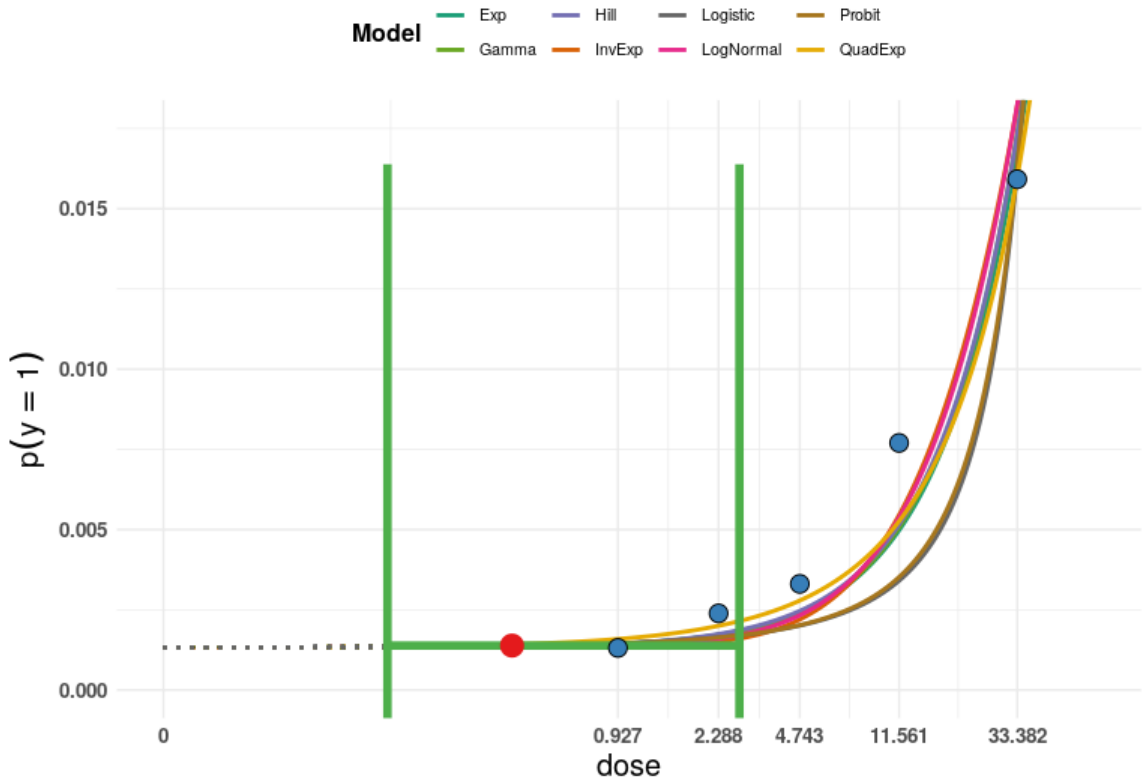
Estimated BMDs per model

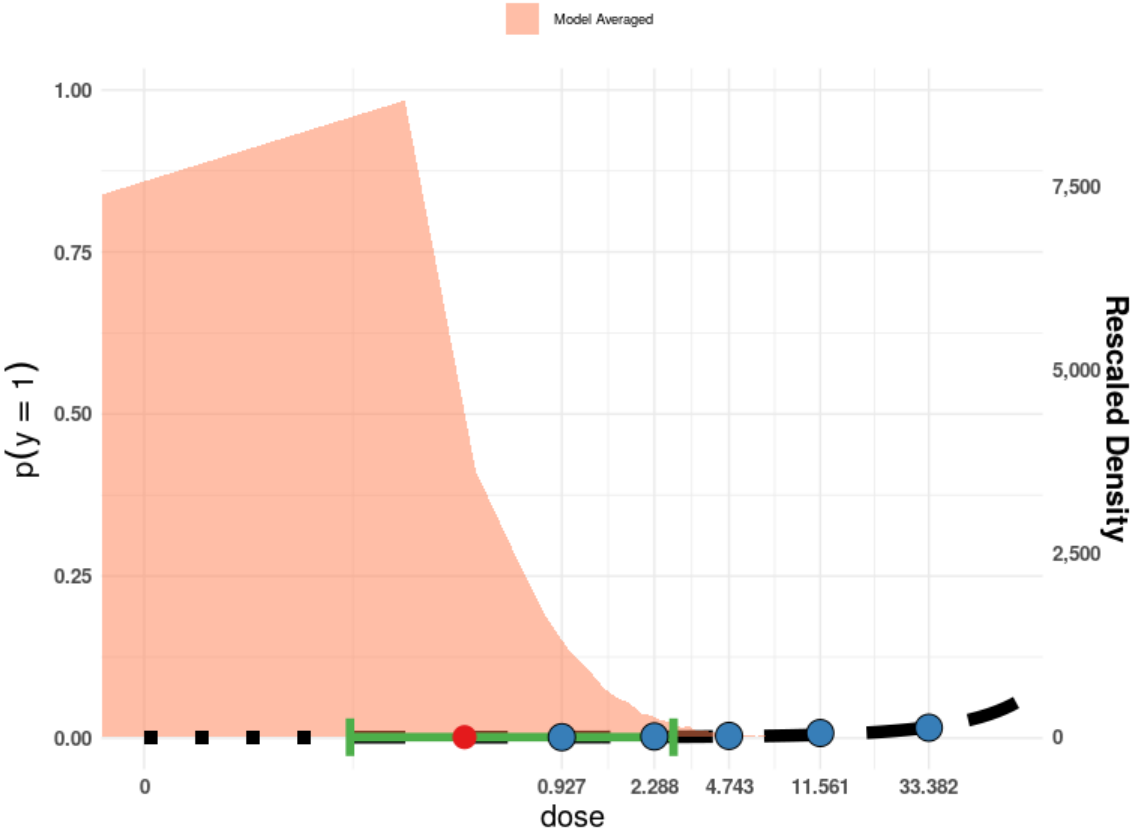
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.091	0.606	3.098	0.140	1
IE4_Q	0.389	1.546	6.102	0.032	1
H4_Q	0.093	0.576	3.182	0.139	1
LN4_Q	0.225	1.073	4.831	0.073	1
G4_Q	0.104	0.631	3.048	0.150	1
QE4_Q	0.124	0.226	0.680	0.434	1
P4_Q	0.037	0.498	6.290	0.019	1
L4_Q	0.031	0.466	5.029	0.013	1

Plots of Fitted Models




Weight
0.4
0.3
0.2
0.1
0.0
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
p(y = 1)
0.015
0.010
0.005
0.000
0
0.927
2.288
4.743
11.561
33.382
dose


Model Averaged
1.00
0.75
0.50
0.25
0.00
p(y = 1)
7,500
5,000
2,500
0
Rescaled Density
0
0.927
2.288
4.743
11.561
33.382
dose

Cherry et al. (2008) stillbirth, relative BMR 5%

Data Description

The endpoint to be analyzed is: Adj.cases for stillbirth

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	N
1.45	492	16860
3.24	386	10669
4.73	177	3455

The 'Value for CES' is set to 0.00150293.

Extended dose range is applied.

Informative background prior: min: 0.02888968; the most likely: 0.02918149; max: 0.02947331. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 1.10e+00).

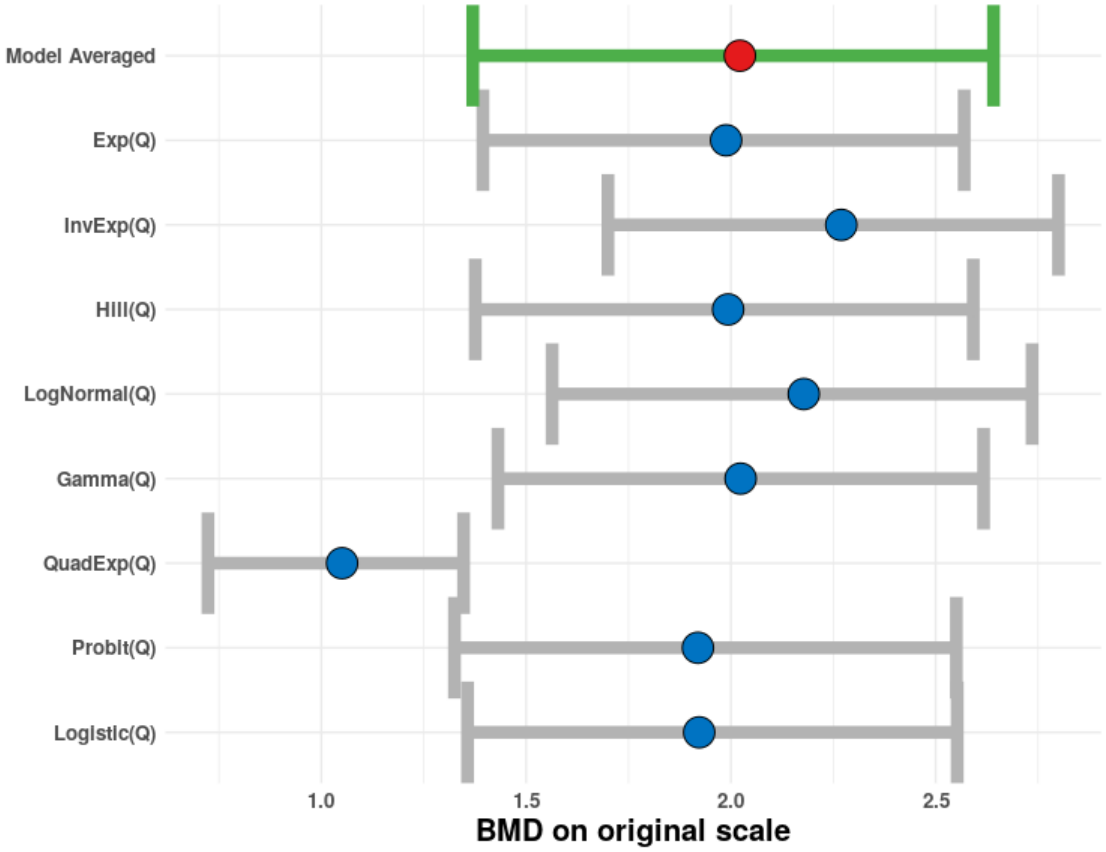
Model Averaged BMD

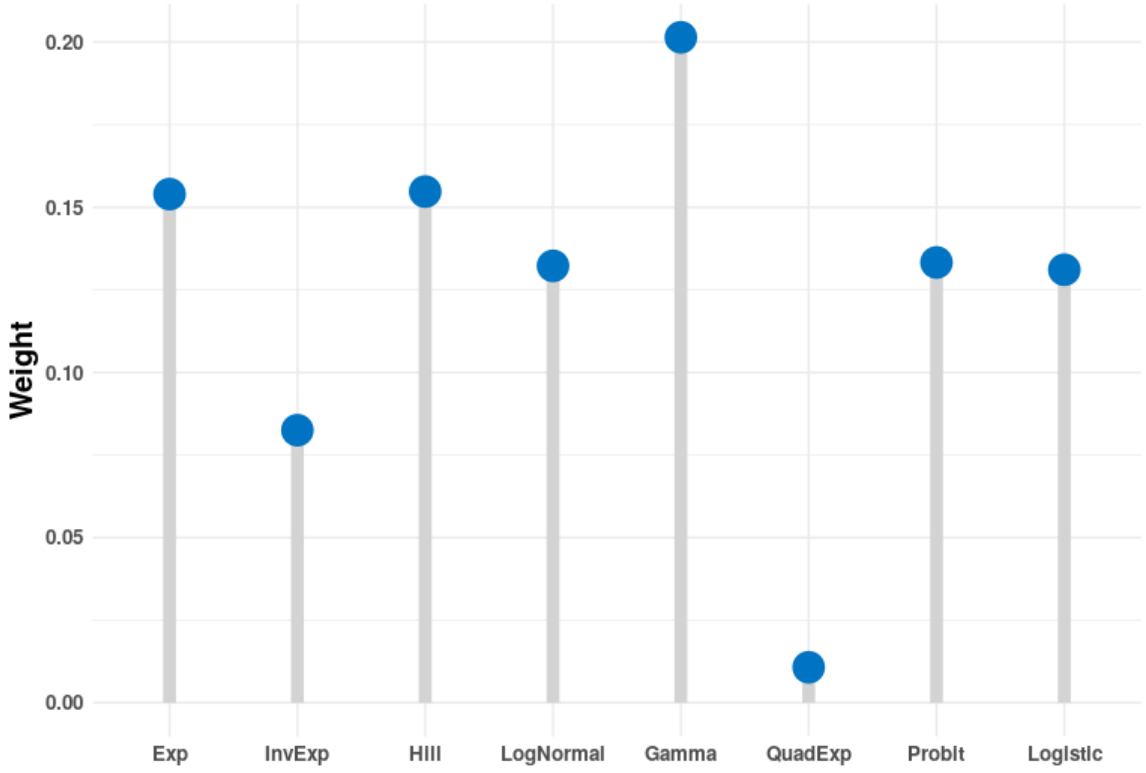
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	1.37	2.022	2.641

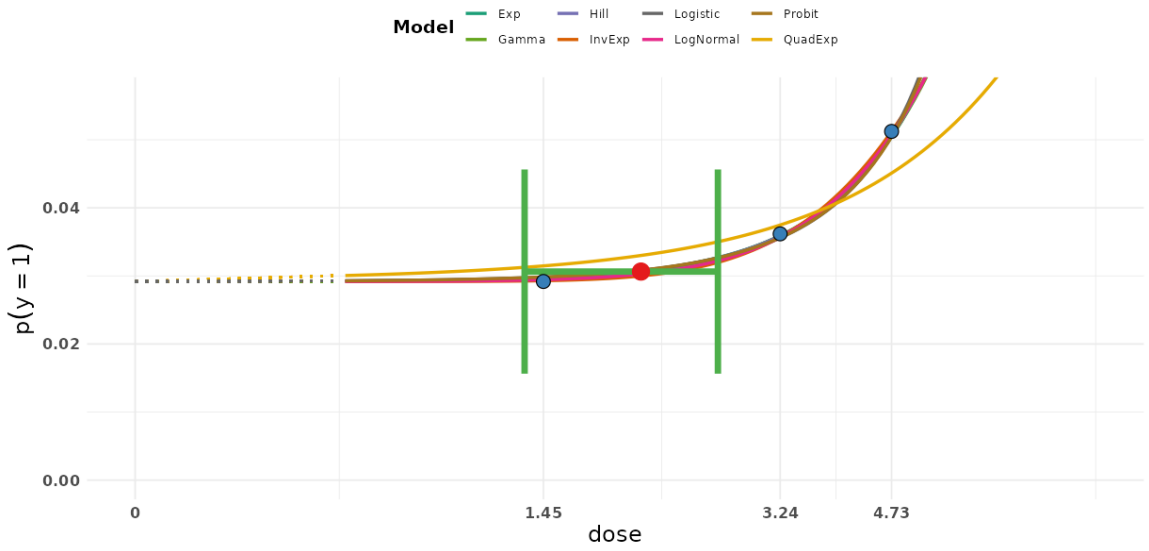
Estimated BMDs per model

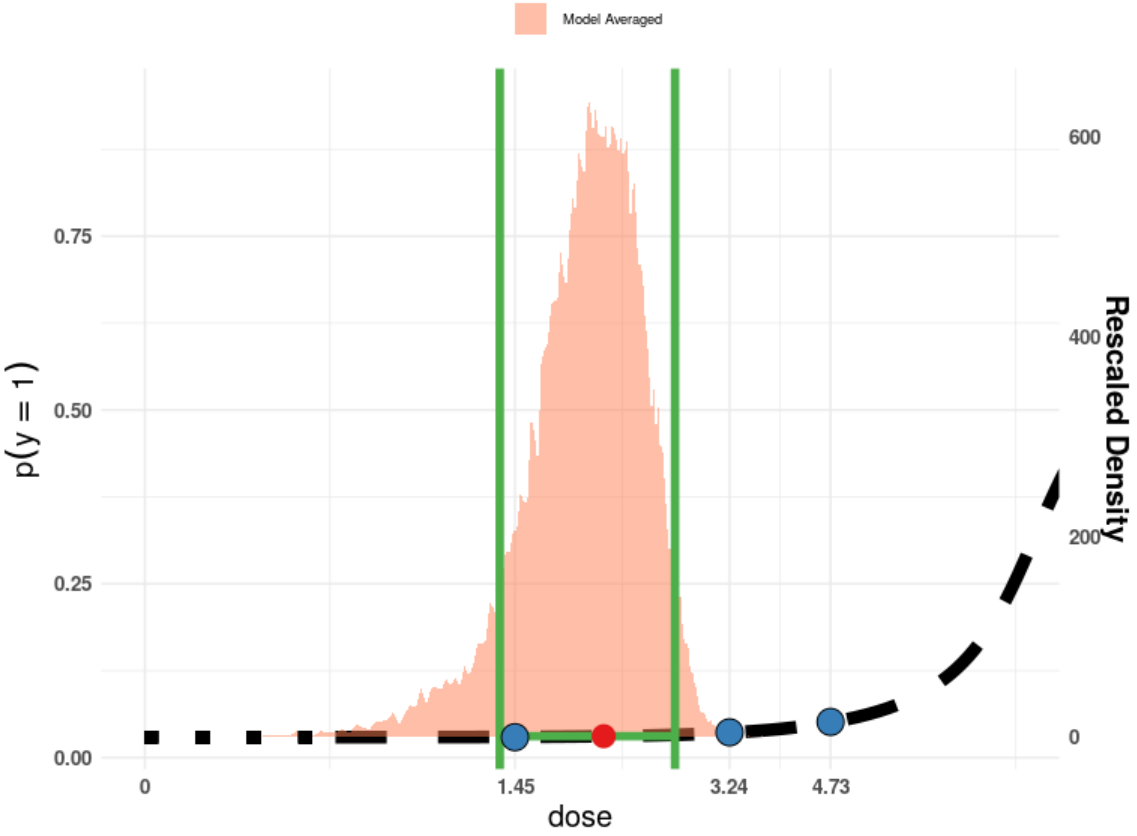
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	1.395	1.988	2.570	0.154	1
IE4_Q	1.700	2.269	2.800	0.083	1
H4_Q	1.376	1.993	2.592	0.155	1
LN4_Q	1.564	2.178	2.736	0.132	1
G4_Q	1.431	2.024	2.617	0.201	1
QE4_Q	0.723	1.051	1.347	0.011	1
P4_Q	1.325	1.920	2.551	0.133	1
L4_Q	1.357	1.923	2.553	0.131	1

Plots of Fitted Models




Weight
0.20
0.15
0.10
0.05
0.00
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
p(y = 1)
0.04
0.02
0.00
0
1.45
3.24
4.73
dose


Model Averaged
p(y = 1)
0.00
0.25
0.50
0.75
0
1.45
3.24
4.73
dose
0
200
400
600
Rescaled Density

Gilbert-Diamond et al. (2013) skin cancer, relative BMR 5%
(the preferred estimate for the study)

Data Description

The endpoint to be analyzed is: Adj.cases for skin cancer

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	N
0.063	96	263307
0.120	90	260846
0.230	137	260846

The 'Value for CES' is set to 1.824e-05.

Extended dose range is not applied.

Informative background prior: min: 0.00034636; the most likely: 0.00036459; max: 0.00038282. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 1.28e+00).

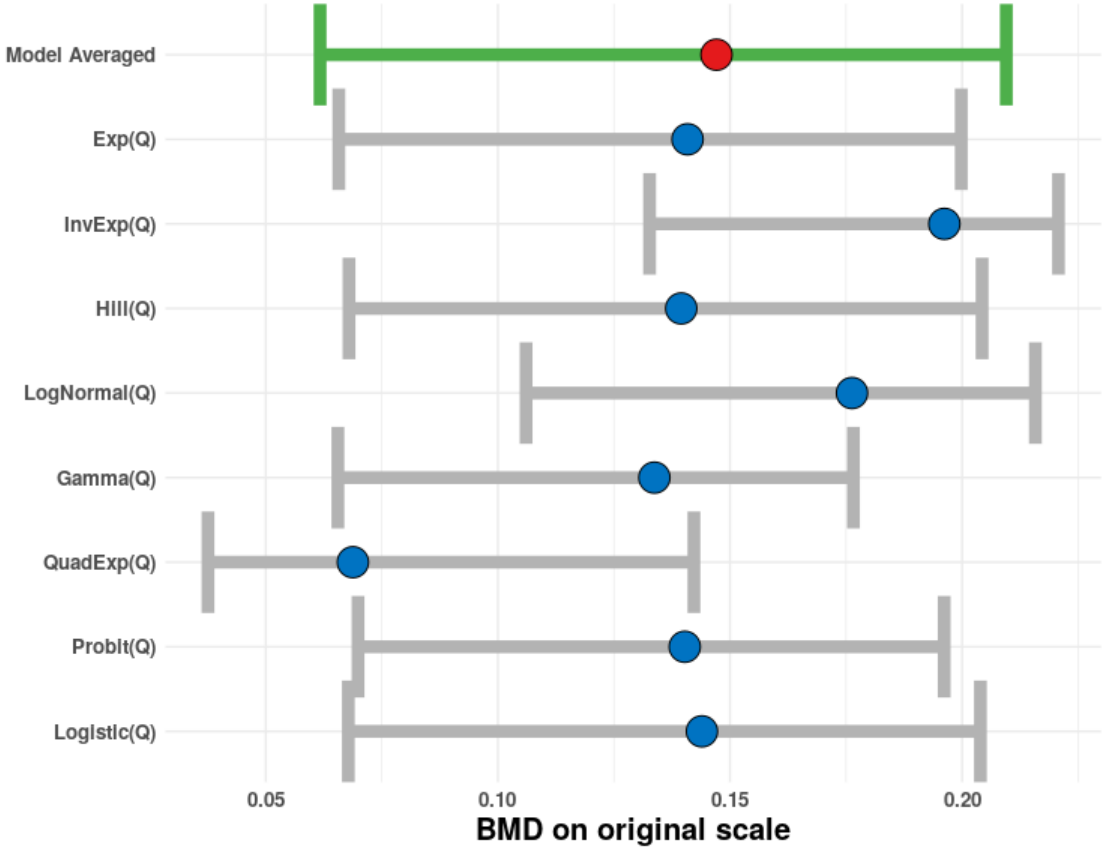
Model Averaged BMD

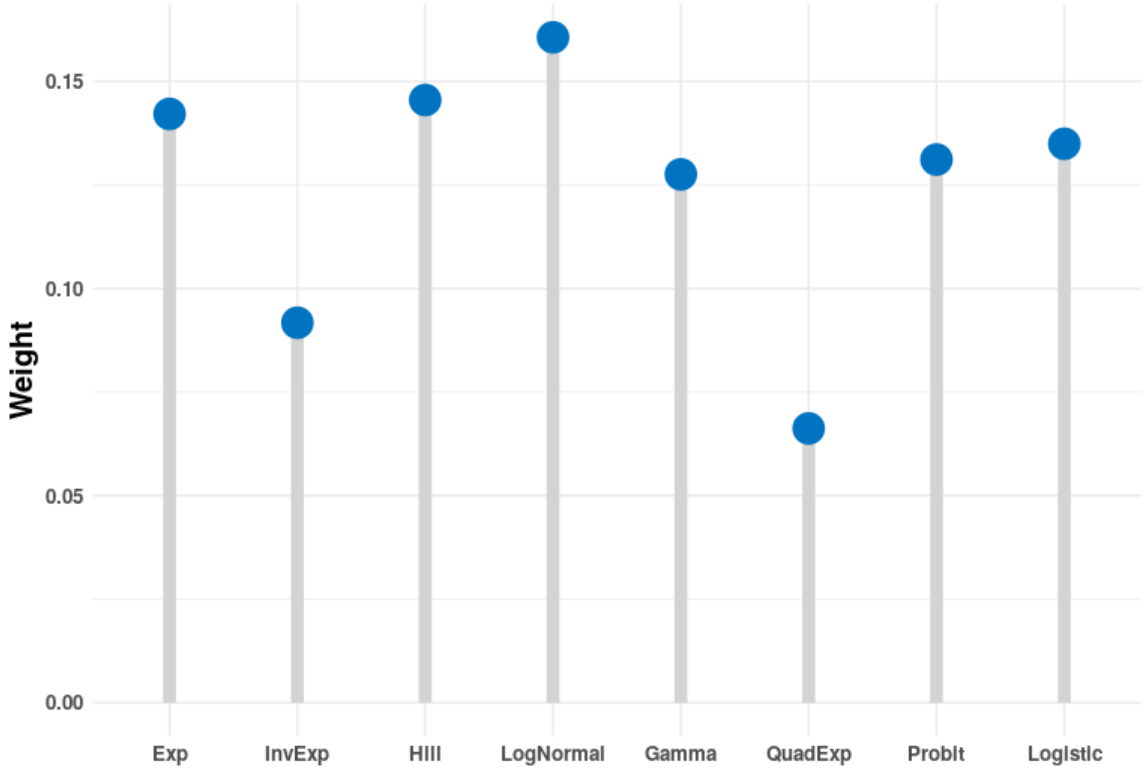
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.062	0.147	0.21

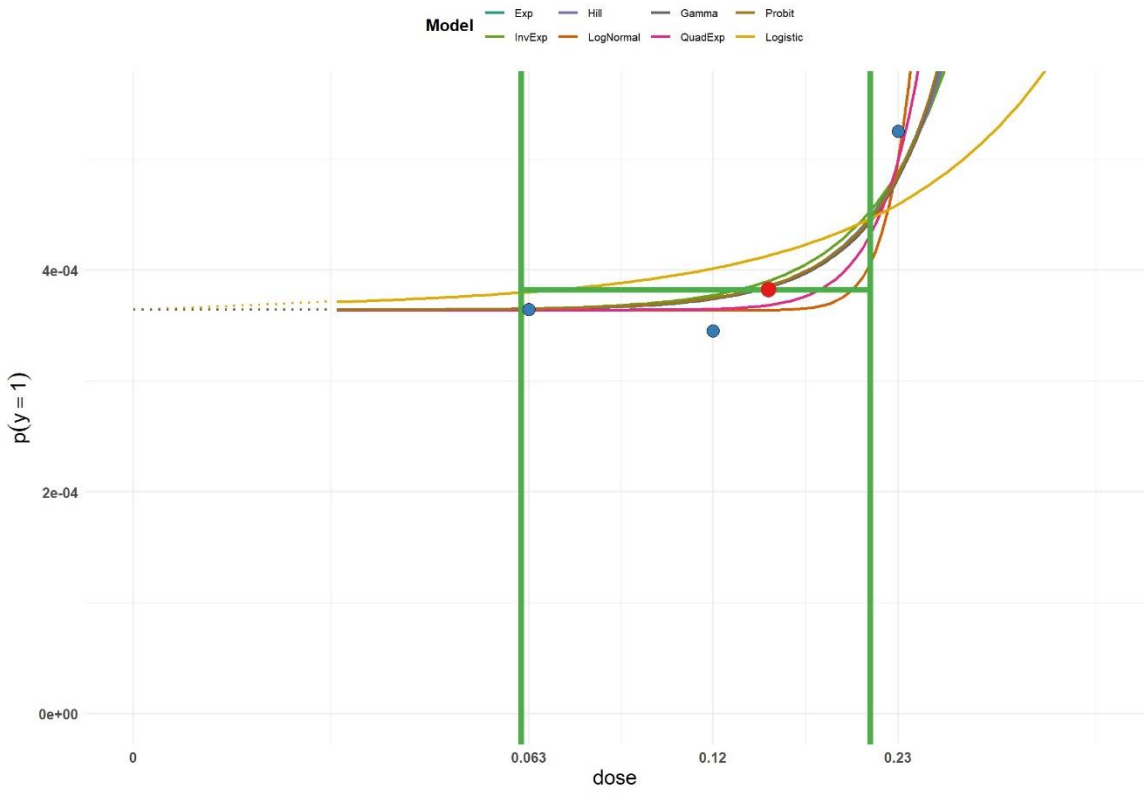
Estimated BMDs per model

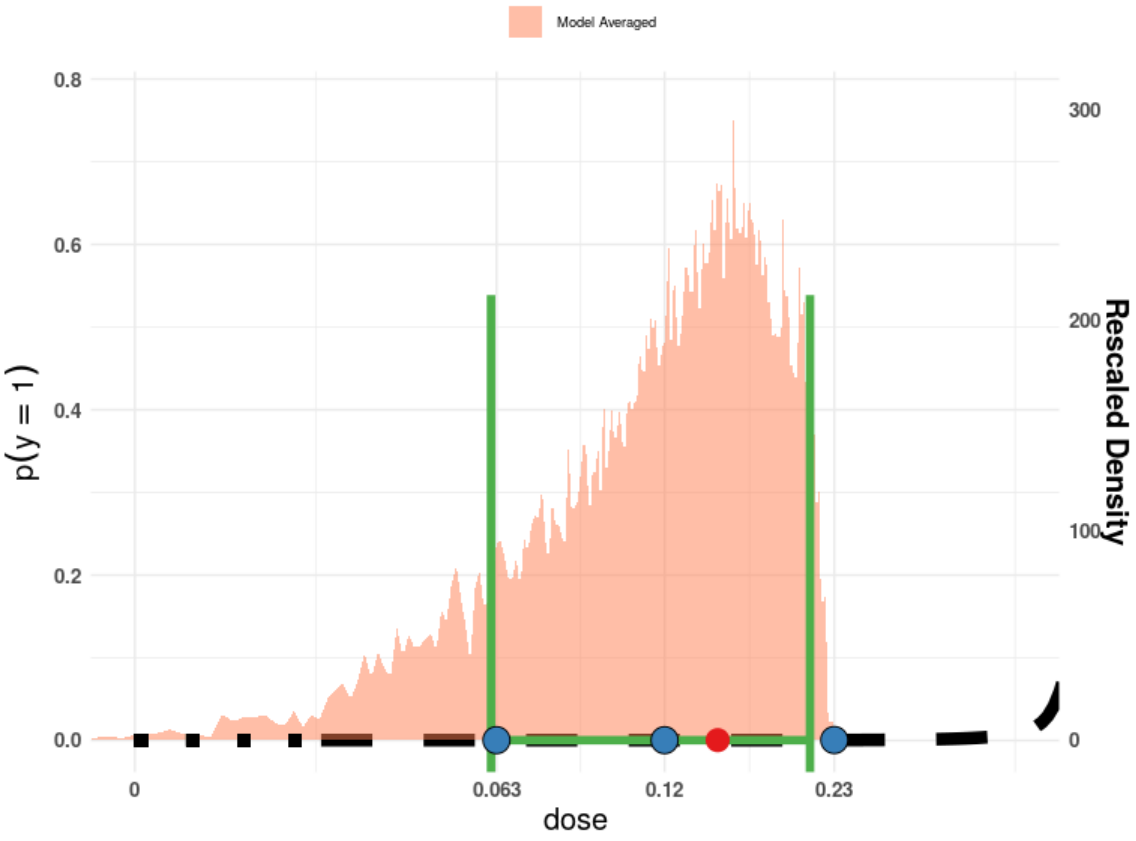
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.066	0.141	0.200	0.142	1
IE4_Q	0.133	0.196	0.221	0.092	1
H4_Q	0.068	0.139	0.204	0.146	1
LN4_Q	0.106	0.176	0.216	0.161	1
G4_Q	0.066	0.134	0.177	0.128	1
QE4_Q	0.038	0.069	0.142	0.066	1
P4_Q	0.070	0.140	0.196	0.131	1
L4_Q	0.068	0.144	0.204	0.135	1

Plots of Fitted Models




0.15
0.10
0.05
0.00
Weight
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic
4e-04
2e-04
0e+00
p(y = 1)
0
0.063
0.12
0.23
dose


Model Averaged
0.8
0.6
0.4
0.2
0.0
p(y = 1)
300
200
100
0
Rescaled Density
0
0.063
0.12
0.23
dose

Gilbert-Diamond et al. (2013) skin cancer, relative BMR 5%

Without an informative background prior (included only in the uncertainty analysis)

Data Description

The endpoint to be analyzed is: Adj.cases for skin cancer

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	N
0.063	96	263307
0.120	90	260846
0.230	137	260846

The 'Value for CES' is set to 1.824e-05.

Extended dose range is not applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 1.79e+00).

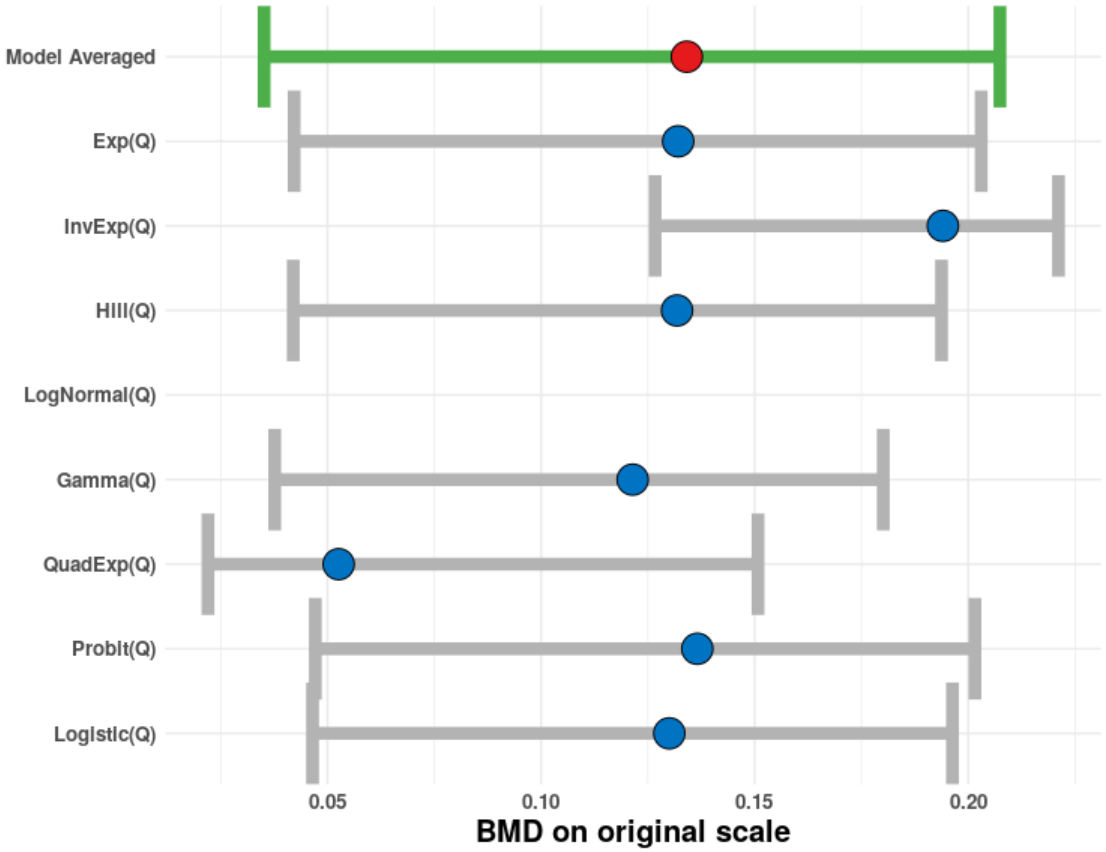
Model Averaged BMD

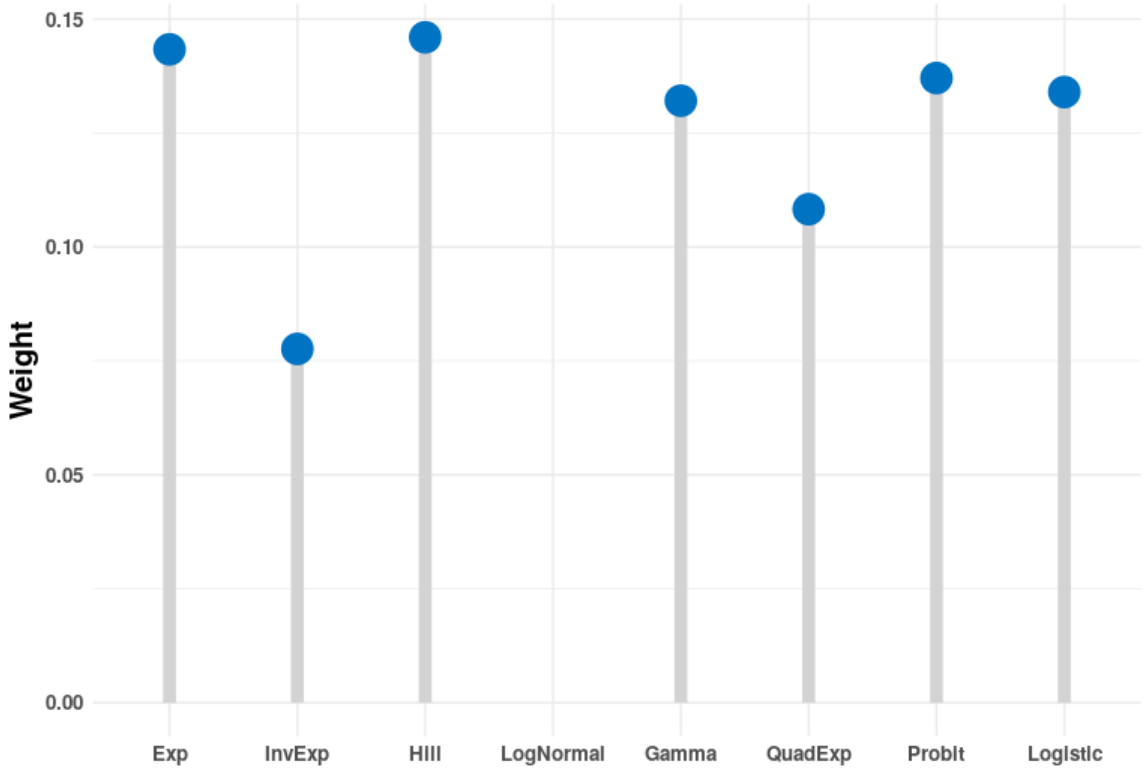
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.035	0.134	0.207

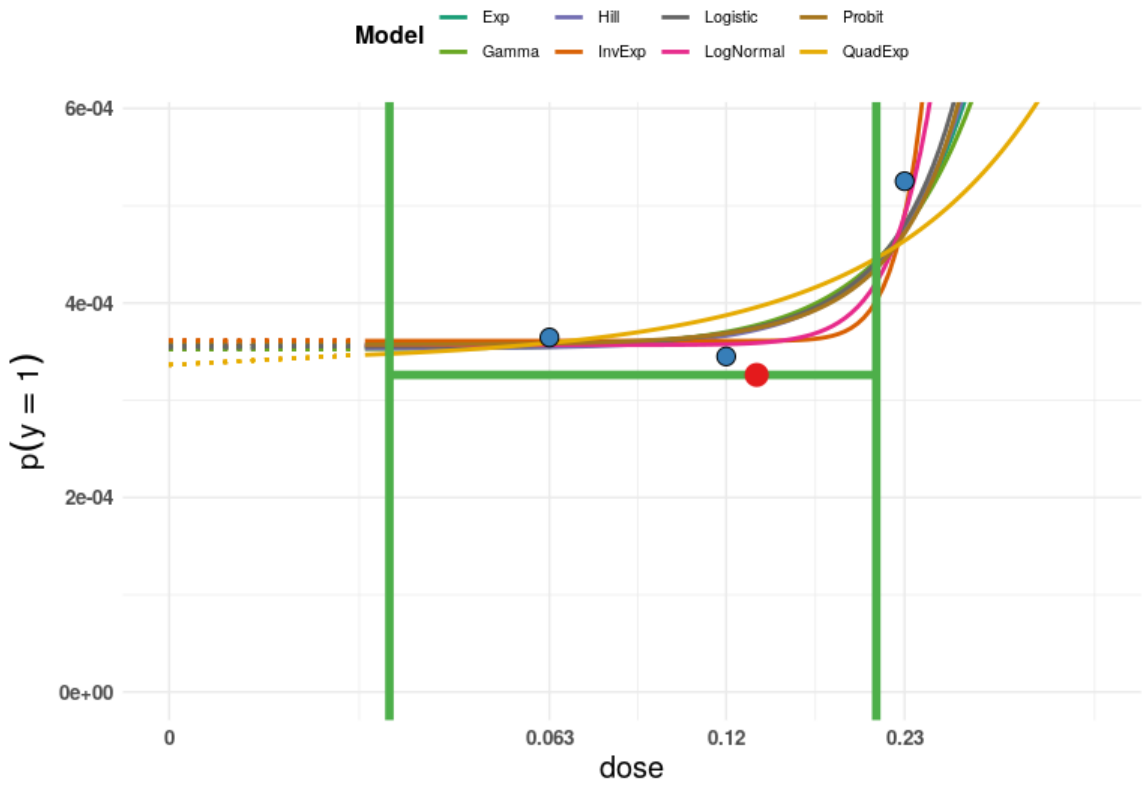
Estimated BMDs per model

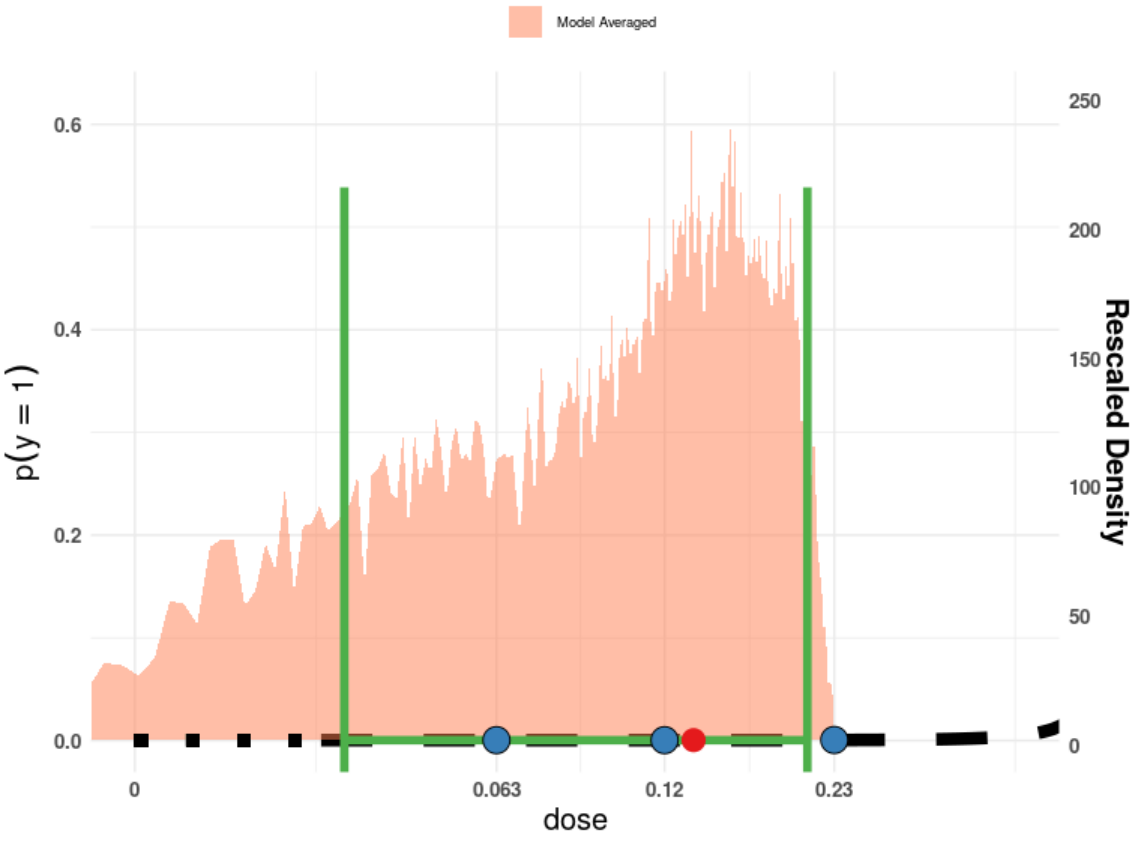
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.042	0.132	0.203	0.143	1
IE4_Q	0.127	0.194	0.221	0.078	1
H4_Q	0.042	0.132	0.194	0.146	1
G4_Q	0.038	0.121	0.180	0.132	1
QE4_Q	0.022	0.053	0.151	0.108	1
P4_Q	0.047	0.137	0.202	0.137	1
L4_Q	0.046	0.130	0.196	0.134	1

Plots of Fitted Models




0.15
0.10
0.05
0.00
Weight
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
6e-04
4e-04
2e-04
0e+00
p(y = 1)
0
0.063
0.12
0.23
dose


Model Averaged
0.6
0.4
0.2
0.0
p(y = 1)
250
200
150
100
50
0
Rescaled Density
0
0.063
0.12
0.23
dose

Gilbert-Diamond et al. (2013) skin cancer, relative BMR 5%

Source population reduced by 10% (only included in the uncertainty analysis)

Data Description

The endpoint to be analyzed is: Adj.cases for skin cancer

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	N
0.063	96	236976
0.120	90	234762
0.230	137	234762

The 'Value for CES' is set to 2.026e-05.

Extended dose range is not applied.

Informative background prior: min: 0.00038485; the most likely: 0.00040510; max: 0.00042536. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 1.30e+00).

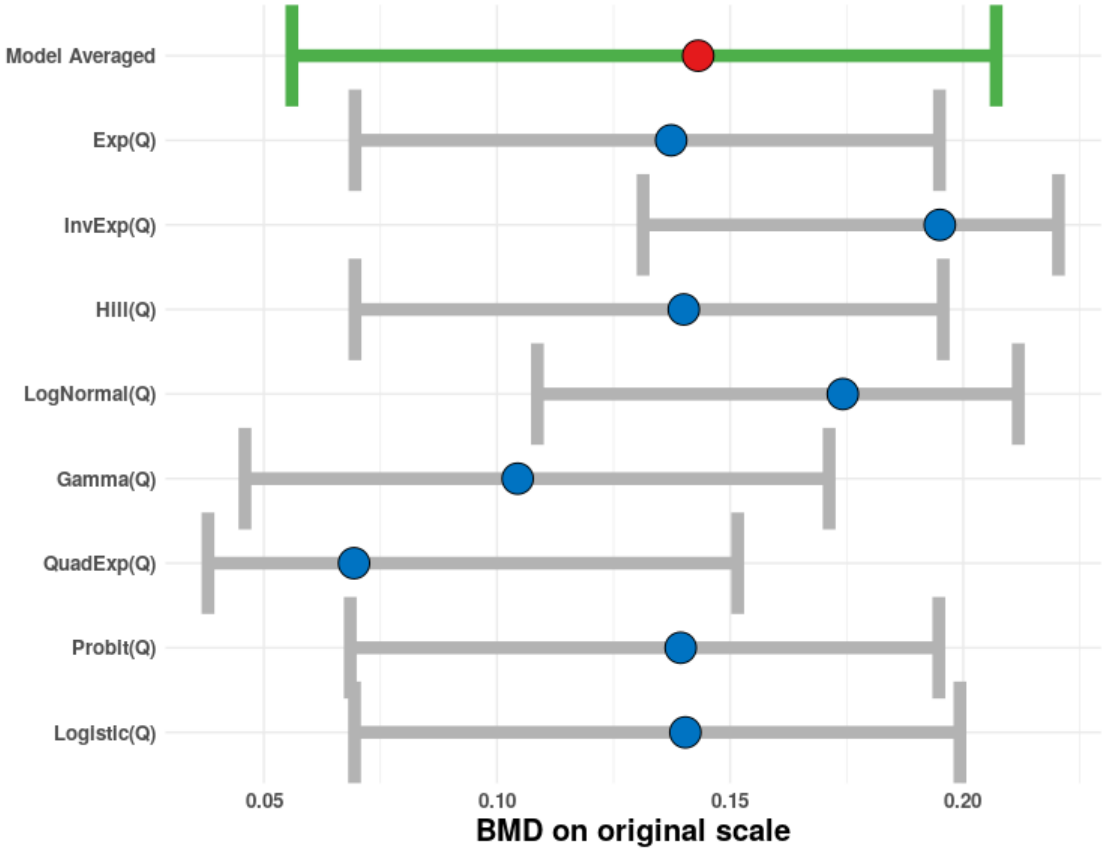
Model Averaged BMD

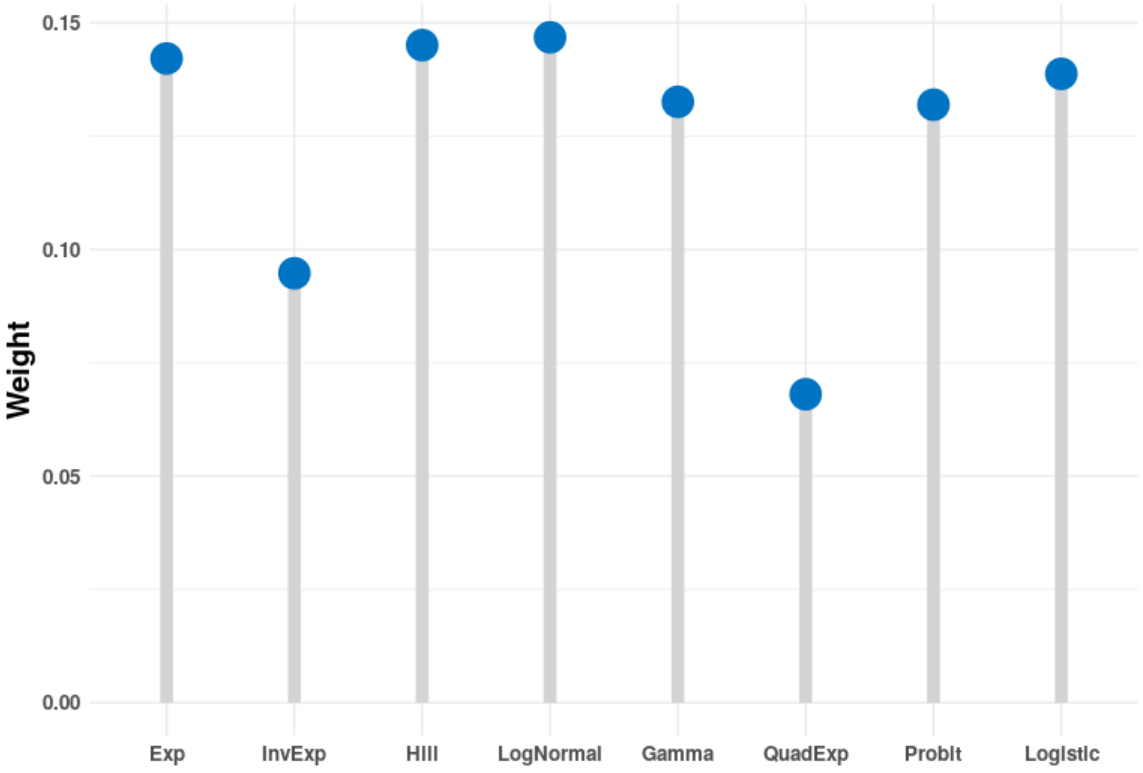
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.056	0.143	0.207

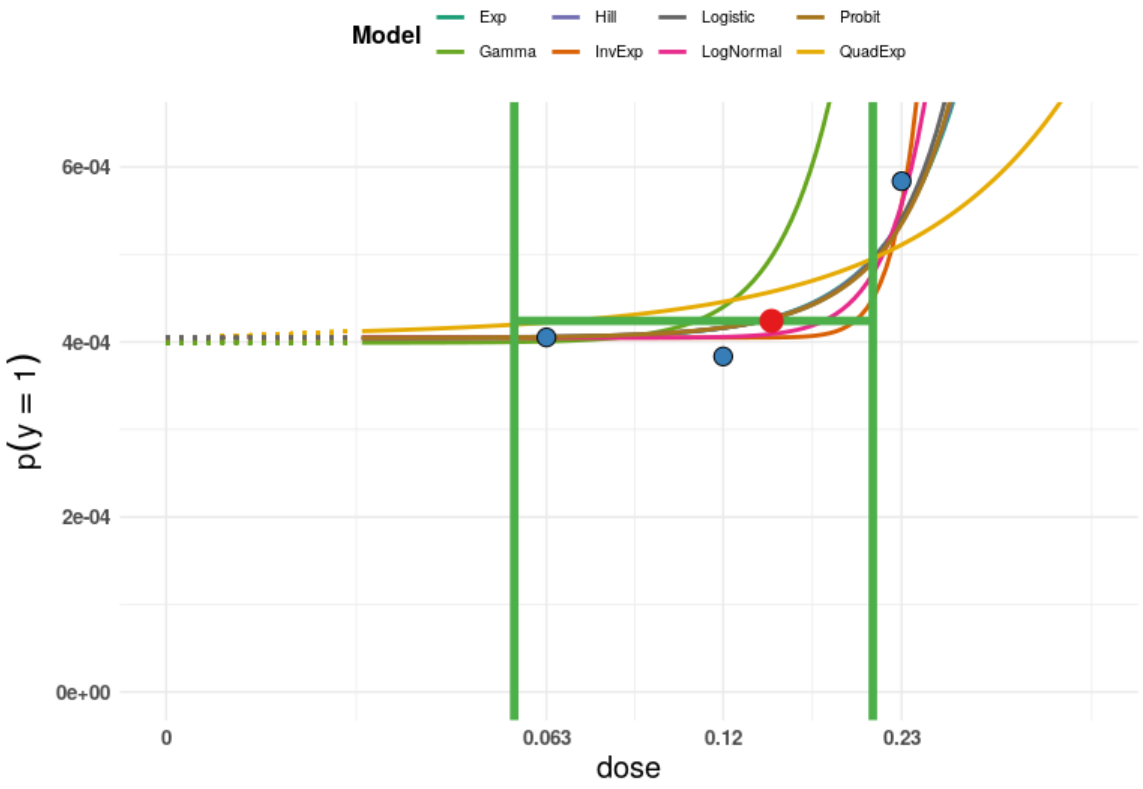
Estimated BMDs per model

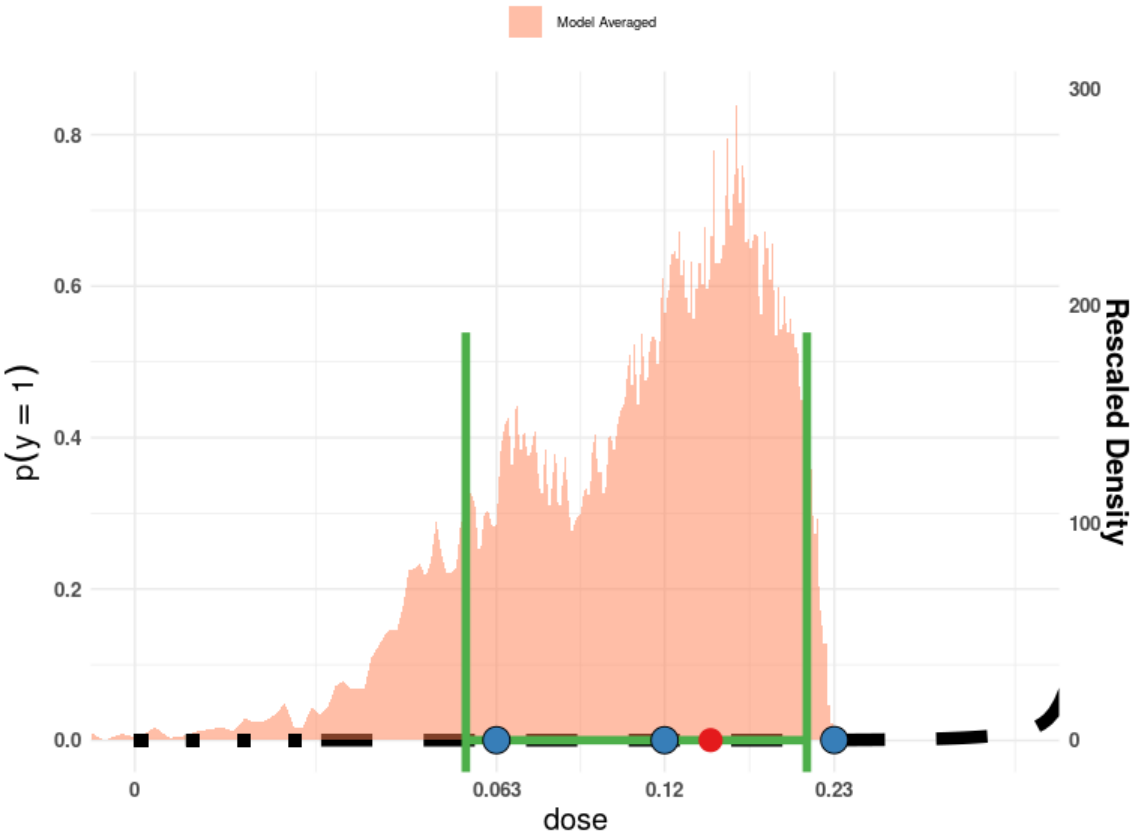
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.070	0.137	0.195	0.142	1
IE4_Q	0.131	0.195	0.220	0.095	1
H4_Q	0.070	0.140	0.196	0.145	1
LN4_Q	0.109	0.174	0.212	0.147	1
G4_Q	0.046	0.104	0.171	0.133	0
QE4_Q	0.038	0.069	0.152	0.068	1
P4_Q	0.069	0.139	0.195	0.132	1
L4_Q	0.069	0.140	0.199	0.139	1

Plots of Fitted Models




0.15
0.10
0.05
0.00
Weight
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
6e-04
4e-04
2e-04
0e+00
p(y = 1)
0
0.063
0.12
0.23
dose


Model Averaged
0.8
0.6
0.4
0.2
0.0
p(y = 1)
300
200
100
0
Rescaled Density
0
0.063
0.12
0.23
dose

Gilbert-Diamond et al. (2013) skin cancer, relative BMR 5%

Source population reduced by 20% (only included in the uncertainty analysis)

Data Description

The endpoint to be analyzed is: Adj.cases for skin cancer

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	N
0.063	96	210646
0.120	90	208677
0.230	137	208677

The 'Value for CES' is set to 2.28e-05.

Extended dose range is not applied.

Informative background prior: min: 0.00043295; the most likely: 0.00045574; max: 0.00047853. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 1.35e+00).

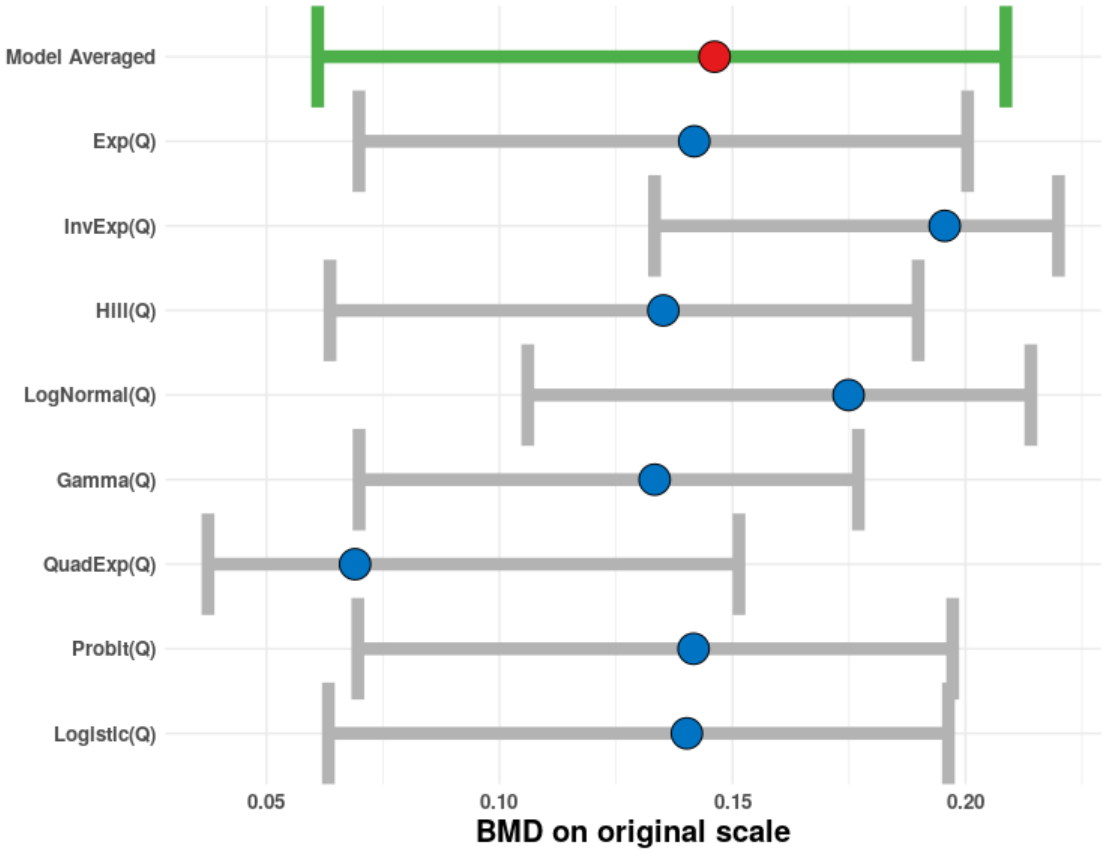
Model Averaged BMD

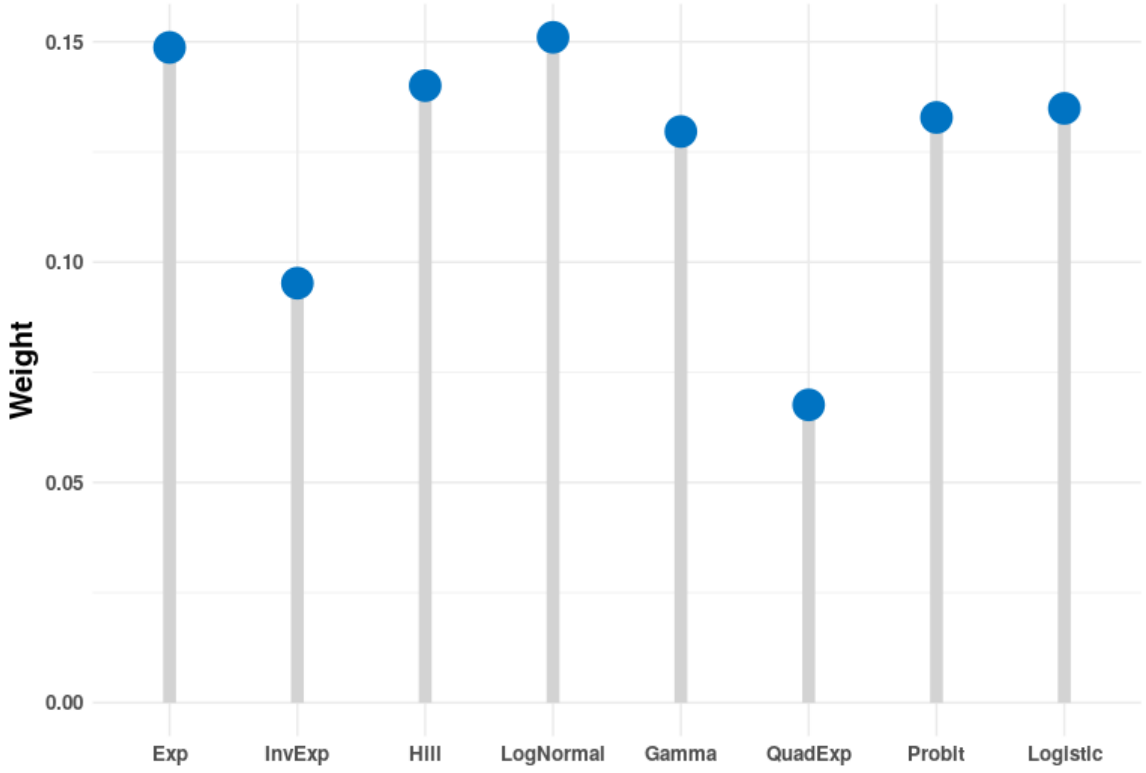
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.061	0.146	0.209

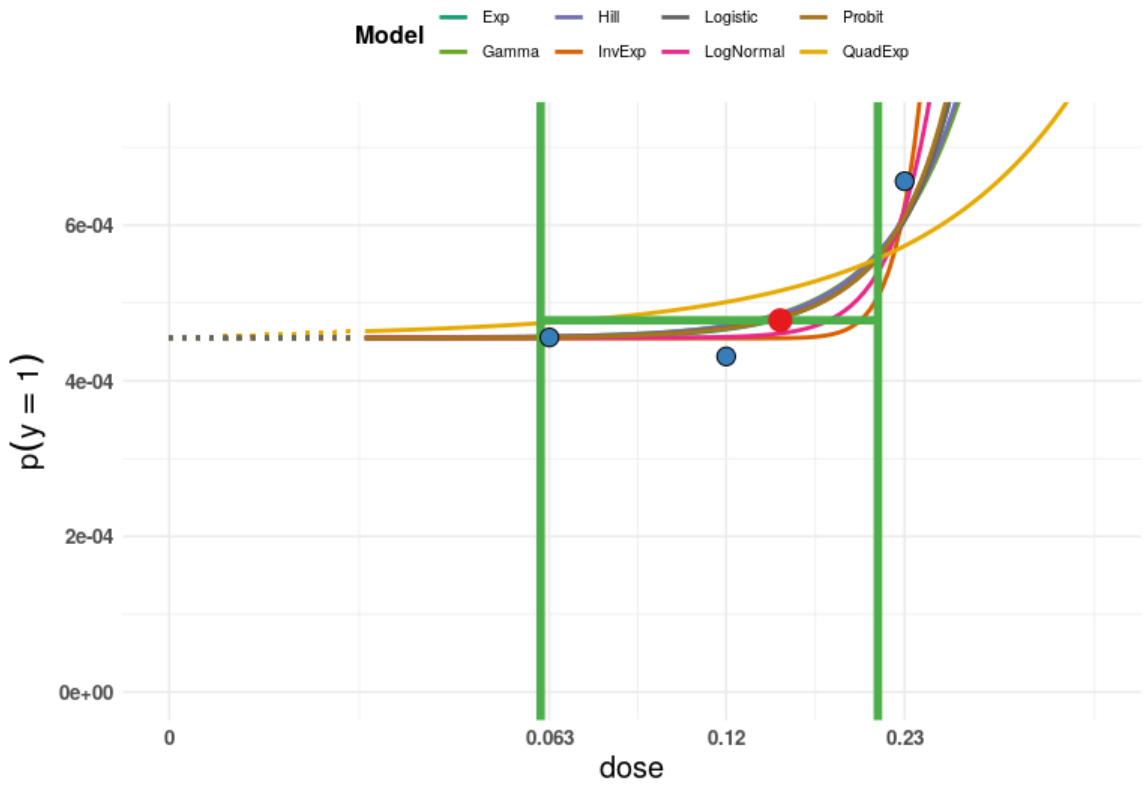
Estimated BMDs per model

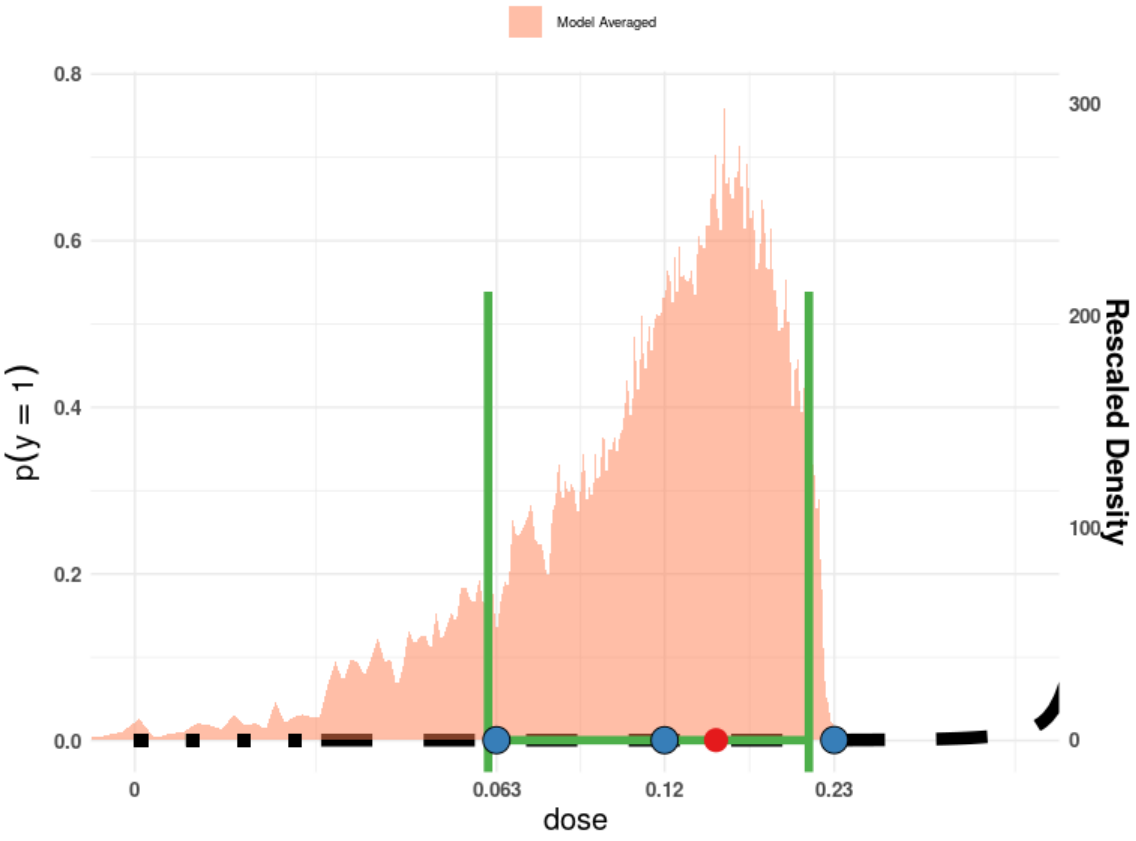
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.070	0.142	0.200	0.149	1
IE4_Q	0.133	0.196	0.220	0.095	1
H4_Q	0.064	0.135	0.190	0.140	1
LN4_Q	0.106	0.175	0.214	0.151	1
G4_Q	0.070	0.133	0.177	0.130	1
QE4_Q	0.037	0.069	0.151	0.068	1
P4_Q	0.070	0.142	0.197	0.133	1
L4_Q	0.063	0.140	0.196	0.135	1

Plots of Fitted Models




0.15
0.10
0.05
0.00
Weight
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
6e-04
4e-04
2e-04
0e+00
p(y = 1)
0
0.063
0.12
0.23
dose


Model Averaged
0.8
0.6
0.4
0.2
0.0
p(y = 1)
300
200
100
0
Rescaled Density
0
0.063
0.12
0.23
dose

Gilbert-Diamond et al. (2013) skin cancer, relative BMR 5%

Source population increased by 10% (only included in the uncertainty analysis)

Data Description

The endpoint to be analyzed is: Adj.cases for skin cancer

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	N
0.063	96	289638
0.120	90	286931
0.230	137	286931

The 'Value for CES' is set to 1.658e-05.

Extended dose range is not applied.

Informative background prior: min: 0.00031488; the most likely: 0.00033145; max: 0.00034802. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 1.40e+00).

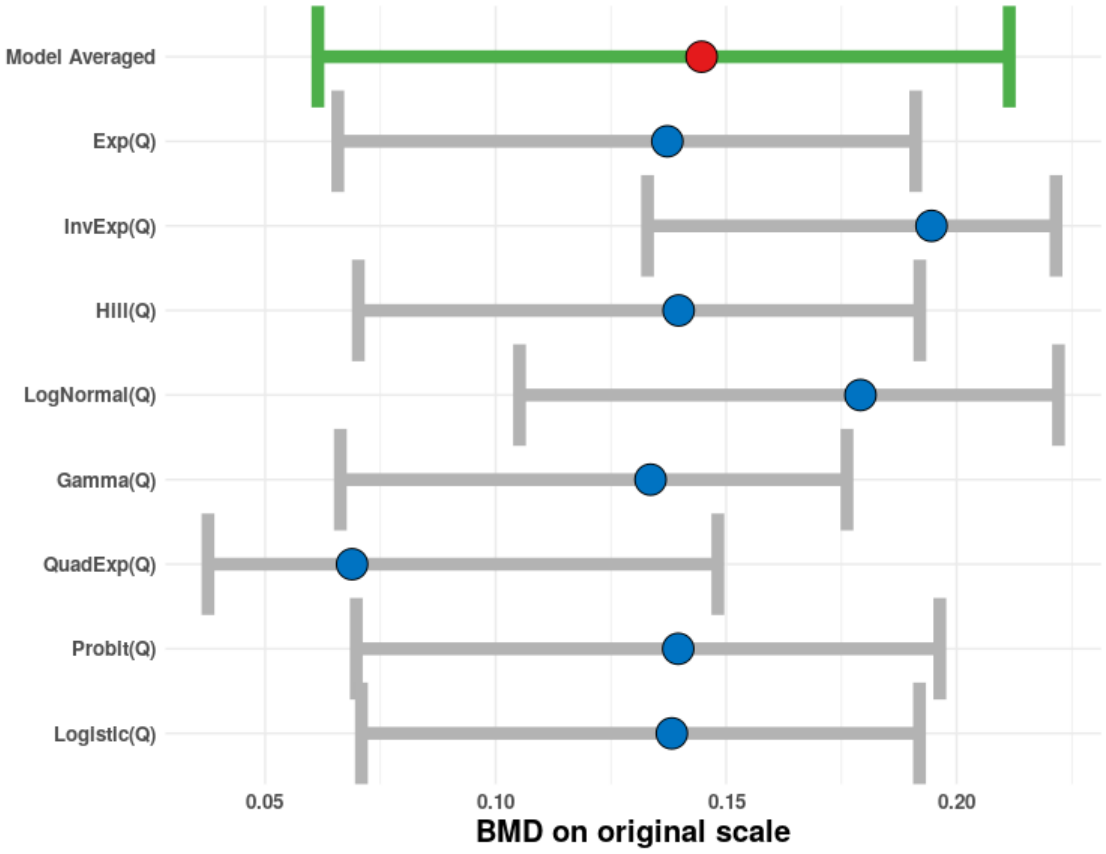
Model Averaged BMD

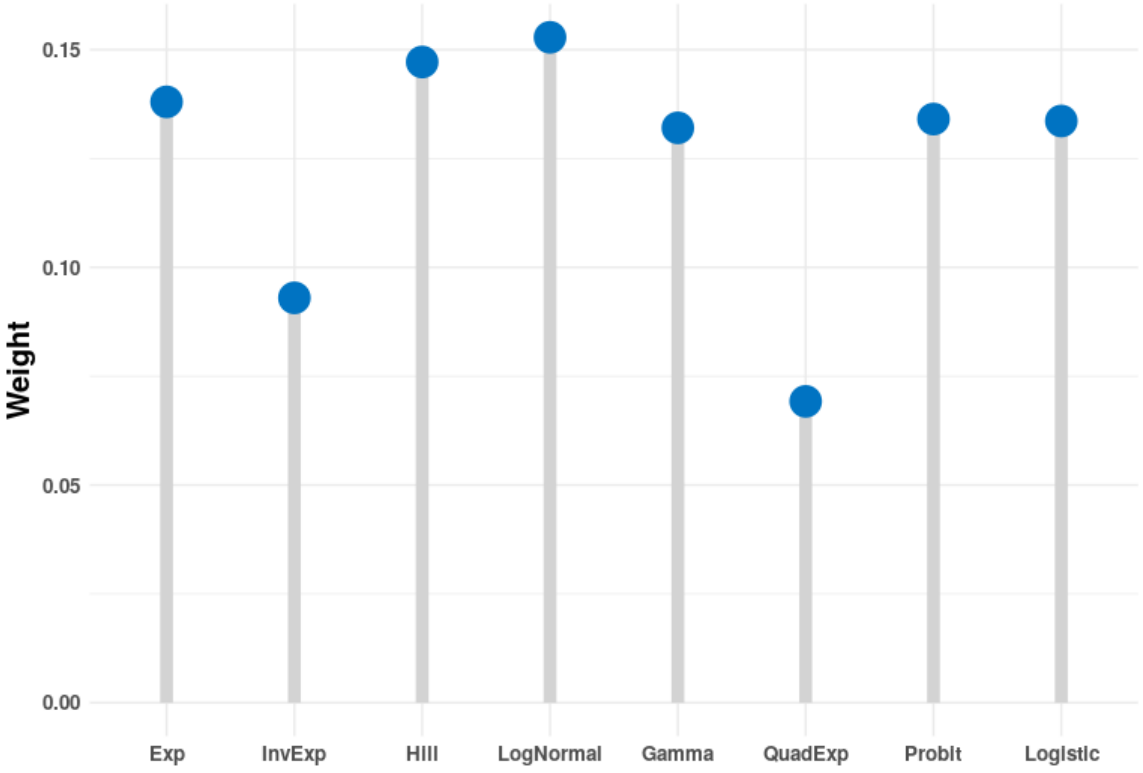
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.061	0.145	0.211

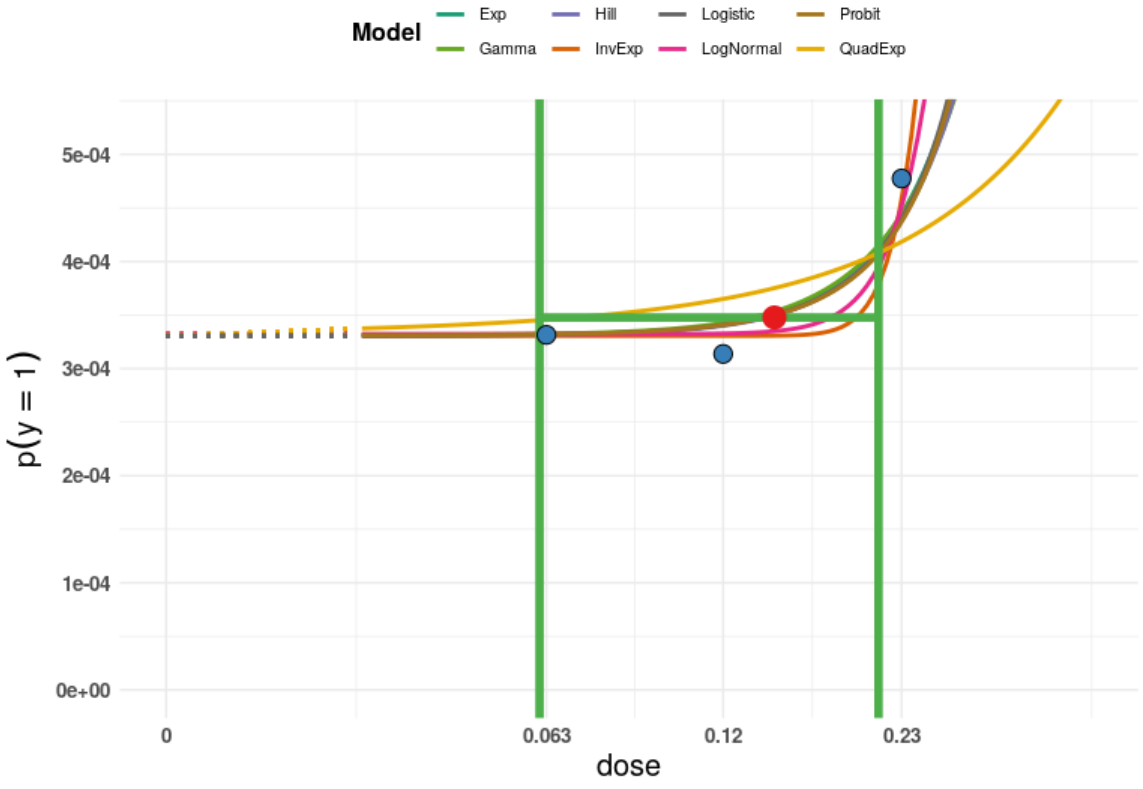
Estimated BMDs per model

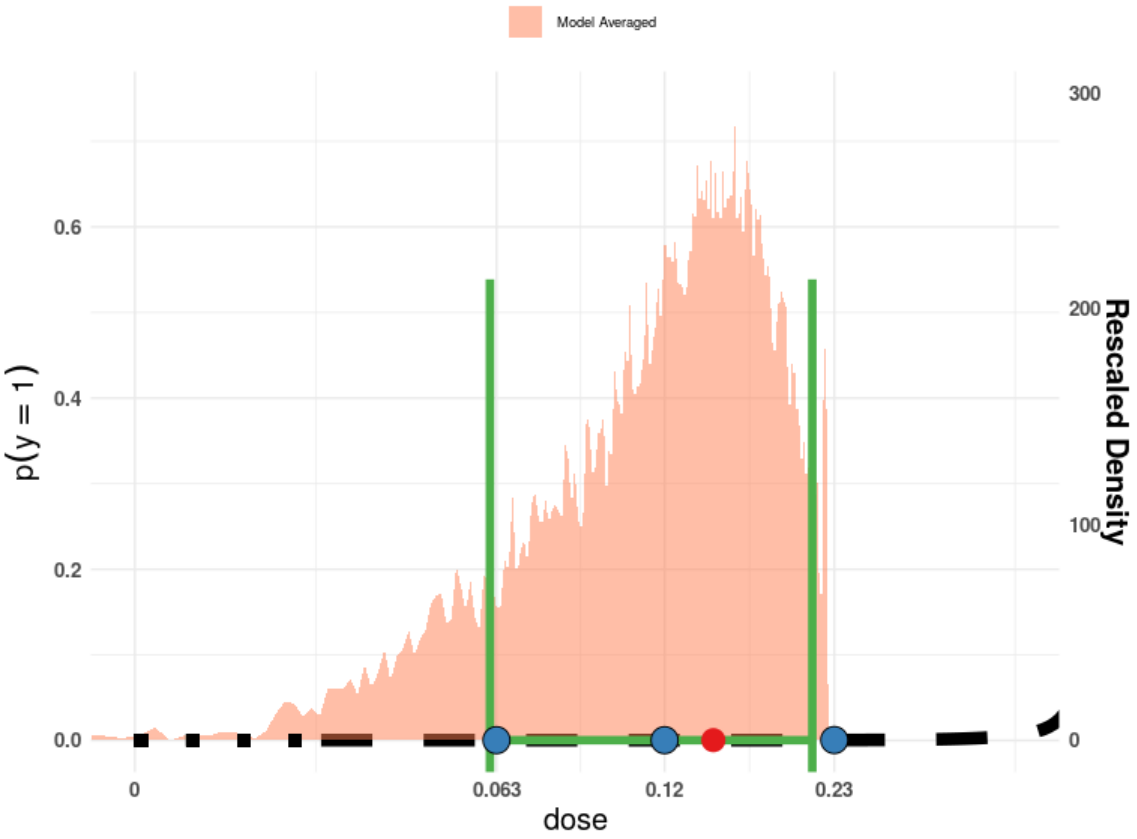
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.066	0.137	0.191	0.138	1
IE4_Q	0.133	0.195	0.222	0.093	1
H4_Q	0.070	0.140	0.192	0.147	1
LN4_Q	0.105	0.179	0.222	0.153	0
G4_Q	0.066	0.134	0.176	0.132	1
QE4_Q	0.038	0.069	0.148	0.069	1
P4_Q	0.070	0.140	0.196	0.134	1
L4_Q	0.071	0.138	0.192	0.134	1

Plots of Fitted Models




0.15
0.10
0.05
0.00
Weight
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
5e-04
4e-04
3e-04
2e-04
1e-04
0e+00
p(y = 1)
0
0.063
0.12
0.23
dose


Model Averaged
p(y = 1)
0.0
0.2
0.4
0.6
0
0.063
0.12
0.23
dose
Rescaled Density
0
100
200
300

Gilbert-Diamond et al. (2013) skin cancer, relative BMR 5%

Source population increased by 20% (only included in the uncertainty analysis)

Data Description

The endpoint to be analyzed is: Adj.cases for skin cancer

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	N
0.063	96	315969
0.120	90	313016
0.230	137	313016

The 'Value for CES' is set to 1.52e-05.

Extended dose range is not applied.

Informative background prior: min: 0.00028864; the most likely: 0.00030383; max: 0.00031902. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 1.34e+00).

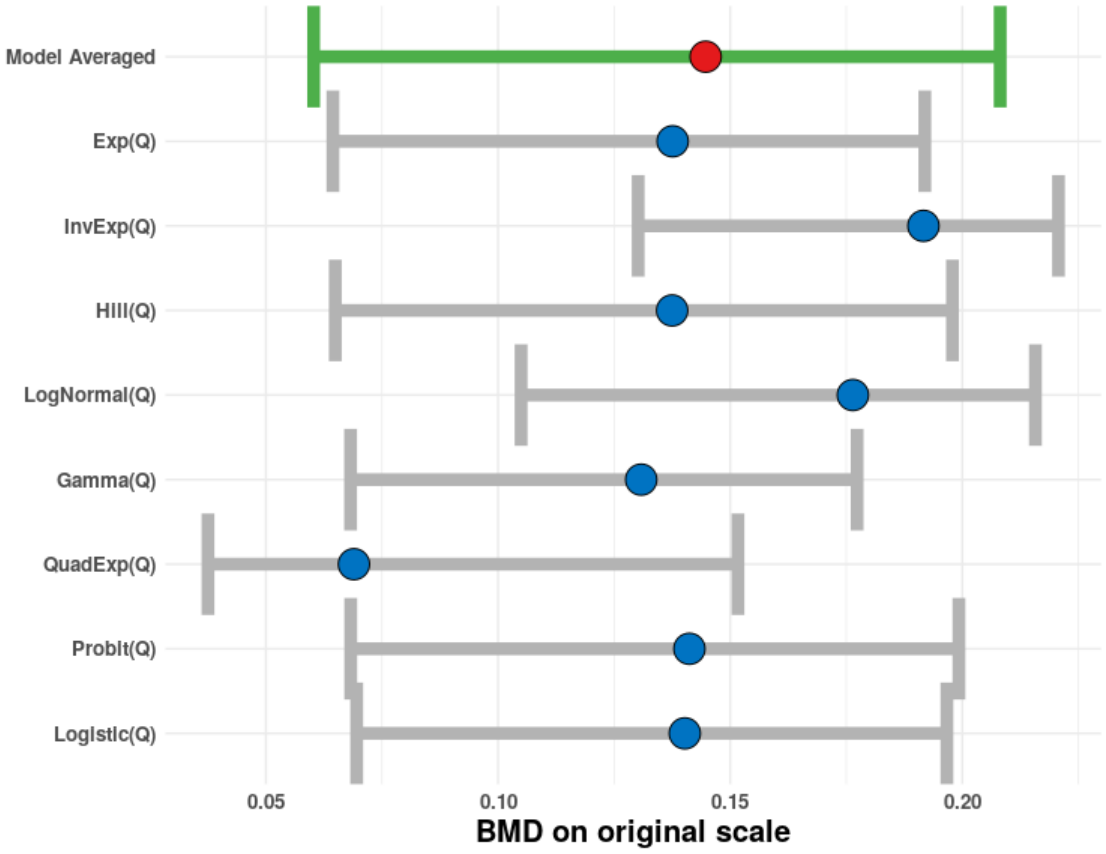
Model Averaged BMD

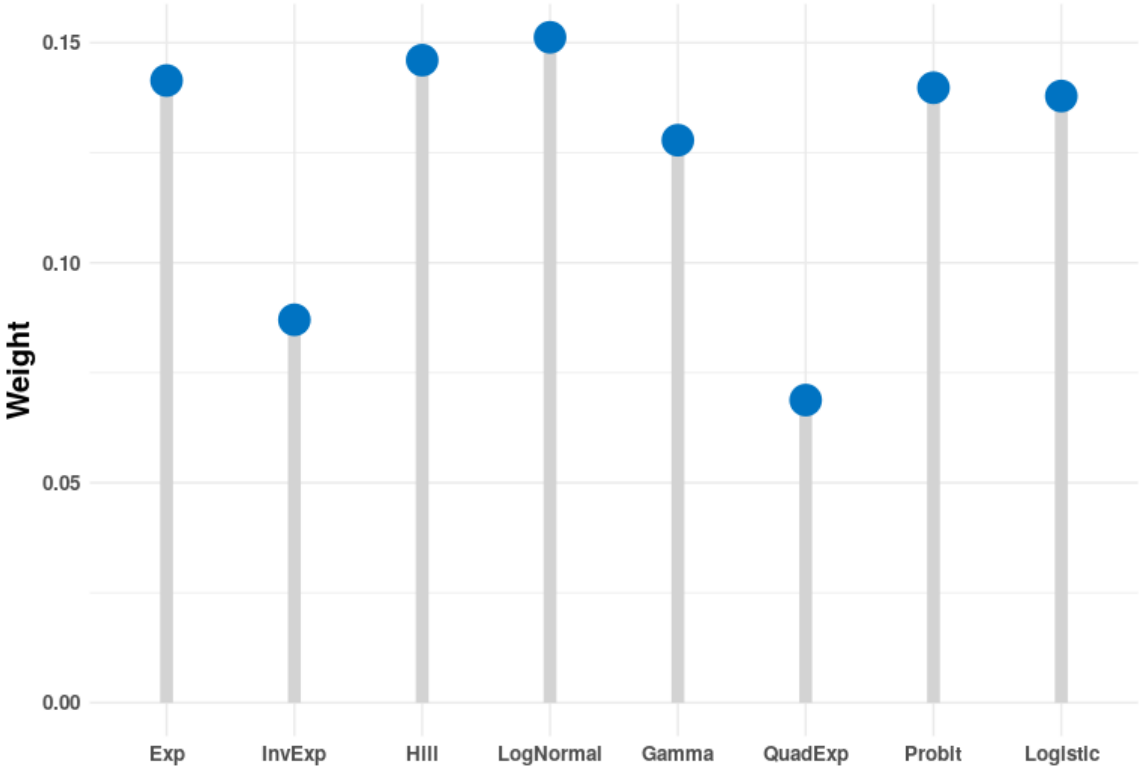
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.06	0.145	0.208

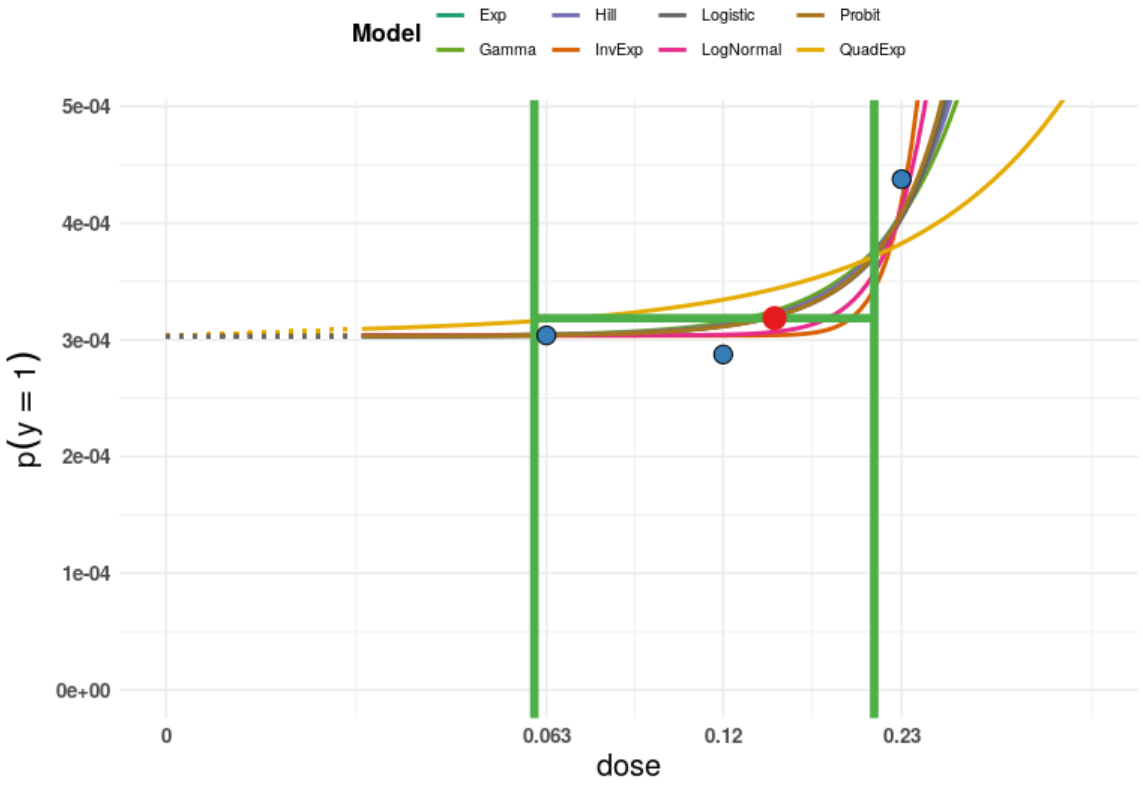
Estimated BMDs per model

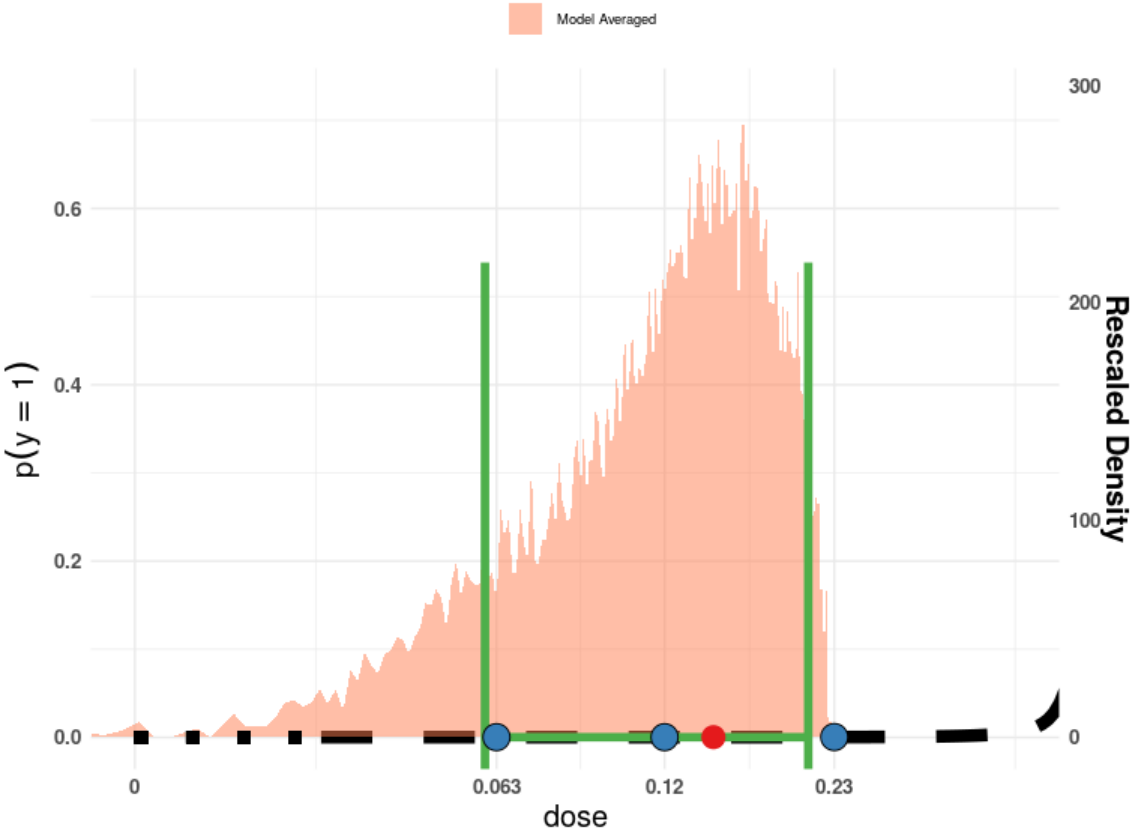
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.064	0.138	0.192	0.141	1
IE4_Q	0.130	0.192	0.221	0.087	0
H4_Q	0.065	0.137	0.198	0.146	1
LN4_Q	0.105	0.176	0.216	0.151	1
G4_Q	0.068	0.131	0.177	0.128	1
QE4_Q	0.038	0.069	0.152	0.069	1
P4_Q	0.068	0.141	0.199	0.140	1
L4_Q	0.070	0.140	0.197	0.138	1

Plots of Fitted Models




0.15
0.10
0.05
0.00
Weight
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
5e-04
4e-04
3e-04
2e-04
1e-04
0e+00
p(y = 1)
0
0.063
0.12
0.23
dose


Model Averaged
p(y = 1)
0.0
0.2
0.4
0.6
Rescaled Density
0
100
200
300
0
0.063
0.12
0.23
dose

Hsueh et al. (2009) chronic kidney disease, relative BMR 5%

Data Description

The endpoint to be analyzed is: Adj.cases for chronic kidney disease

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	N
0.13	18	655022
0.36	27	681223
0.46	80	663755

The 'Value for CES' is set to 1.37e-06.

Extended dose range is not applied.

Informative background prior: min: 0.00002721; the most likely: 0.00002748; max: 0.00002775. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 4.59e-01).

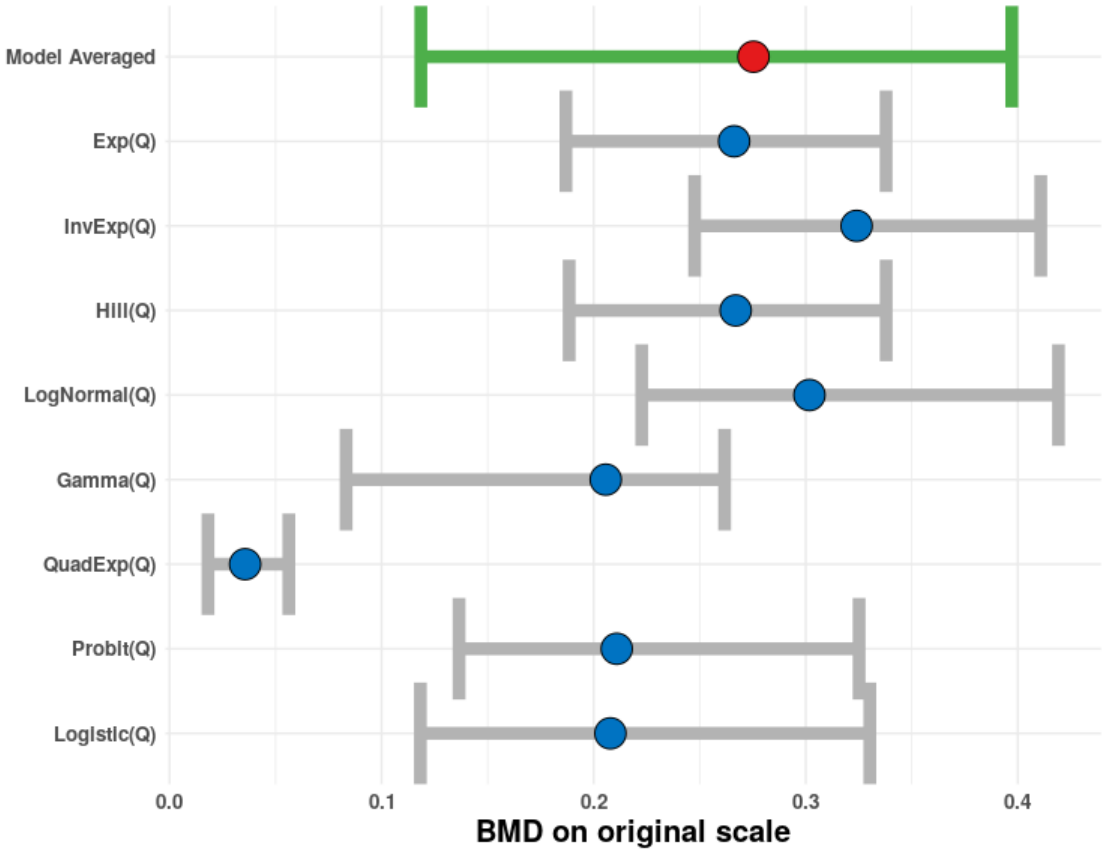
Model Averaged BMD

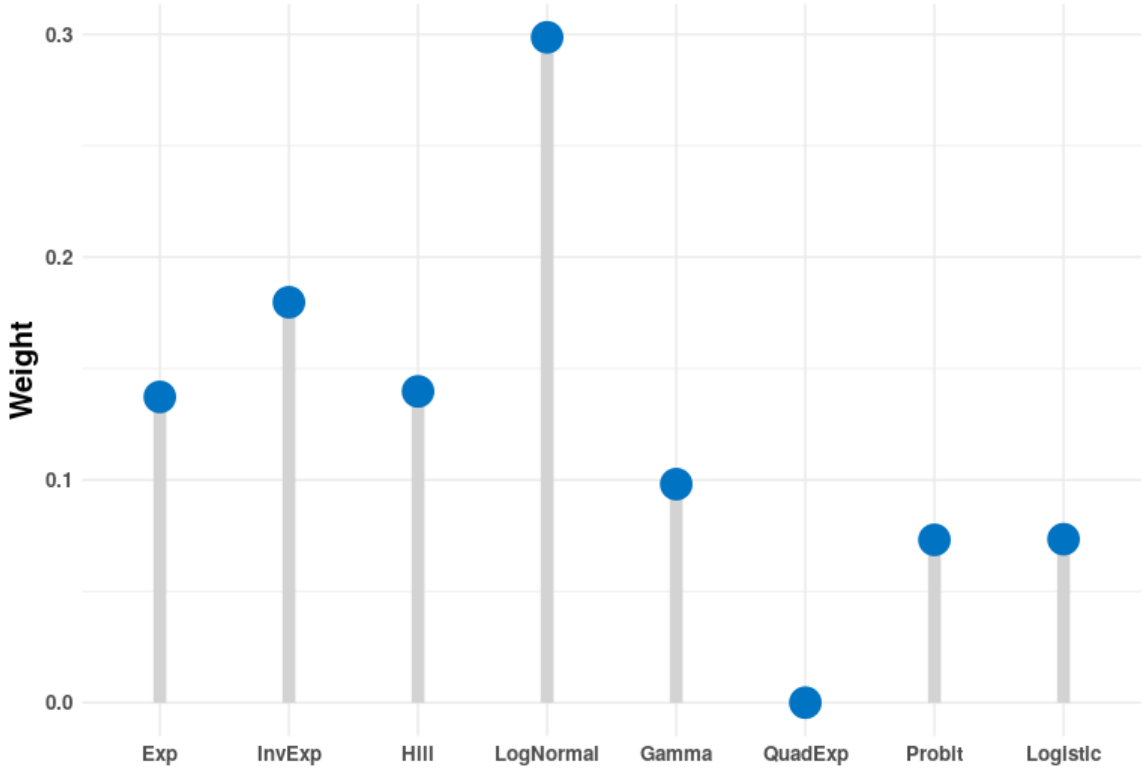
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.119	0.275	0.397

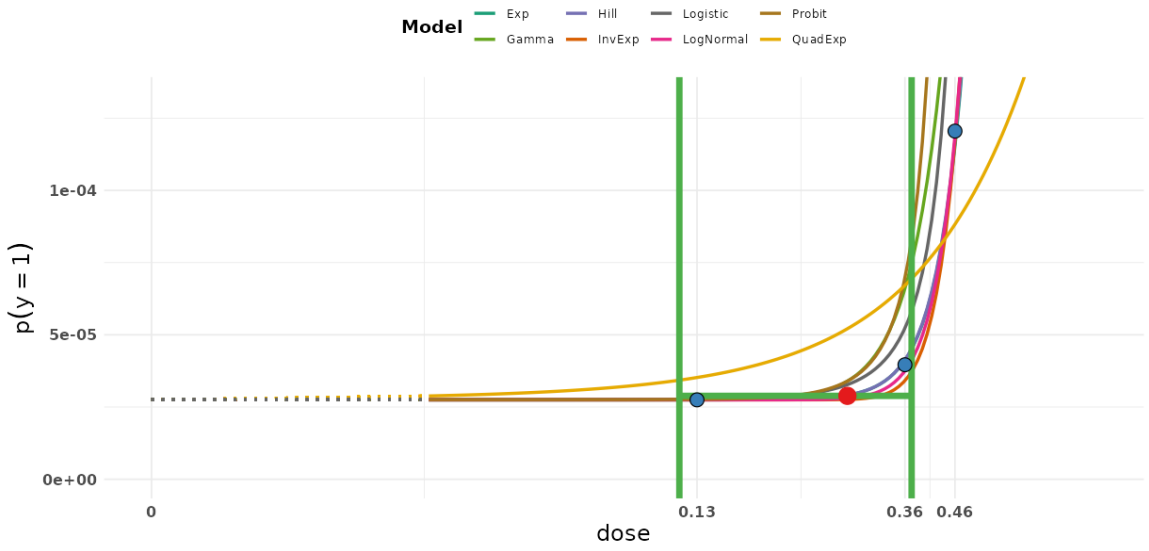
Estimated BMDs per model

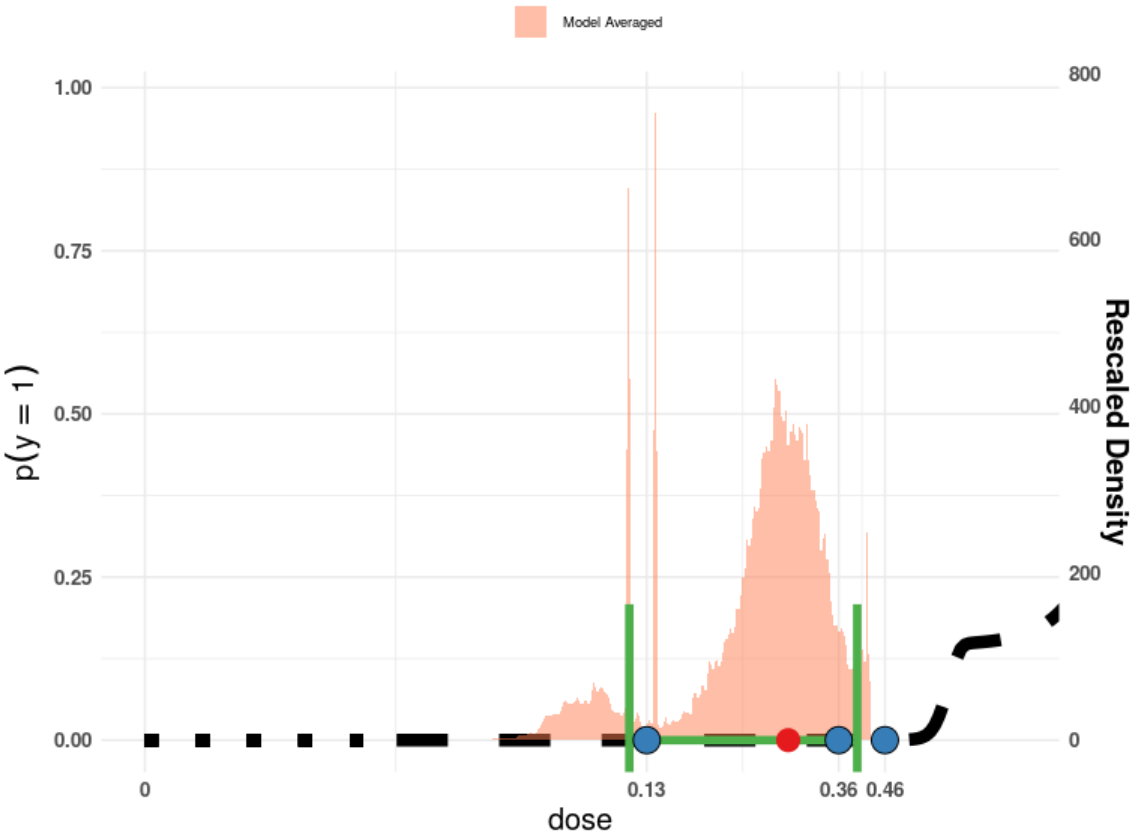
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.187	0.266	0.338	0.137	1
IE4_Q	0.248	0.324	0.411	0.180	1
H4_Q	0.188	0.267	0.338	0.140	1
LN4_Q	0.223	0.302	0.419	0.299	0
G4_Q	0.083	0.206	0.262	0.098	0
QE4_Q	0.018	0.036	0.056	0.000	1
P4_Q	0.137	0.211	0.325	0.073	0
L4_Q	0.118	0.208	0.330	0.073	0

Plots of Fitted Models




0.3
0.2
0.1
0.0
Weight
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
1e-04
5e-05
0e+00
p(y = 1)
0
0.13
0.36
0.46
dose


Model Averaged
1.00
0.75
0.50
0.25
0.00
p(y = 1)
800
600
400
200
0
Rescaled Density
0
0.13
0.36
0.46
dose

James et al. (2015) ischemic heart disease, relative BMR 5%

Data Description

The endpoint to be analyzed is: Adj.cases for ischemic heart disease

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	Person.years
0.34	58	4806
0.76	20	1335
0.97	14	534
1.30	4	98

The 'Value for CES' is set to 0.00061078.

Extended dose range is not applied.

Informative background prior: min: 0.01194757; the most likely: 0.01206825; max: 0.01218893. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 2.11e-02).

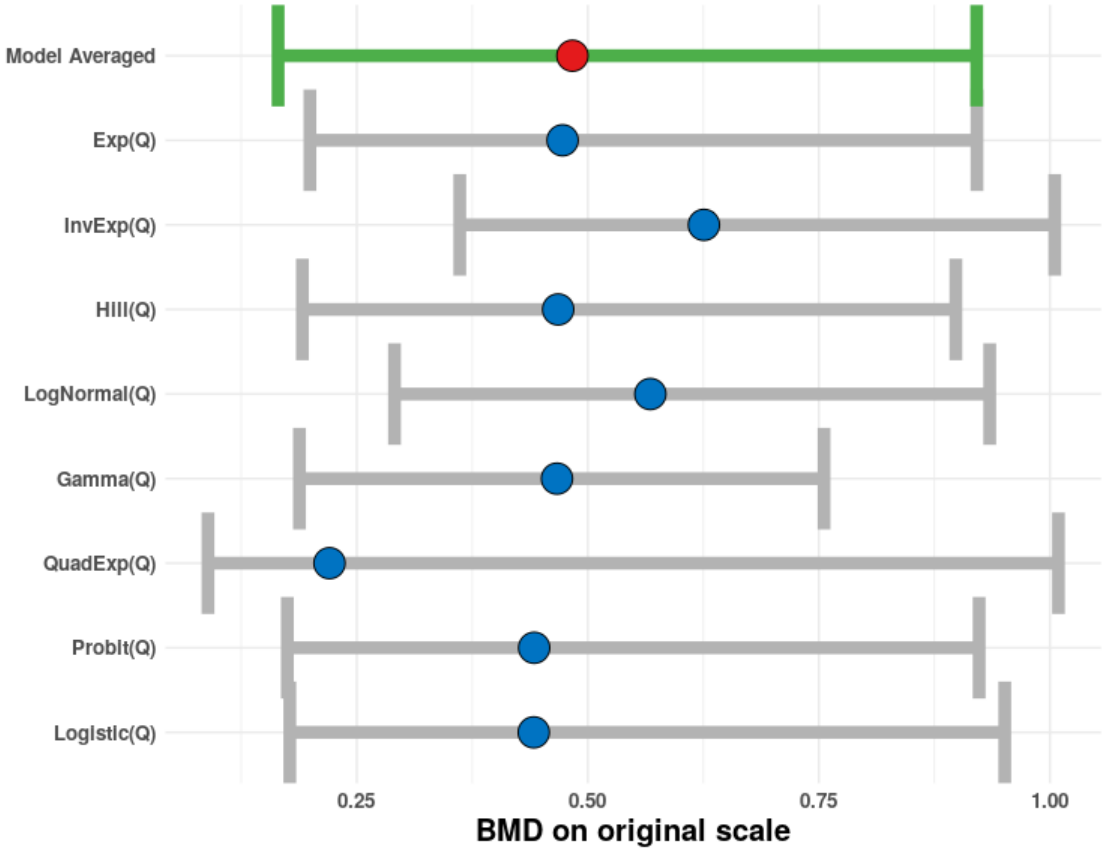
Model Averaged BMD

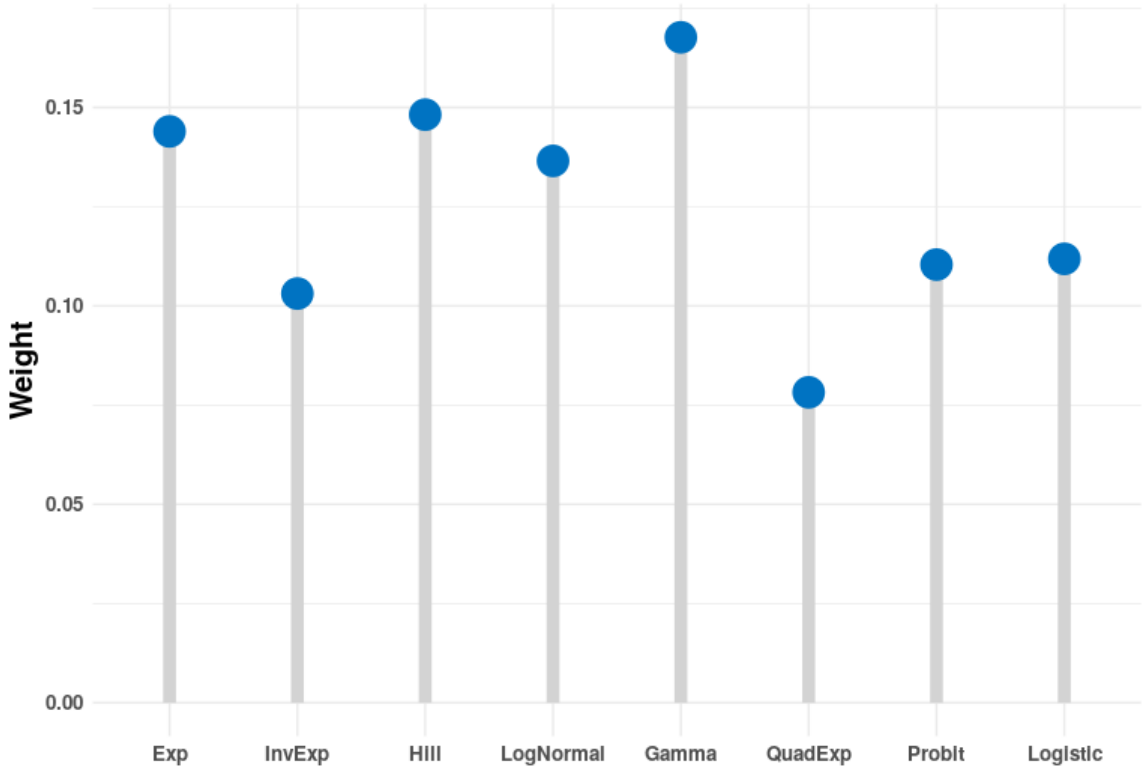
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.165	0.483	0.921

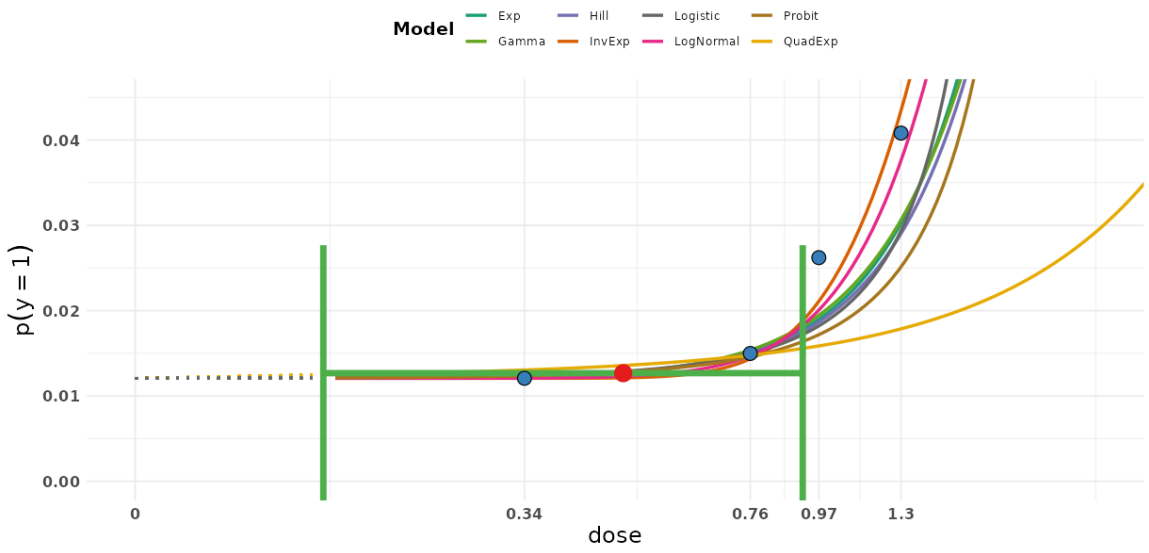
Estimated BMDs per model

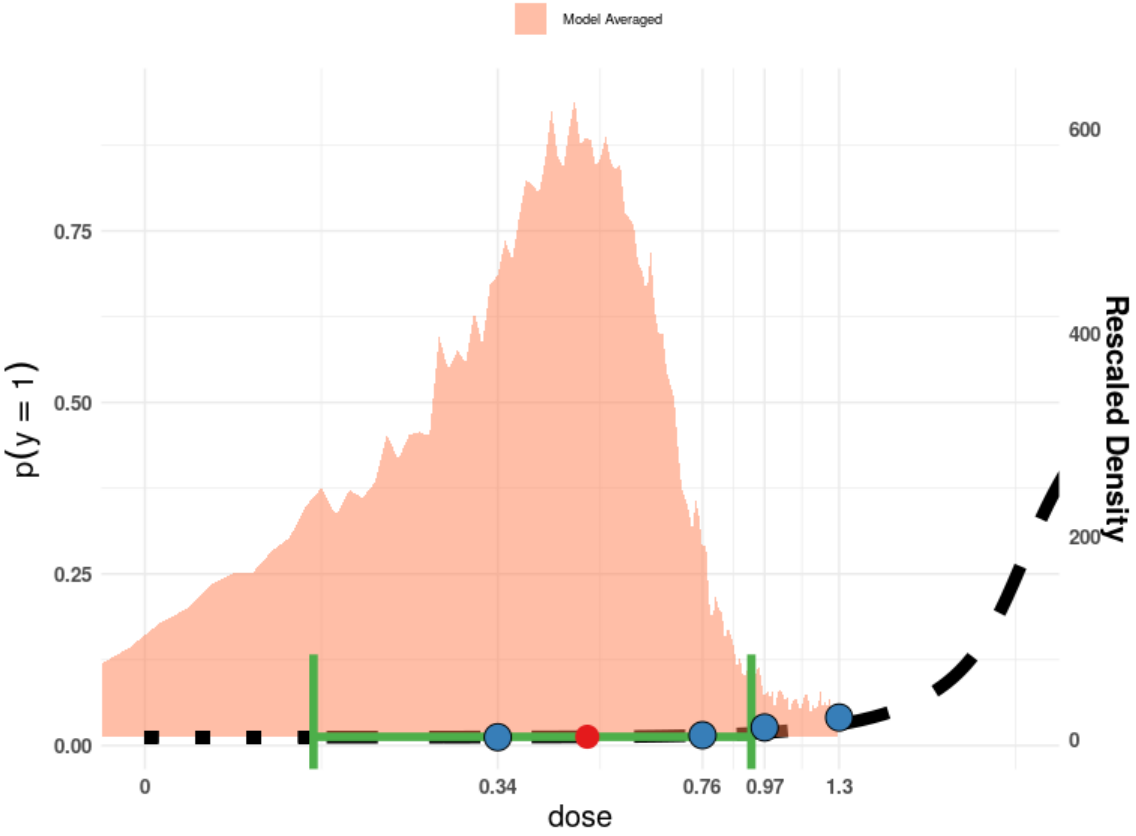
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.199	0.473	0.921	0.144	1
IE4_Q	0.361	0.626	1.005	0.103	1
H4_Q	0.191	0.468	0.898	0.148	1
LN4_Q	0.291	0.568	0.935	0.137	1
G4_Q	0.188	0.467	0.756	0.168	1
QE4_Q	0.089	0.220	1.009	0.078	1
P4_Q	0.175	0.442	0.923	0.110	1
L4_Q	0.178	0.441	0.951	0.112	1

Plots of Fitted Models




Weight
0.15
0.10
0.05
0.00
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
p(y = 1)
0.04
0.03
0.02
0.01
0.00
0
0.34
0.76
0.97
1.3
dose


Model Averaged
p(y = 1)
0.00
0.25
0.50
0.75
0
0.34
0.76
0.97
1.3
dose
0
200
400
600
Rescaled Density

Leonardi et al. (2012) skin cancer, relative BMR 5%

Data Description

The endpoint to be analyzed is: Adj.cases for skin cancer

Data used for analysis:

Exposure	Adj.cases	N
0.12	59	4e+05
0.13	82	4e+05
0.20	70	4e+05
0.39	101	4e+05
2.11	179	4e+05

The 'Value for CES' is set to 7.38e-06.

Extended dose range is not applied.

Informative background prior: min: 0.00014603; the most likely: 0.00014750; max: 0.00014898. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 9.72e-06).

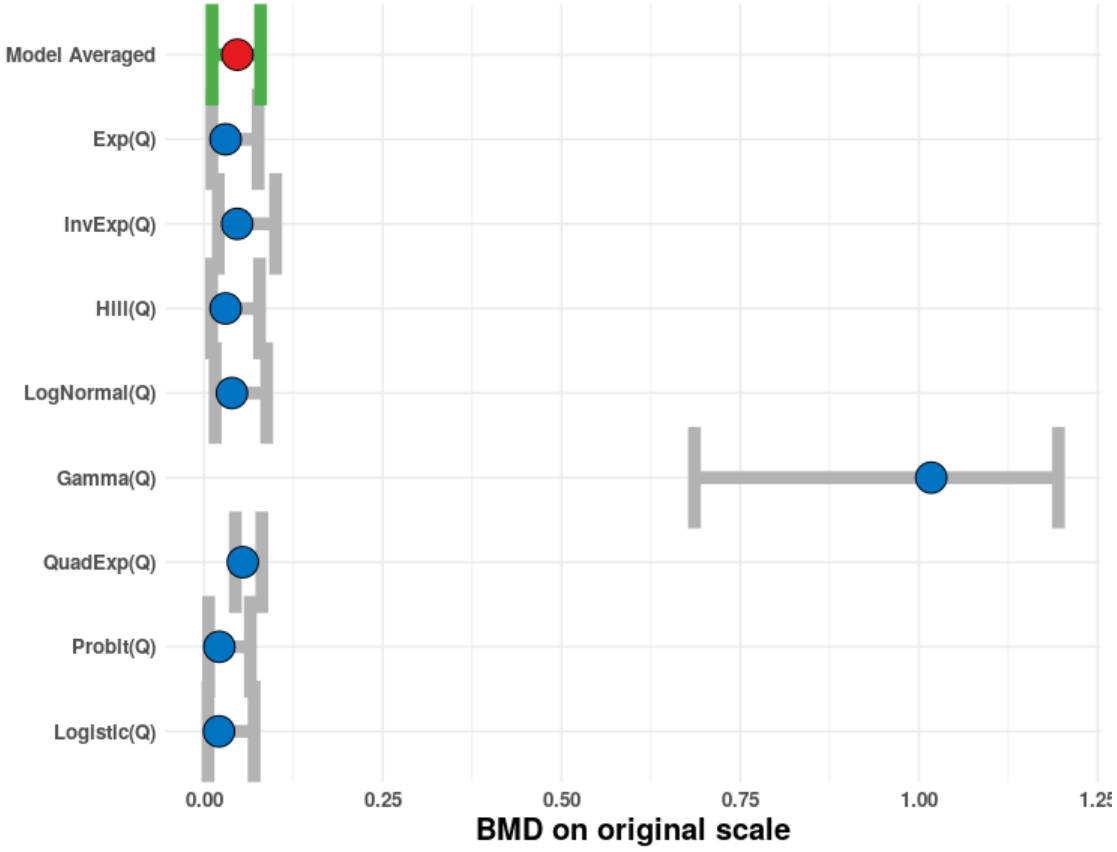
Model Averaged BMD

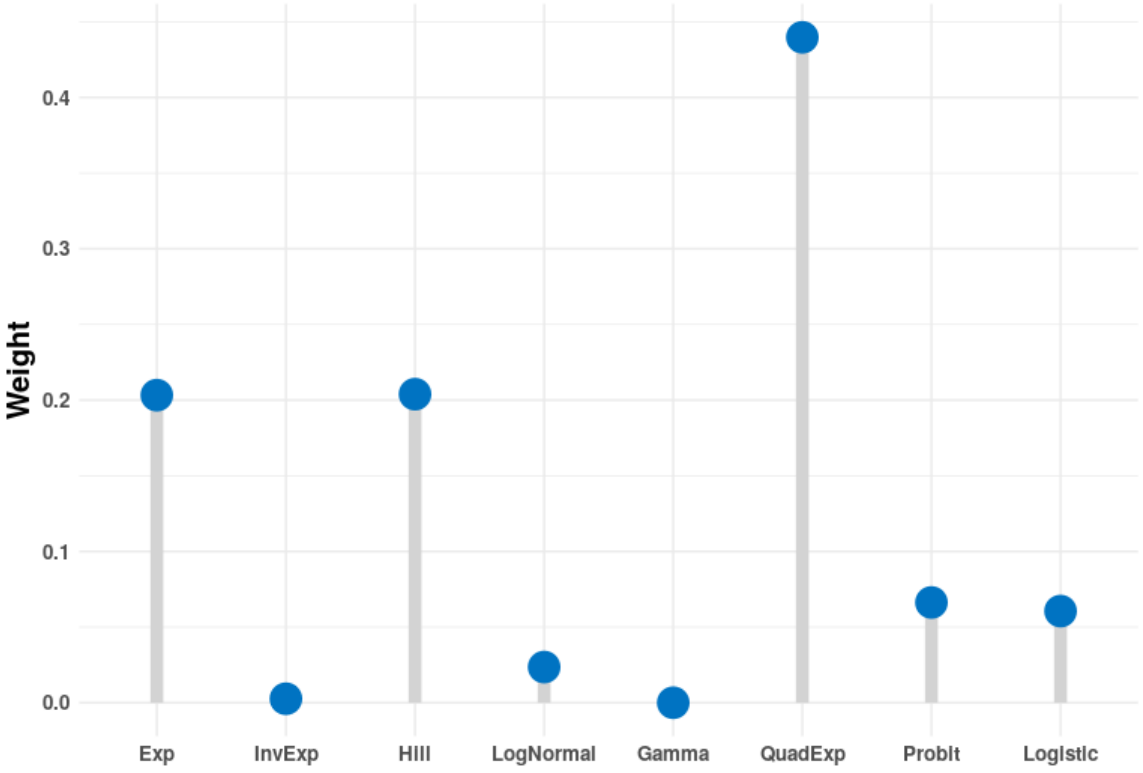
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.011	0.047	0.079

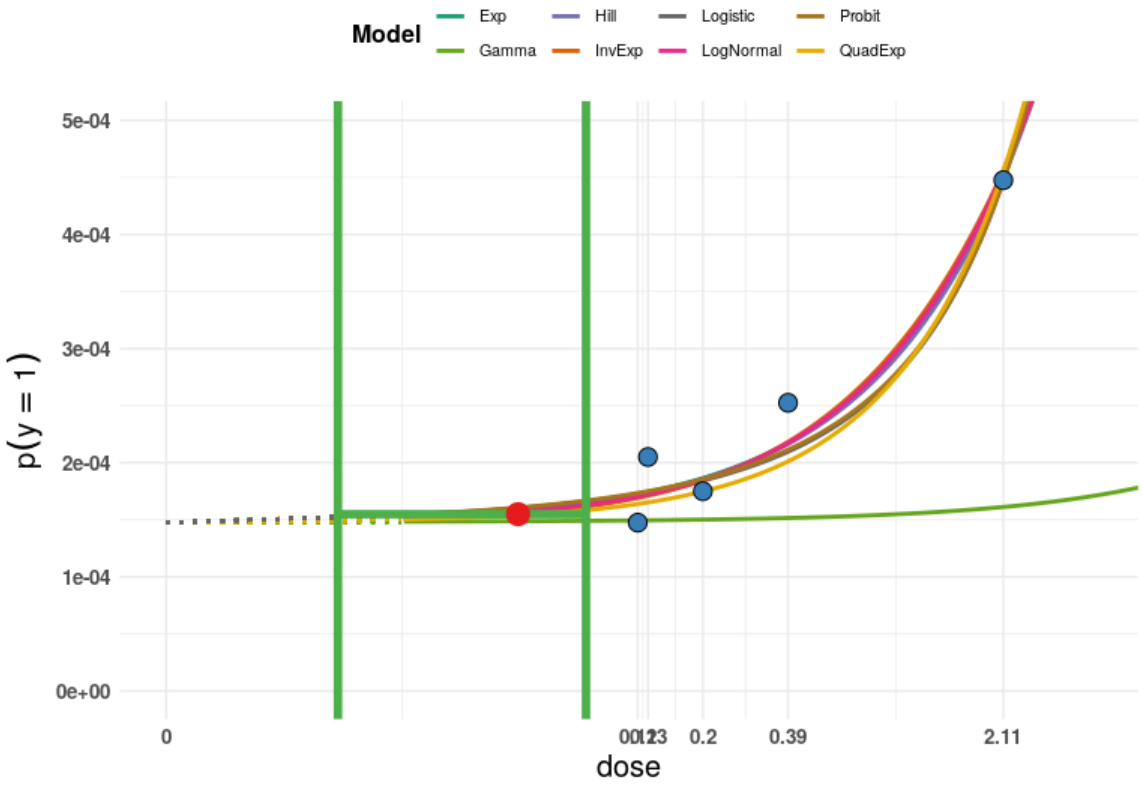
Estimated BMDs per model

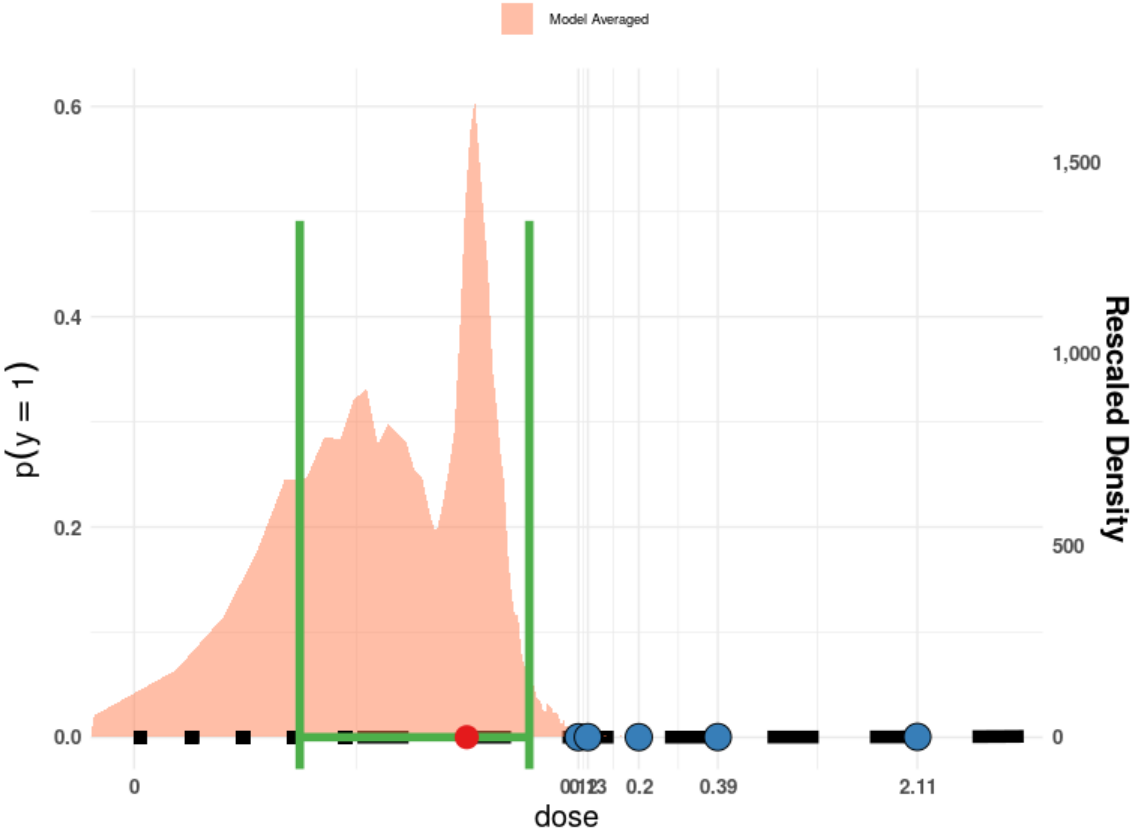
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.011	0.030	0.076	0.203	1
IE4_Q	0.020	0.046	0.100	0.003	1
H4_Q	0.011	0.030	0.078	0.204	1
LN4_Q	0.016	0.039	0.088	0.024	1
G4_Q	0.686	1.017	1.195	0.000	0
QE4_Q	0.044	0.054	0.081	0.440	1
P4_Q	0.006	0.021	0.065	0.066	1
L4_Q	0.006	0.021	0.070	0.061	1

Plots of Fitted Models




Weight
0.4
0.3
0.2
0.1
0.0
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
p(y = 1)
5e-04
4e-04
3e-04
2e-04
1e-04
0e+00
0
0.2
0.39
2.11
dose


Model Averaged
0.6
0.4
0.2
0.0
p(y = 1)
1,500
1,000
500
0
Rescaled Density
0
0.2
0.39
2.11
dose

Milton et al. (2005) neonatal death, relative BMR 5%

Data Description

The endpoint to be analyzed is: Adj.cases for neonatal death

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	N
2.91	19	176
6.58	14	53
8.36	53	304

The 'Value for CES' is set to 0.006050955.

Extended dose range is not applied.

Informative background prior: min: 0.10255682; the most likely: 0.107954545; max: 0.113352273. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

The results do not fulfill the EFSA BMD guidance (EFSA Scientific Committee, 2022) criteria since none of the candidate models fit the data sufficiently well.

Goodness of Fit

None of the models provide an adequate fit do the data (Bayes factor is 1.08e+01).

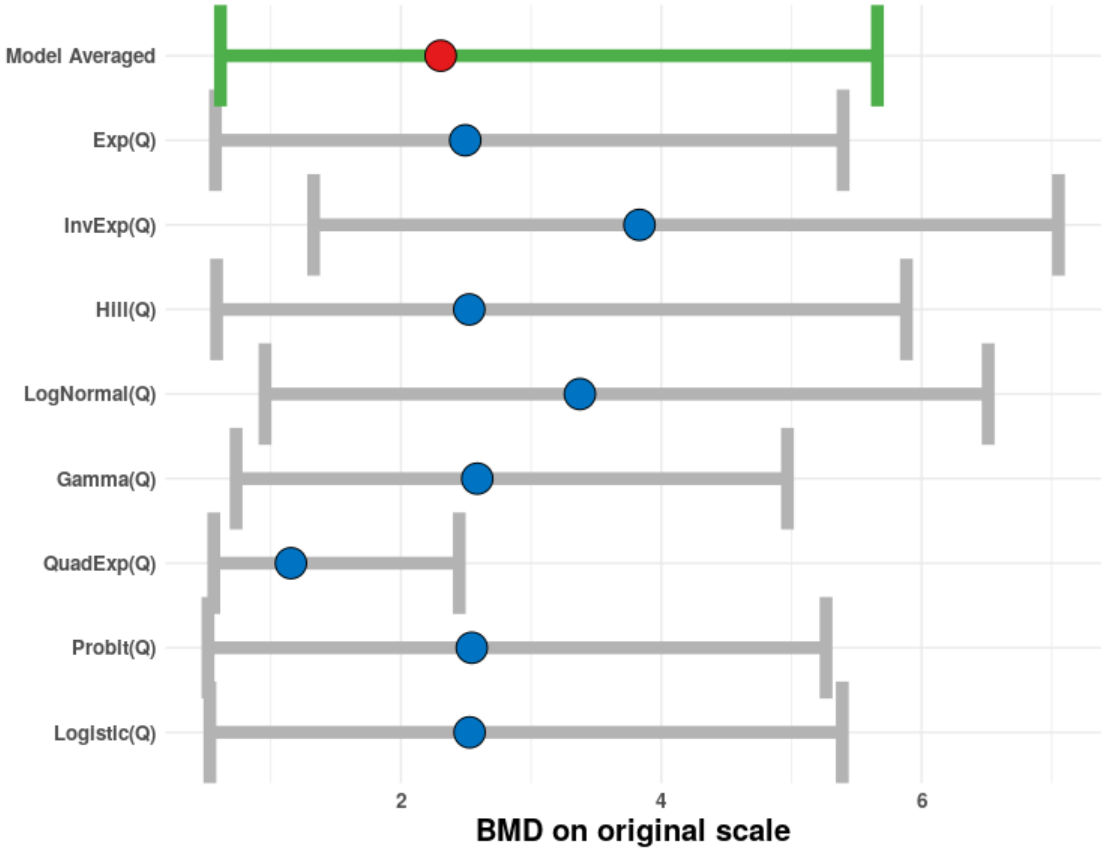
Model Averaged BMD

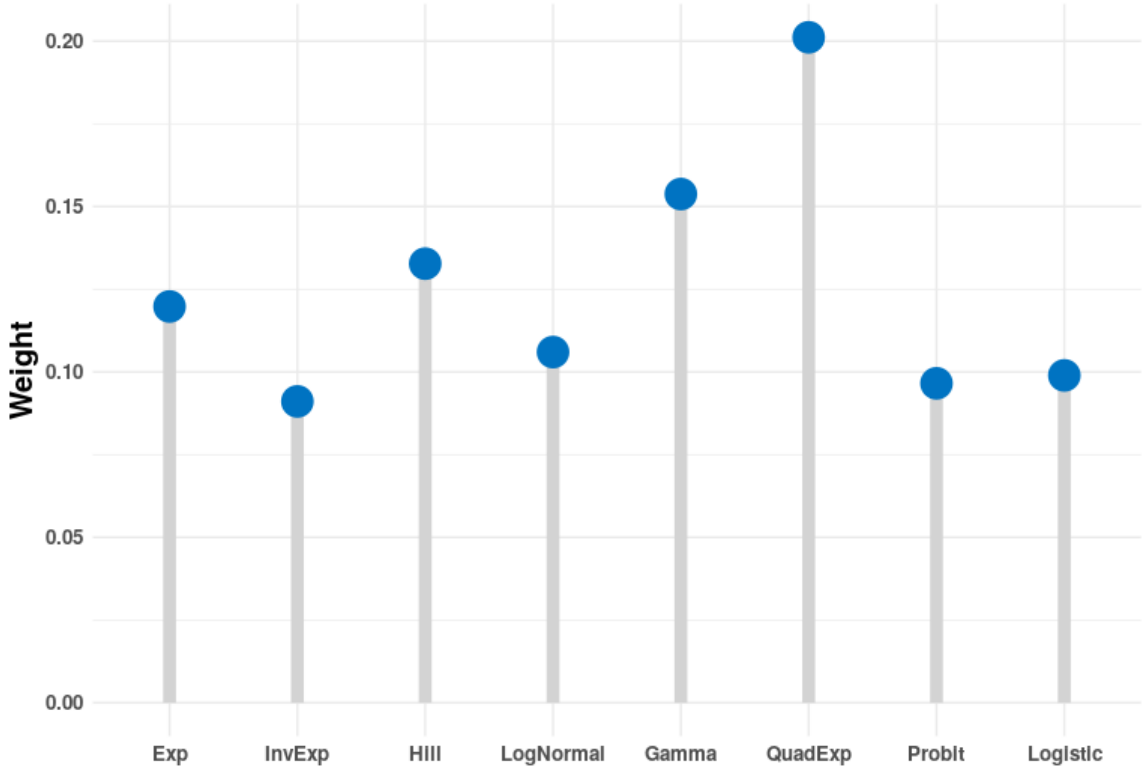
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.613	2.305	5.661

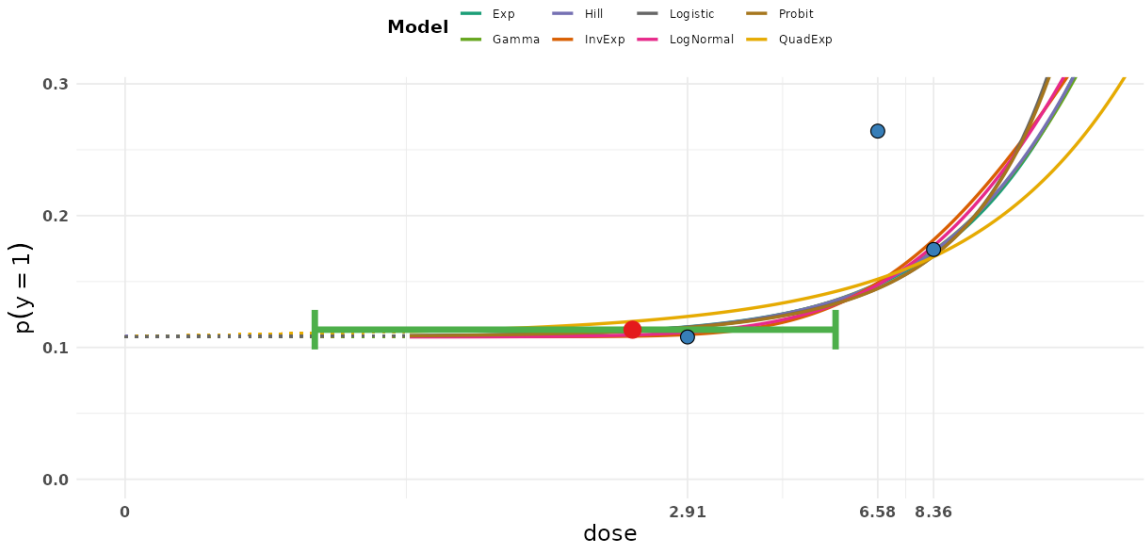
Estimated BMDs per model

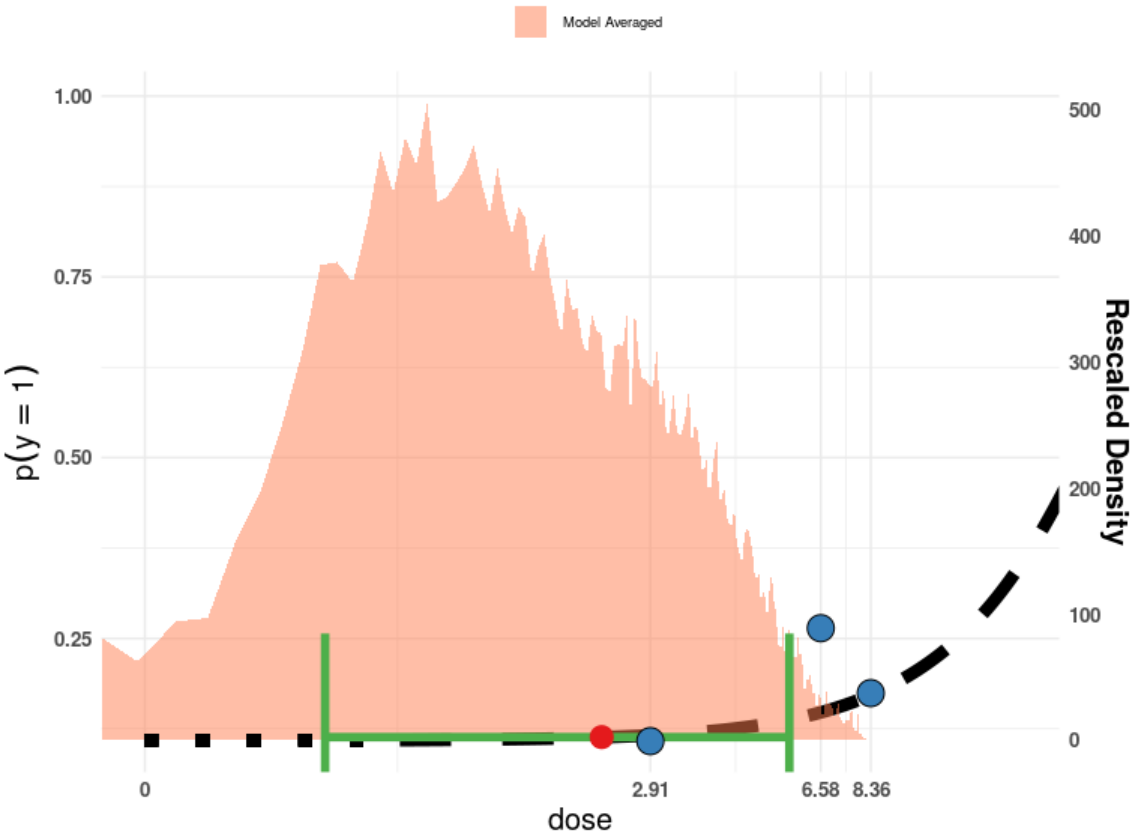
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.575	2.494	5.397	0.120	1
IE4_Q	1.329	3.833	7.052	0.091	1
H4_Q	0.584	2.525	5.884	0.133	1
LN4_Q	0.956	3.375	6.512	0.106	1
G4_Q	0.734	2.586	4.970	0.154	1
QE4_Q	0.562	1.155	2.448	0.201	1
P4_Q	0.518	2.544	5.266	0.097	1
L4_Q	0.532	2.527	5.391	0.099	1

Plots of Fitted Models




Weight
0.20
0.15
0.10
0.05
0.00
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
p(y = 1)
0.3
0.2
0.1
0.0
0
2.91
6.58
8.36
dose


Model Averaged
1.00
0.75
0.50
0.25
p(y = 1)
500
400
300
200
100
0
Rescaled Density
0
2.91
6.58
8.36
dose

Milton et al. (2005) spontaneous abortion, relative BMR 5%

Data Description

The endpoint to be analyzed is: Adj.cases for spontaneous abortion

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	N
2.91	17	176
6.58	11	53
8.36	63	304

The 'Value for CES' is set to 0.00534591.

Extended dose range is not applied.

Informative background prior: min: 0.09562500; the most likely; 0.09659091; max: 0.09755682. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 1.56e+00).

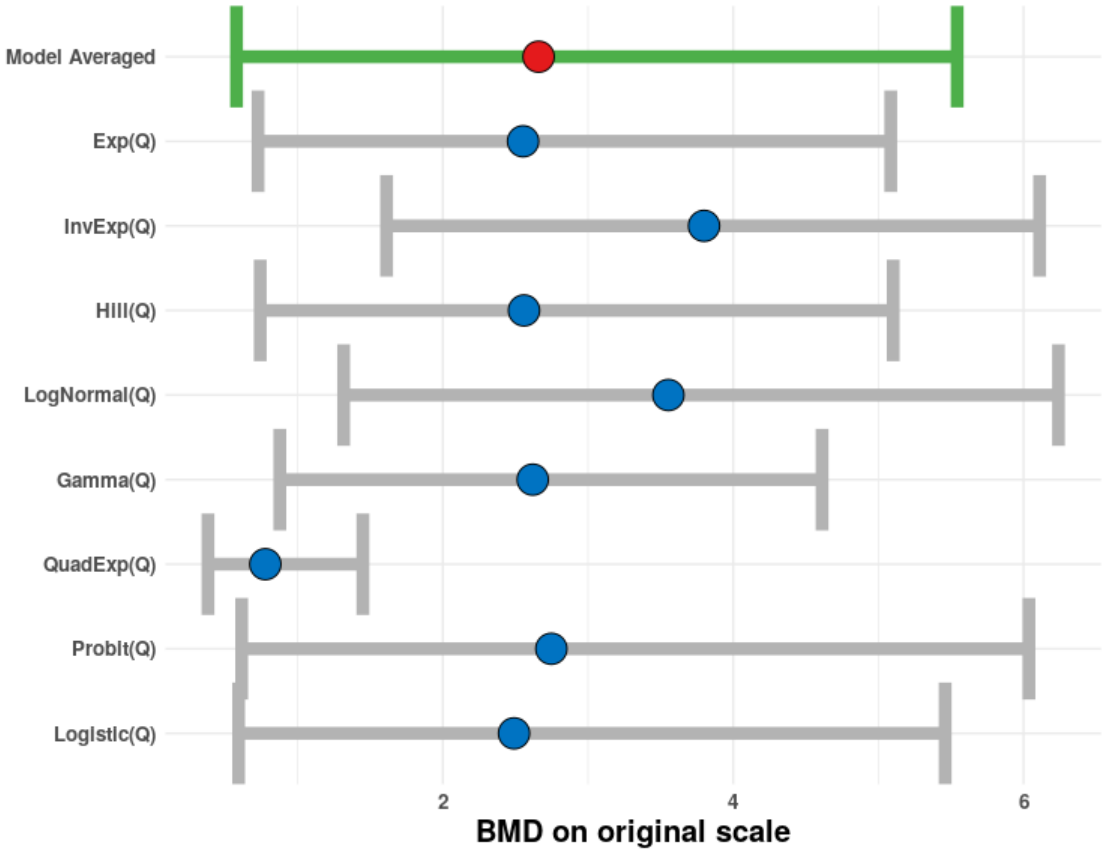
Model Averaged BMD

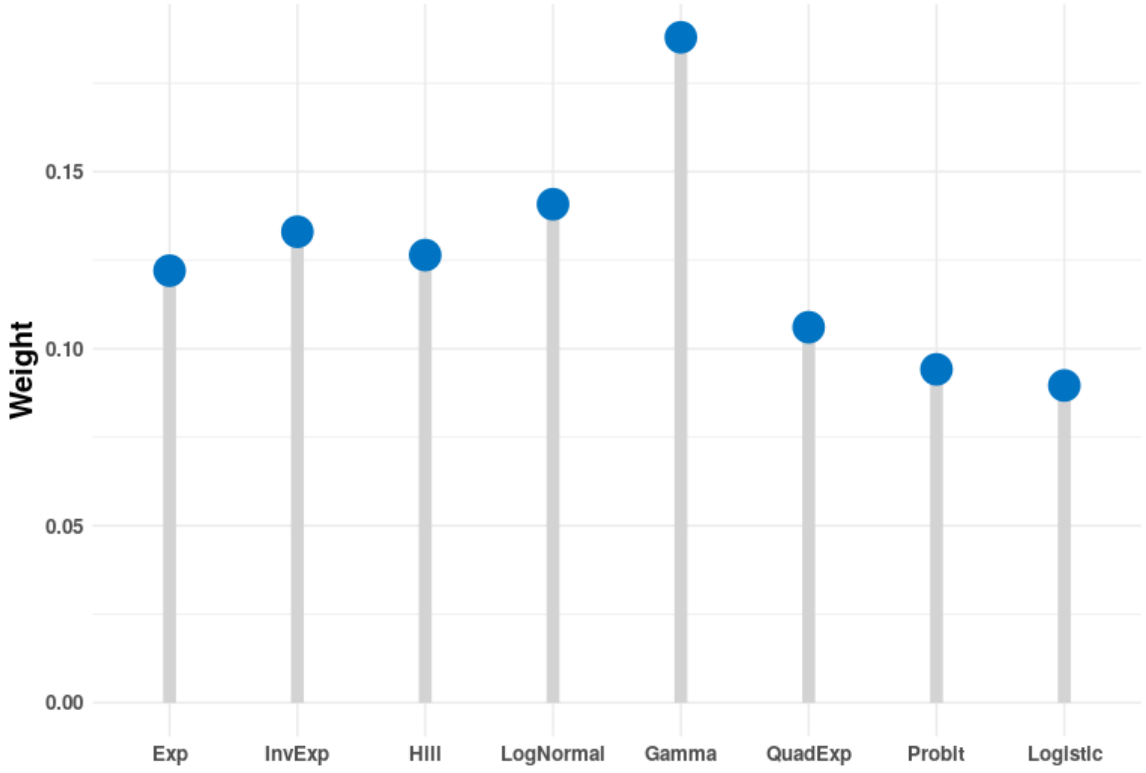
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.579	2.66	5.543

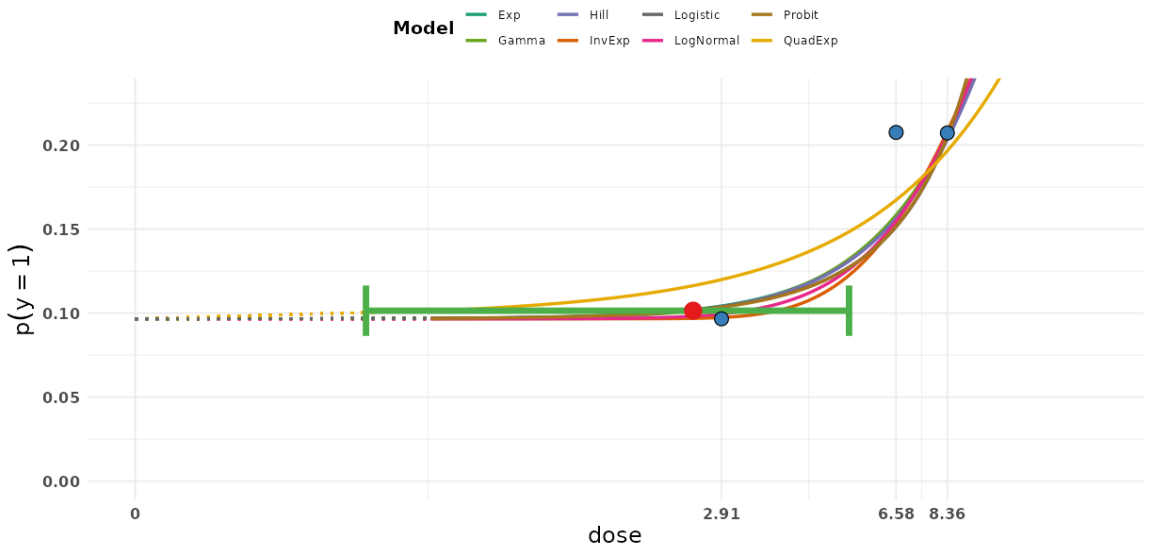
Estimated BMDs per model

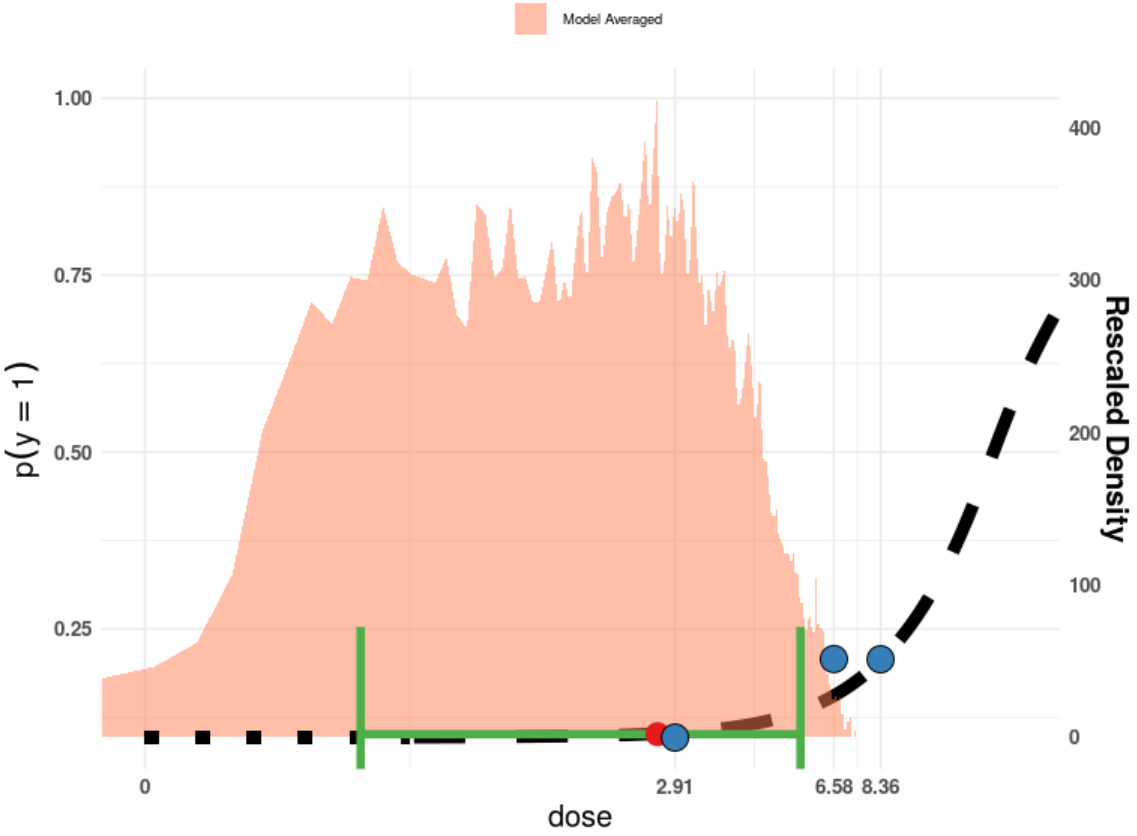
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.727	2.553	5.085	0.122	1
IE4_Q	1.613	3.799	6.110	0.133	1
H4_Q	0.743	2.559	5.102	0.126	1
LN4_Q	1.317	3.554	6.240	0.141	1
G4_Q	0.877	2.619	4.612	0.188	0
QE4_Q	0.383	0.778	1.450	0.106	1
P4_Q	0.615	2.747	6.037	0.094	0
L4_Q	0.593	2.491	5.460	0.090	1

Plots of Fitted Models




Weight
0.15
0.10
0.05
0.00
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
p(y = 1)
0.20
0.15
0.10
0.05
0.00
0
2.91
6.58
8.36
dose


Model Averaged
1.00
0.75
0.50
0.25
p(y = 1)
400
300
200
100
0
Rescaled Density
0
2.91
6.58
8.36
dose

Milton et al. (2005) stillbirth, relative BMR 5%

Data Description

The endpoint to be analyzed is: Adj.cases for stillbirth

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	N
2.91	11	176
6.58	4	53
8.36	48	304

The 'Value for CES' is set to 0.00333333.

Extended dose range is not applied.

Informative background prior: min: 0.06187500; the most likely; 0.06250000; max: 0.06312500. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 9.91e-01).

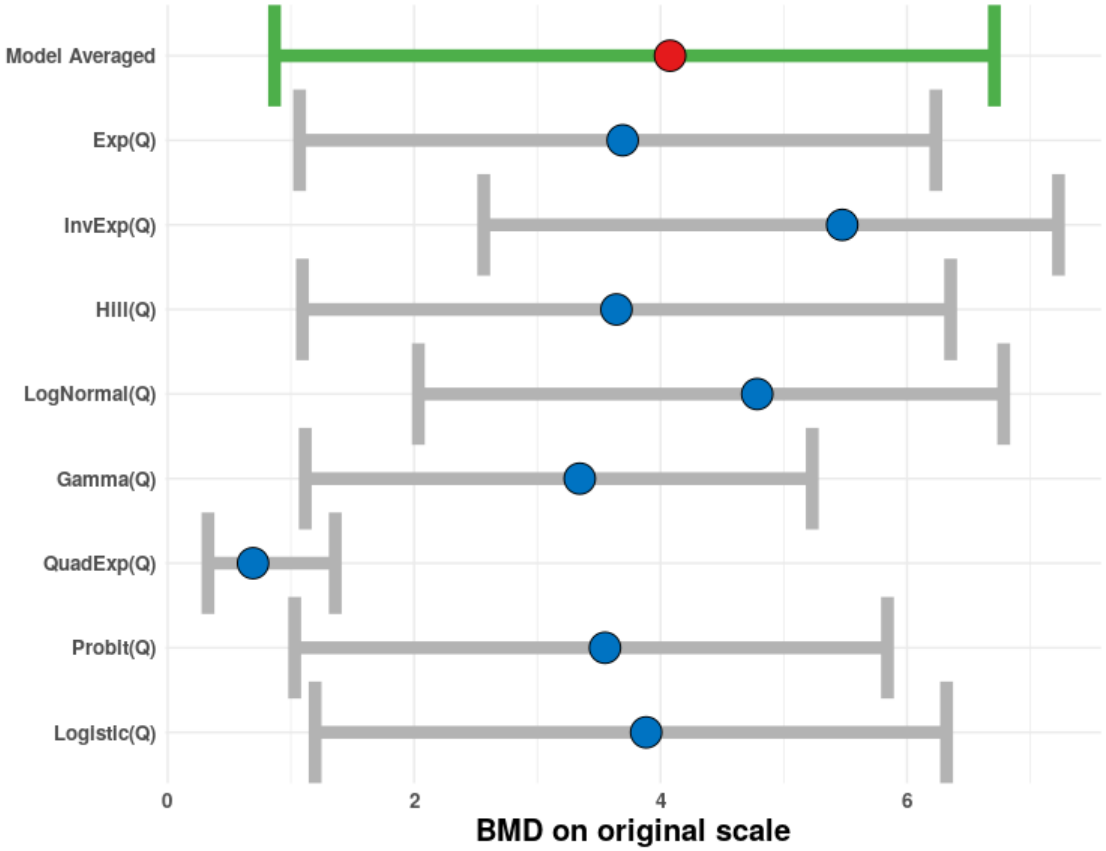
Model Averaged BMD

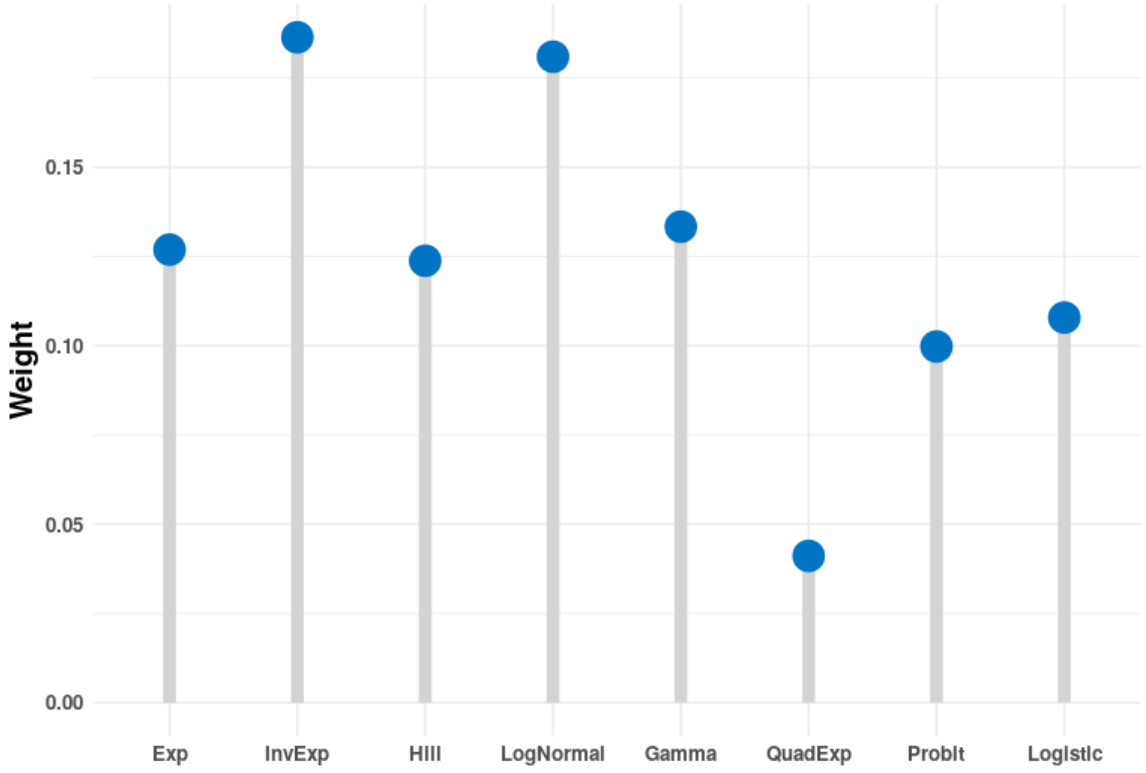
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.867	4.077	6.709

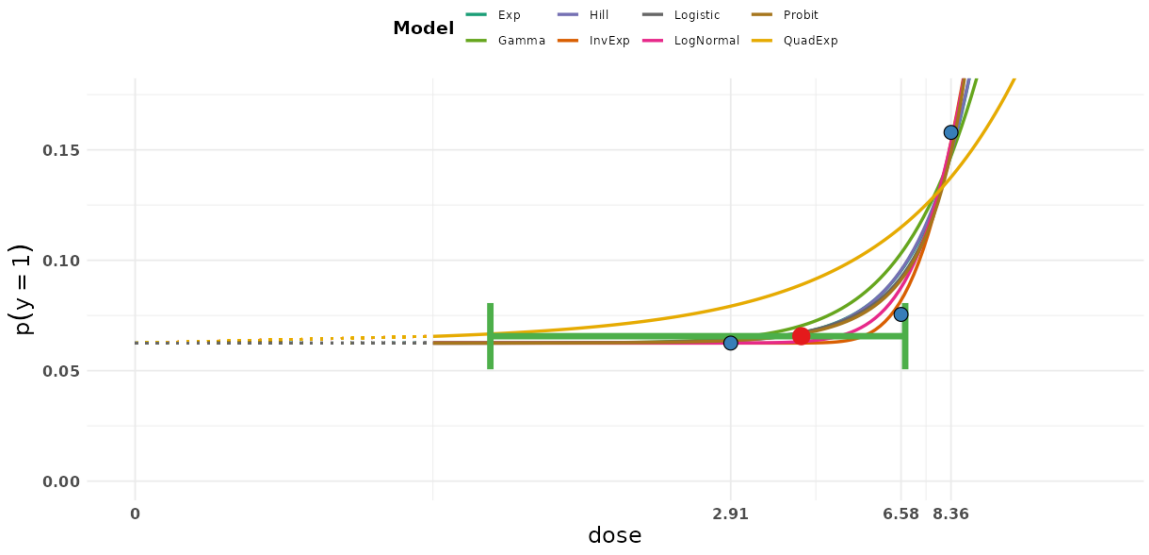
Estimated BMDs per model

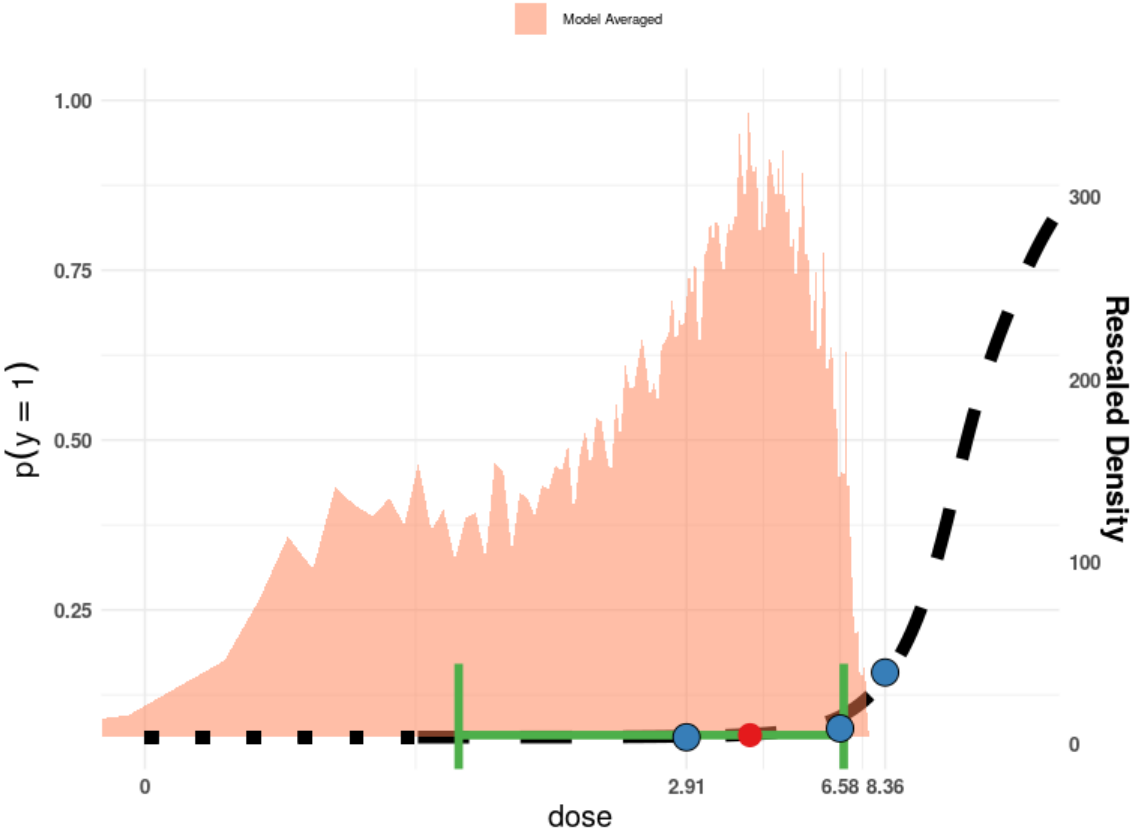
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	1.071	3.693	6.234	0.127	1
IE4_Q	2.565	5.474	7.229	0.186	1
H4_Q	1.094	3.642	6.354	0.124	1
LN4_Q	2.035	4.784	6.785	0.181	1
G4_Q	1.117	3.344	5.231	0.133	1
QE4_Q	0.327	0.693	1.360	0.041	1
P4_Q	1.031	3.549	5.842	0.100	1
L4_Q	1.197	3.883	6.321	0.108	1

Plots of Fitted Models




Weight
0.15
0.10
0.05
0.00
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
p(y = 1)
0.15
0.10
0.05
0.00
0
2.91
6.58
8.36
dose


Model Averaged
1.00
0.75
0.50
0.25
p(y = 1)
300
200
100
0
Rescaled Density
0
2.91
6.58
8.36
dose

Moon et al. (2013) ischemic heart disease, relative BMR 5%

Data Description

The endpoint to be analyzed is: Adj.cases for ischemic heart disease

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	Person.years
0.089	207	12447
0.150	212	12136
0.250	187	11805
0.440	240	11075

The 'Value for CES' is set to 0.00084559.

Extended dose range is not applied.

Informative background prior: min: 0.01646421; the most likely; 0.01663051; max: 0.01679682. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 9.18e-03).

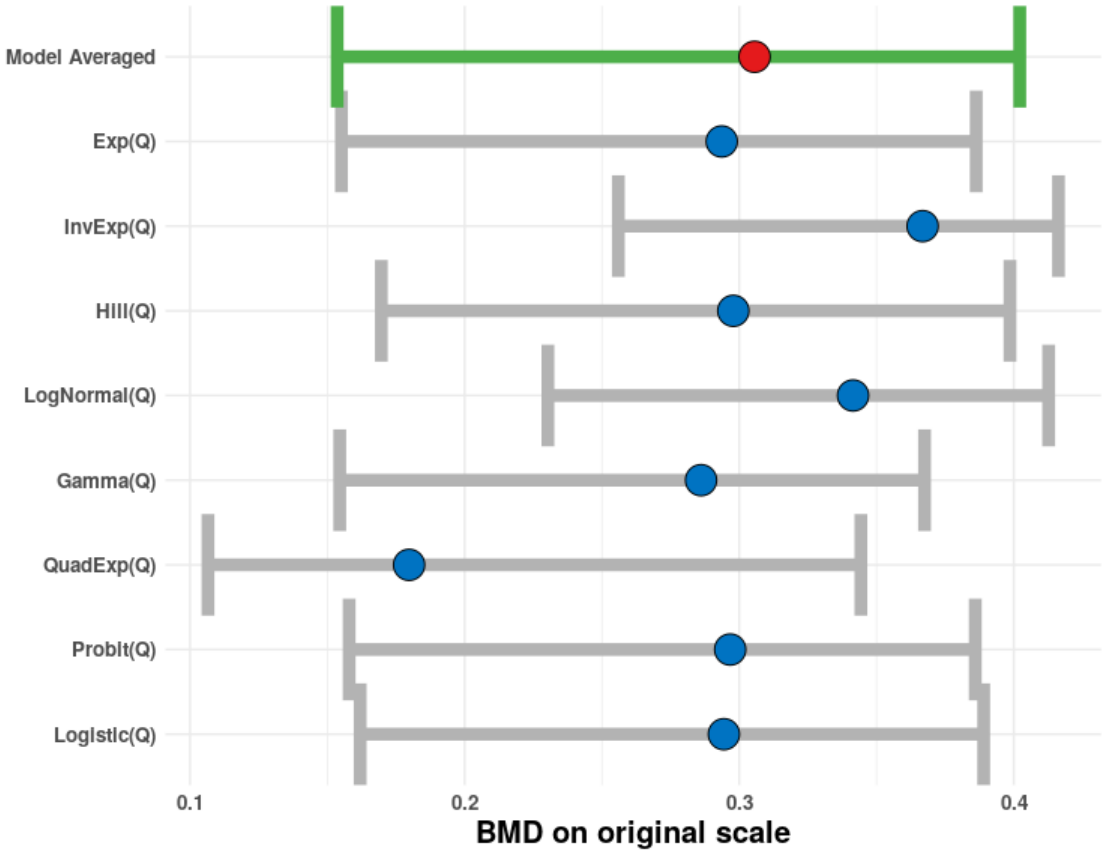
Model Averaged BMD

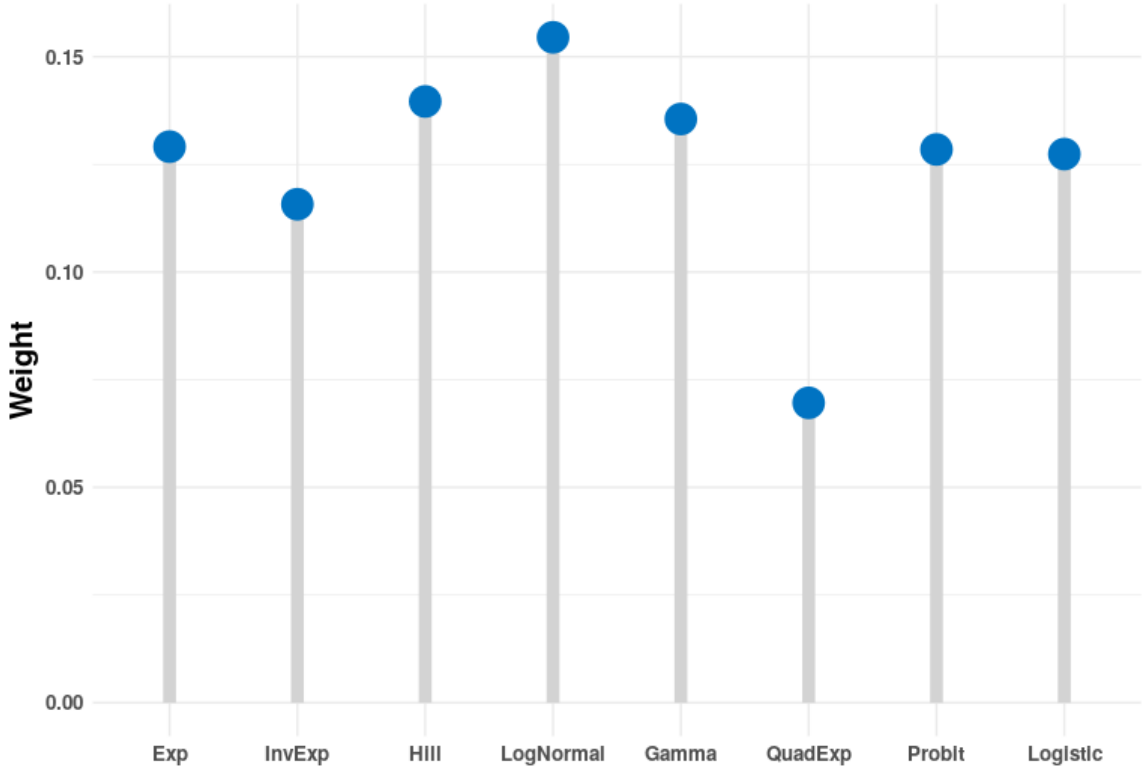
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.154	0.306	0.402

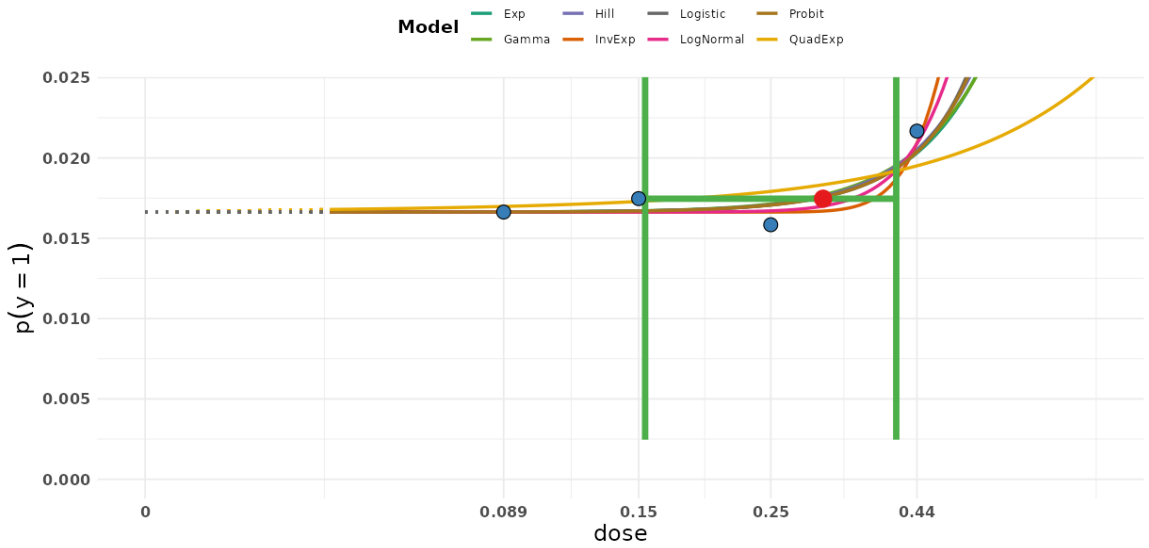
Estimated BMDs per model

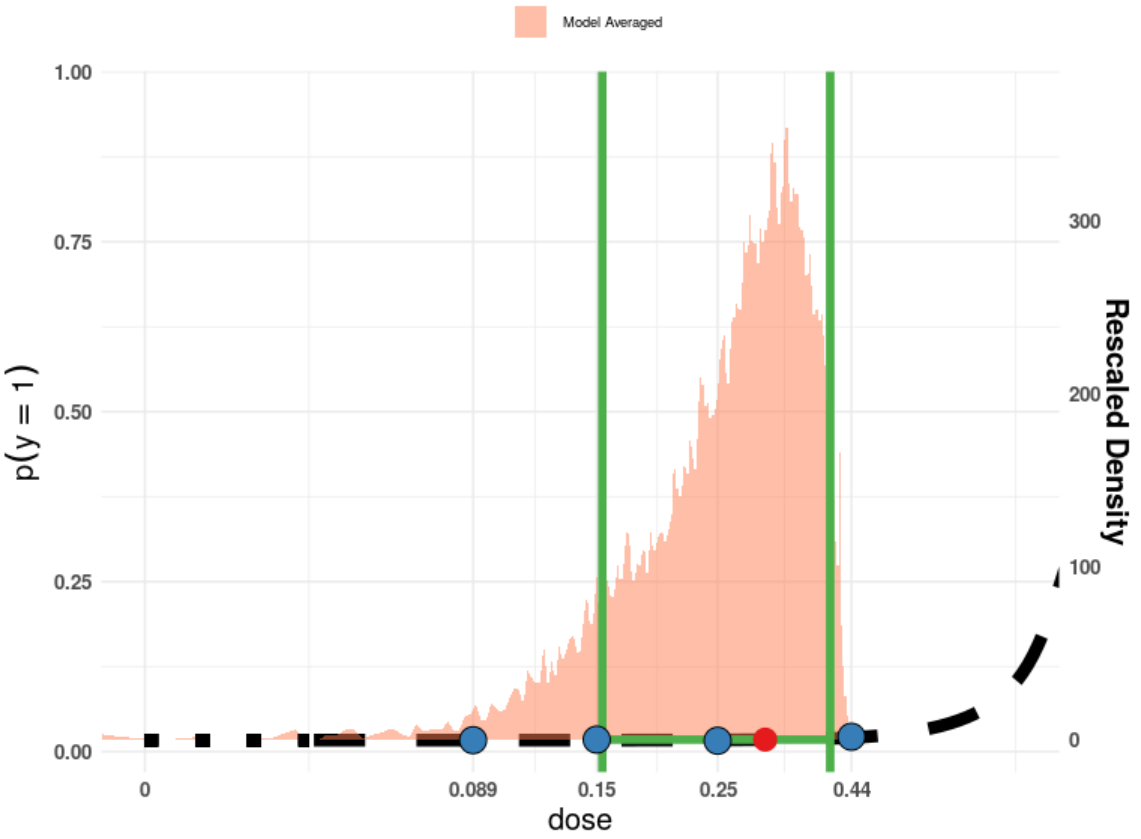
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.155	0.294	0.386	0.129	1
IE4_Q	0.256	0.367	0.416	0.116	1
H4_Q	0.170	0.298	0.399	0.140	1
LN4_Q	0.230	0.341	0.413	0.155	1
G4_Q	0.155	0.286	0.367	0.136	1
QE4_Q	0.107	0.180	0.344	0.070	1
P4_Q	0.158	0.297	0.386	0.128	1
L4_Q	0.162	0.294	0.389	0.127	1

Plots of Fitted Models




Weight
0.15
0.10
0.05
0.00
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
p(y = 1)
0.025
0.020
0.015
0.010
0.005
0.000
0
0.089
0.15
0.25
0.44
dose


Model Averaged
1.00
0.75
0.50
0.25
0.00
p(y = 1)
300
200
100
0
Rescaled Density
0
0.089
0.15
0.25
0.44
dose

Parvez et al. (2013) FEV1 (lung function), BMR 5%

Data Description

The endpoint to be analyzed is: FEV1 response

Data used for analysis:

Dose	Response	SD	N
1.78	1574	522	312
5.31	1541	522	315
8.15	1494	525	315

The 'Value for CES' is set to 0.05.

Extended dose range is not applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

The results do not fulfill the EFSA BMD guidance (EFSA Scientific Committee, 2022) recommendations since none of the candidate models fit the data sufficiently well.

Check for constant variance coefficient of variation

Distributional assumption of constant variance is met, Bartlett test p-value is 0.9932

Distributional assumption of constant variance (on log-scale) is met, Bartlett test p-value is 0.6173

Goodness of Fit

None of the models provide an adequate fit do the data (Bayes factor is 3.24e+01).

Model Averaged BMD

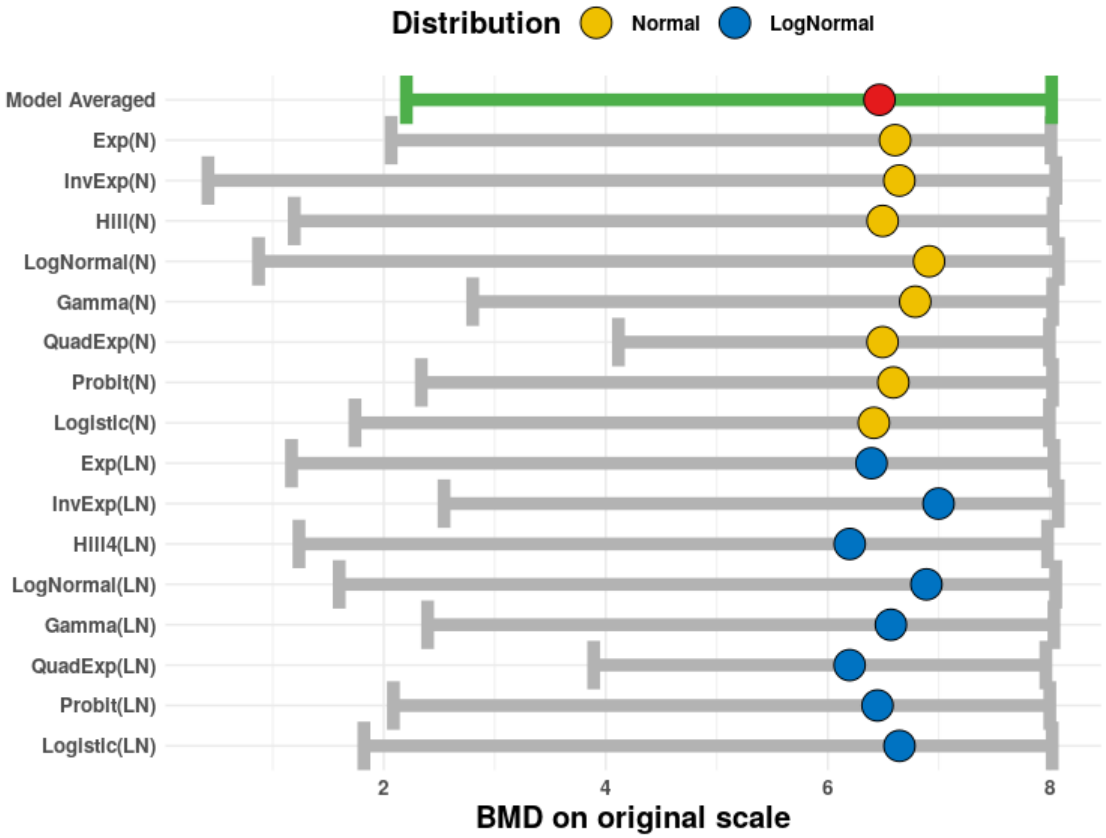
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	2.204	6.465	8.015

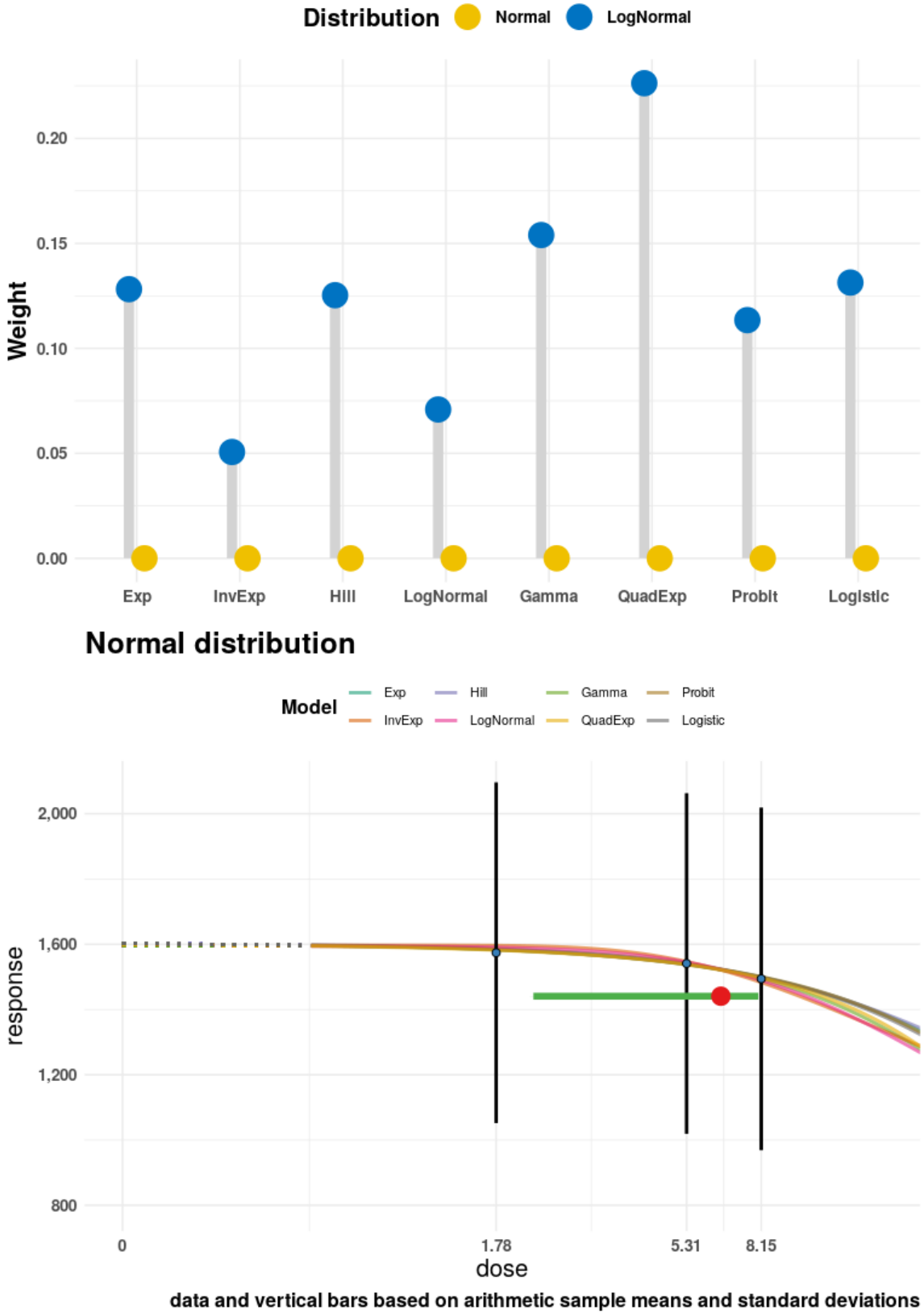
Estimated BMDs per model

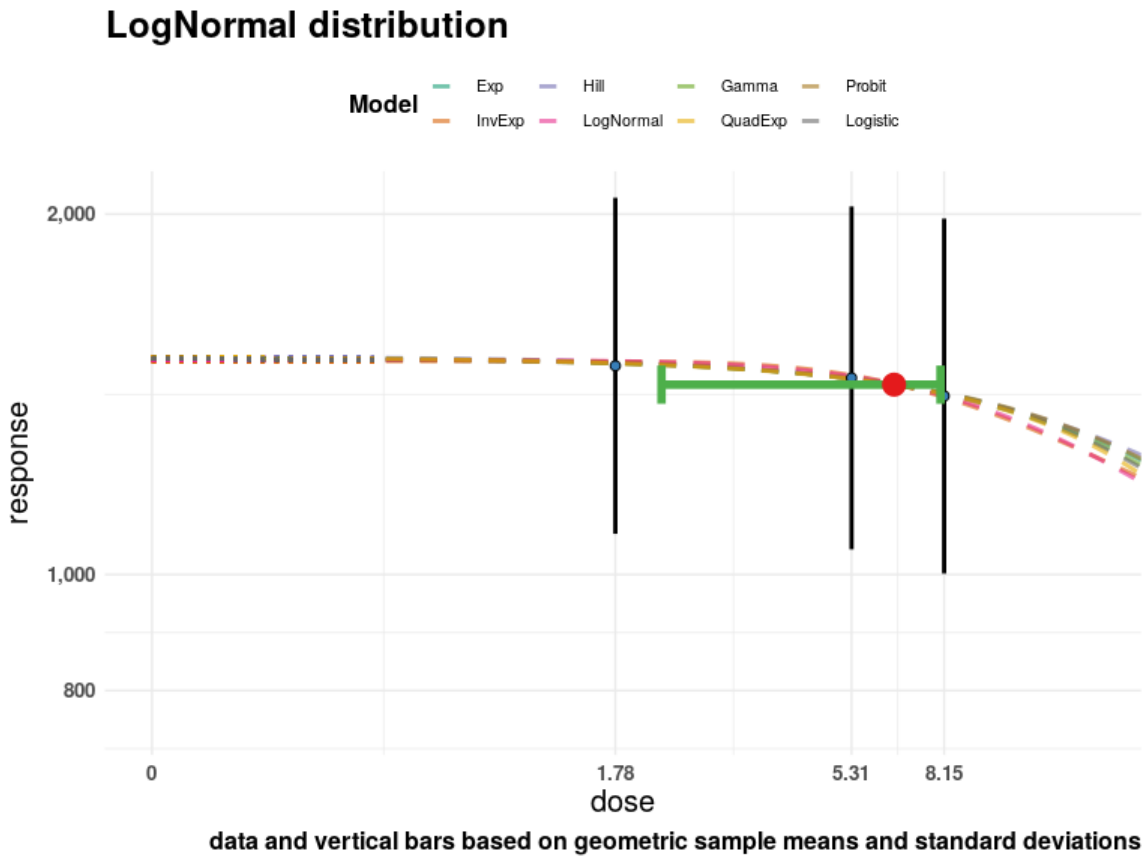
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_N	2.067	6.606	8.010	0.000	1
IE4_N	0.417	6.644	8.055	0.000	0
H4_N	1.194	6.494	8.029	0.000	0
LN4_N	0.873	6.912	8.077	0.000	0
G4_N	2.801	6.787	8.025	0.000	1
QE4_N	4.114	6.493	7.996	0.000	1
P4_N	2.339	6.590	8.024	0.000	1

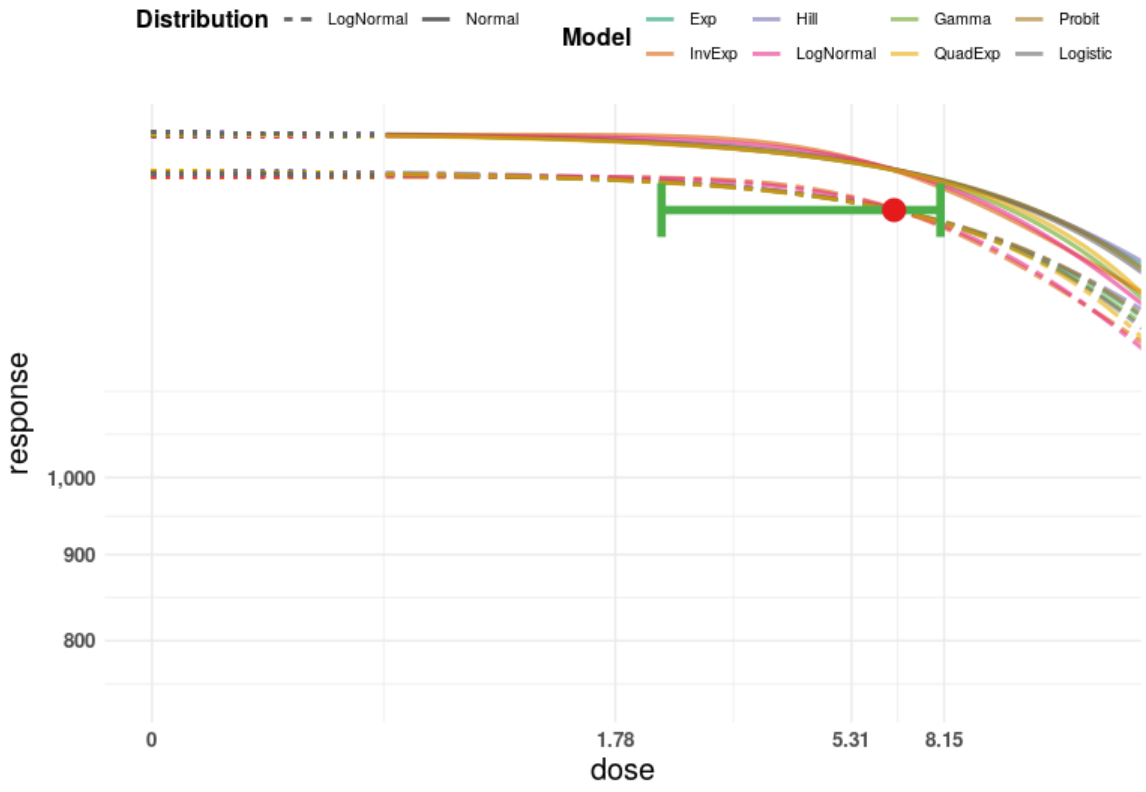
L4_N	1.741	6.414	7.996	0.000	0
E4_LN	1.169	6.393	8.036	0.128	0
IE4_LN	2.543	6.997	8.075	0.051	1
H4_LN	1.237	6.197	7.979	0.125	0
LN4_LN	1.599	6.888	8.053	0.071	0
G4_LN	2.395	6.568	8.037	0.154	1
QE4_LN	3.891	6.196	7.964	0.226	1
P4_LN	2.087	6.447	7.999	0.113	1
L4_LN	1.821	6.645	8.021	0.131	1

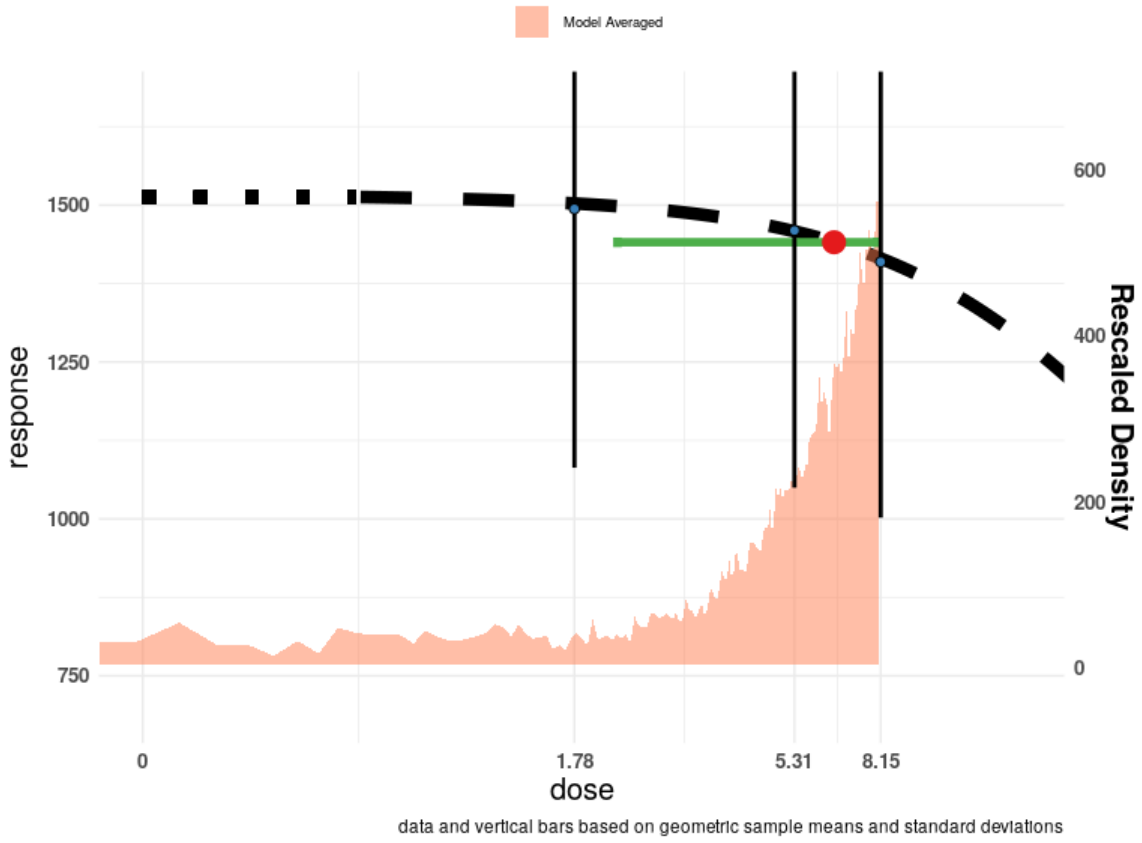
Plots of Fitted Models




Distribution
Normal
LogNormal
Weight
0.20
0.15
0.10
0.05
0.00
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic
Normal distribution
Model
Exp
Hill
Gamma
Probit
InvExp
LogNormal
QuadExp
Logistic
response
2,000
1,600
1,200
800
0
1.78
5.31
8.15
dose
data and vertical bars based on arithmetic sample means and standard deviations


LogNormal distribution
Model
Exp
Hill
Gamma
Probit
InvExp
LogNormal
QuadExp
Logistic
2,000
1,000
800
response
0
1.78
5.31
8.15
dose
data and vertical bars based on geometric sample means and standard deviations


Distribution
LogNormal
Normal
Model
Exp
Hill
Gamma
Probit
InvExp
LogNormal
QuadExp
Logistic
1,000
900
800
response
0
1.78
5.31
8.15
dose


Model Averaged
1500
1250
1000
750
response
600
400
200
0
Rescaled Density
0
1.78
5.31
8.15
dose
data and vertical bars based on geometric sample means and standard deviations

Parvez et al. (2013) FVC (lung function), BMR 5%

Data Description

The endpoint to be analyzed is: FVC response

Data used for analysis:

Dose	Response	SD	N
1.78	2268	538	312
5.31	2254	539	315
8.15	2170	541	315

The 'Value for CES' is set to 0.05.

Extended dose range is not applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

The results do not fulfill the EFSA BMD guidance (EFSA Scientific Committee, 2022) recommendations since none of the candidate models fit the data sufficiently well.

Check for constant variance coefficient of variation

Distributional assumption of constant variance is met, Bartlett test p-value is 0.995

Distributional assumption of constant variance (on log-scale) is met, Bartlett test p-value is 0.6541

Goodness of Fit

None of the models provide an adequate fit do the data (Bayes factor is 5.67e+01).

Model Averaged BMD

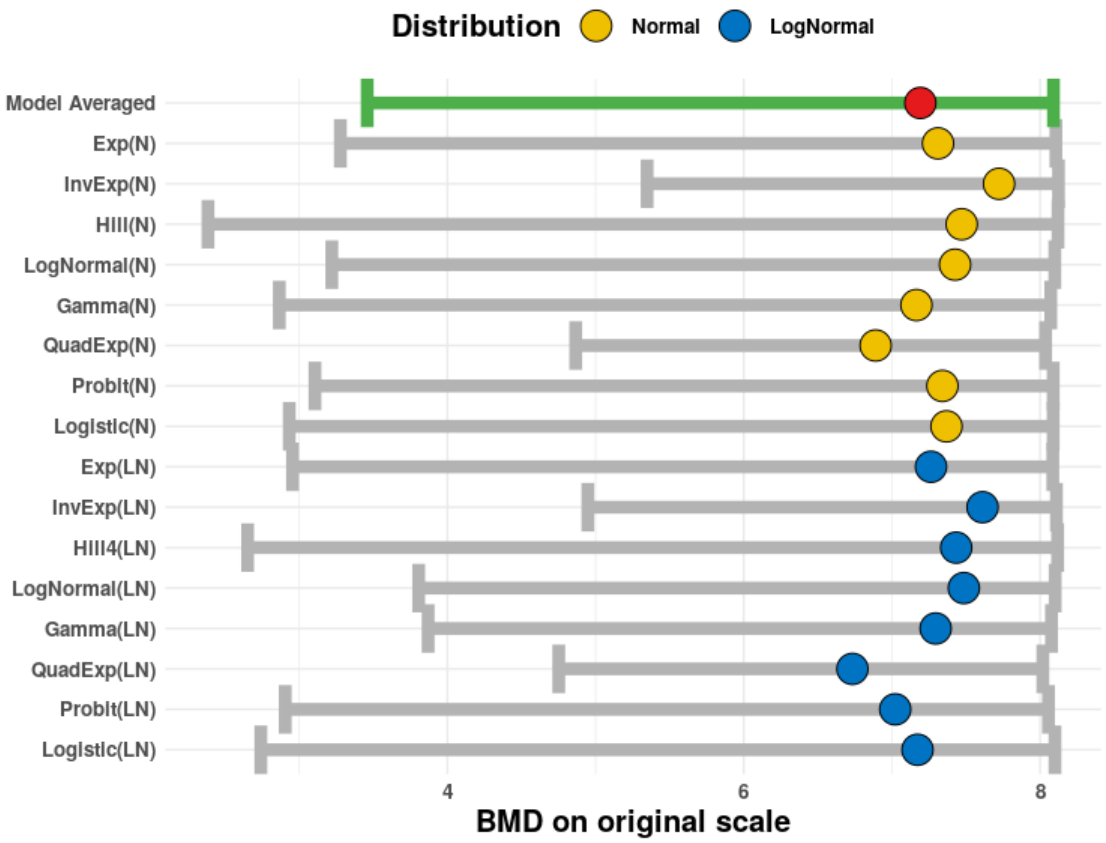
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	3.459	7.192	8.091

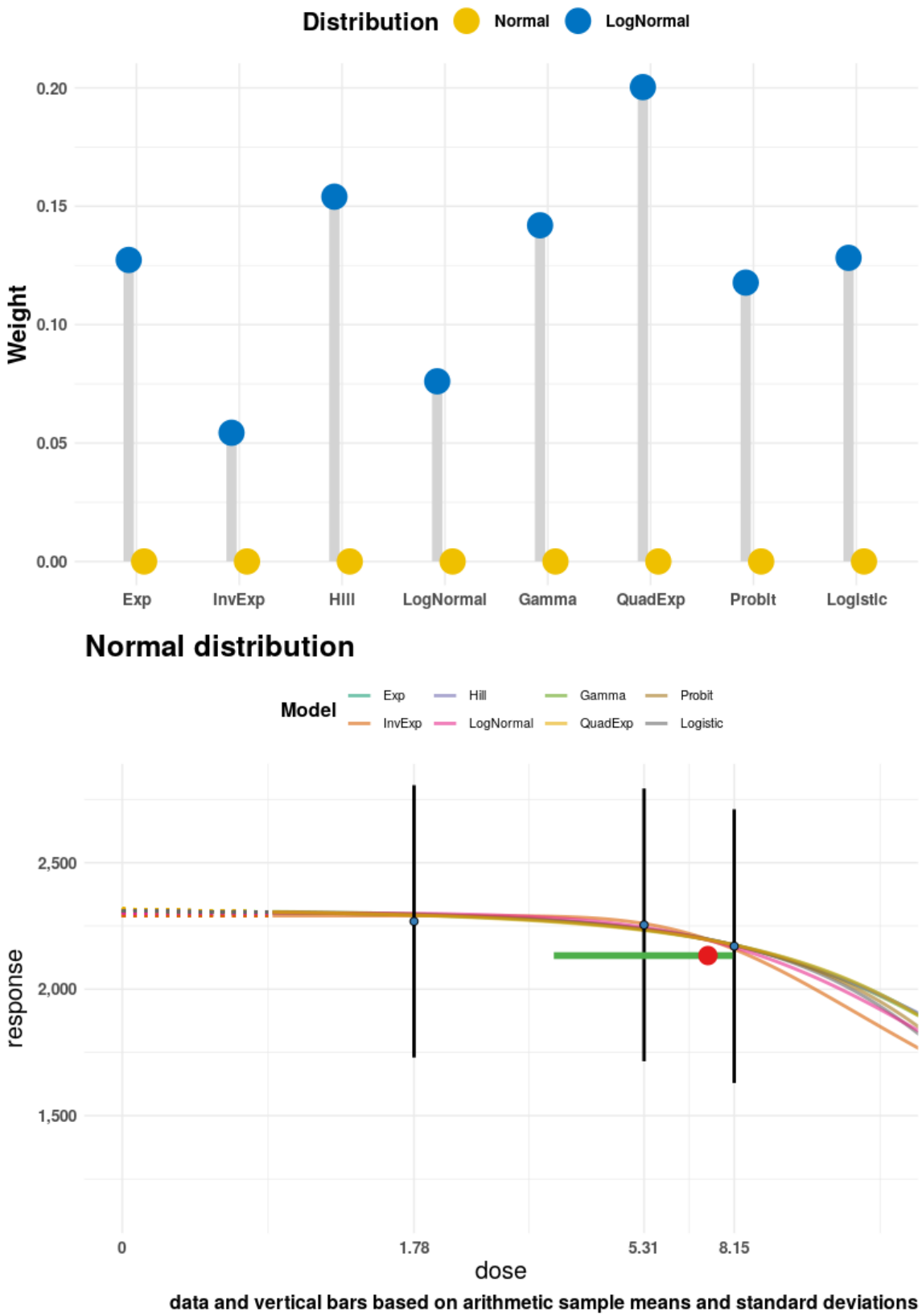
Estimated BMDs per model

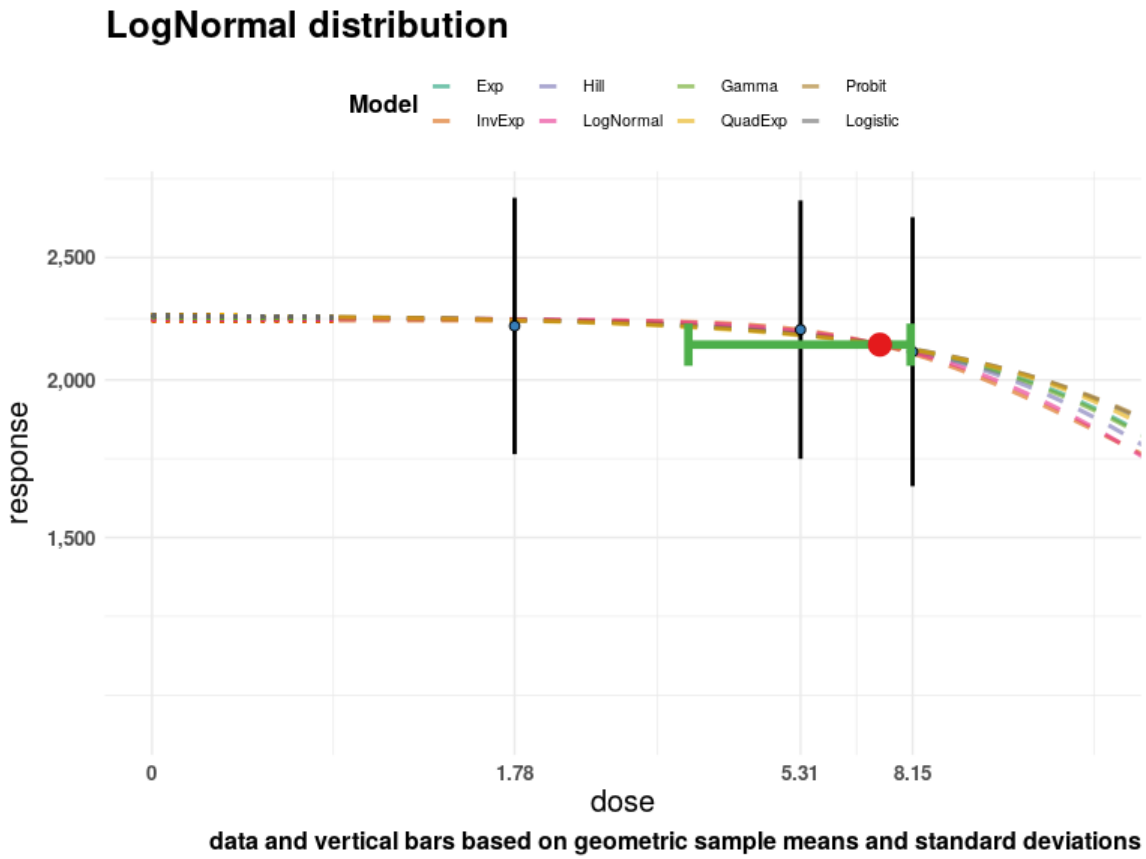
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_N	3.277	7.311	8.107	0.000	0
IE4_N	5.348	7.723	8.124	0.000	0
H4_N	2.384	7.471	8.121	0.000	0
LN4_N	3.220	7.426	8.099	0.000	0
G4_N	2.865	7.166	8.072	0.000	0
QE4_N	4.866	6.890	8.037	0.000	1
P4_N	3.106	7.341	8.089	0.000	1
L4_N	2.933	7.368	8.089	0.000	0

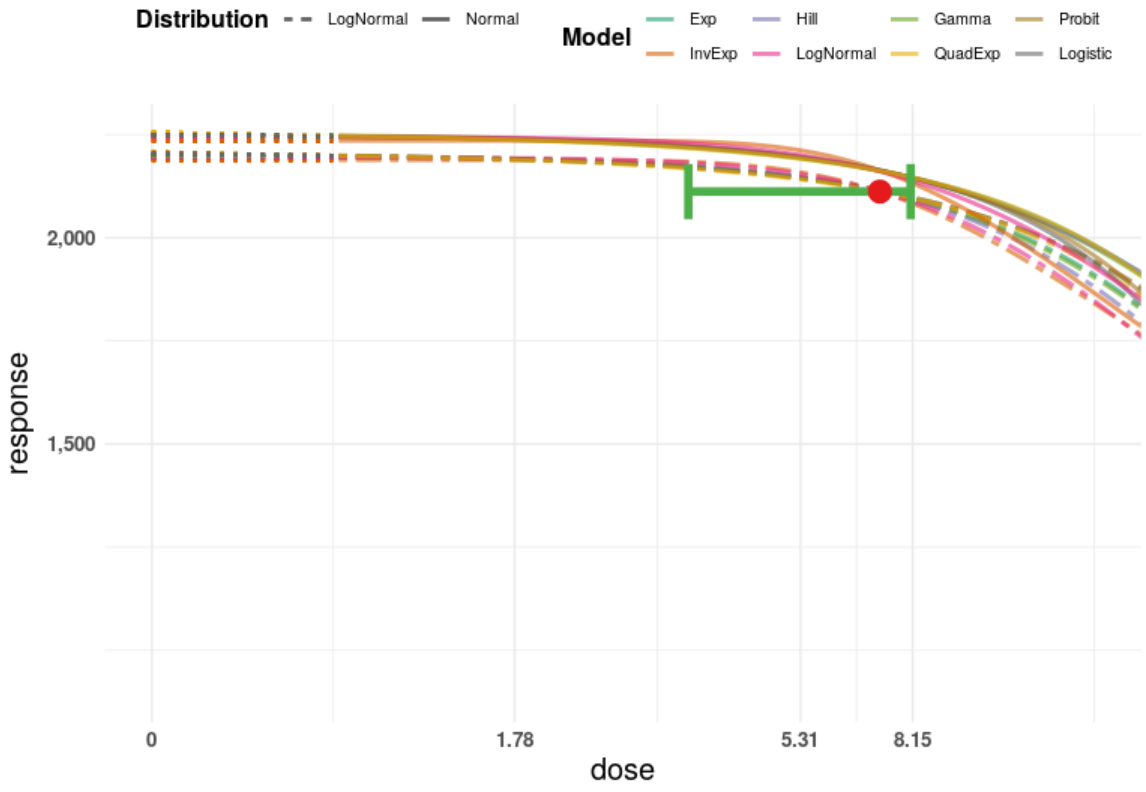
E4_LN	2.954	7.264	8.086	0.127	0
IE4_LN	4.948	7.612	8.111	0.054	0
H4_LN	2.651	7.434	8.119	0.154	0
LN4_LN	3.806	7.486	8.102	0.076	0
G4_LN	3.870	7.295	8.077	0.142	1
QE4_LN	4.751	6.734	8.019	0.200	1
P4_LN	2.905	7.022	8.057	0.118	1
L4_LN	2.741	7.173	8.100	0.128	0

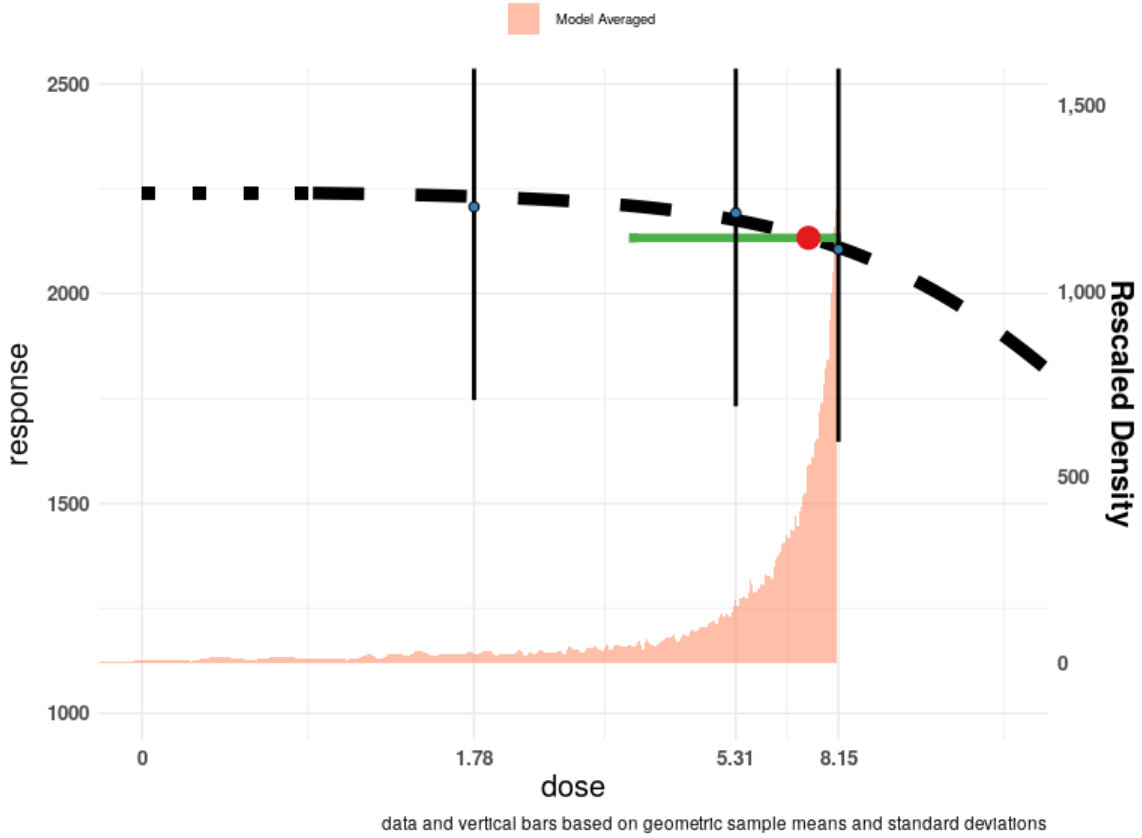
Plots of Fitted Models




Distribution
Normal
LogNormal
Weight
0.20
0.15
0.10
0.05
0.00
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic
Normal distribution
Model
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic
response
2,500
2,000
1,500
0
1.78
5.31
8.15
dose
data and vertical bars based on arithmetic sample means and standard deviations


LogNormal distribution
Model
Exp
Hill
Gamma
Probit
InvExp
LogNormal
QuadExp
Logistic
2,500
2,000
1,500
response
0
1.78
5.31
8.15
dose
data and vertical bars based on geometric sample means and standard deviations


Distribution
LogNormal
Normal
Model
Exp
Hill
Gamma
Probit
InvExp
LogNormal
QuadExp
Logistic
2,000
1,500
response
0
1.78
5.31
8.15
dose


Model Averaged
2500
2000
1500
1000
response
1,500
1,000
500
0
Rescaled Density
0
1.78
5.31
8.15
dose
data and vertical bars based on geometric sample means and standard deviations

Pierce et al. (2011) skin lesions, relative BMR 5%

Data Description

The endpoint to be analyzed is: Adj.cases for skin lesions

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	N
1.46	117	2358
3.28	123	2118
6.55	145	1726
12.00	314	2855
15.64	115	617

The 'Value for CES' is set to 0.00261044.

Extended dose range is not applied.

Informative background prior: min: 0.04912214; the most likely; 0.04961832; max: 0.05011450. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 6.63e-03).

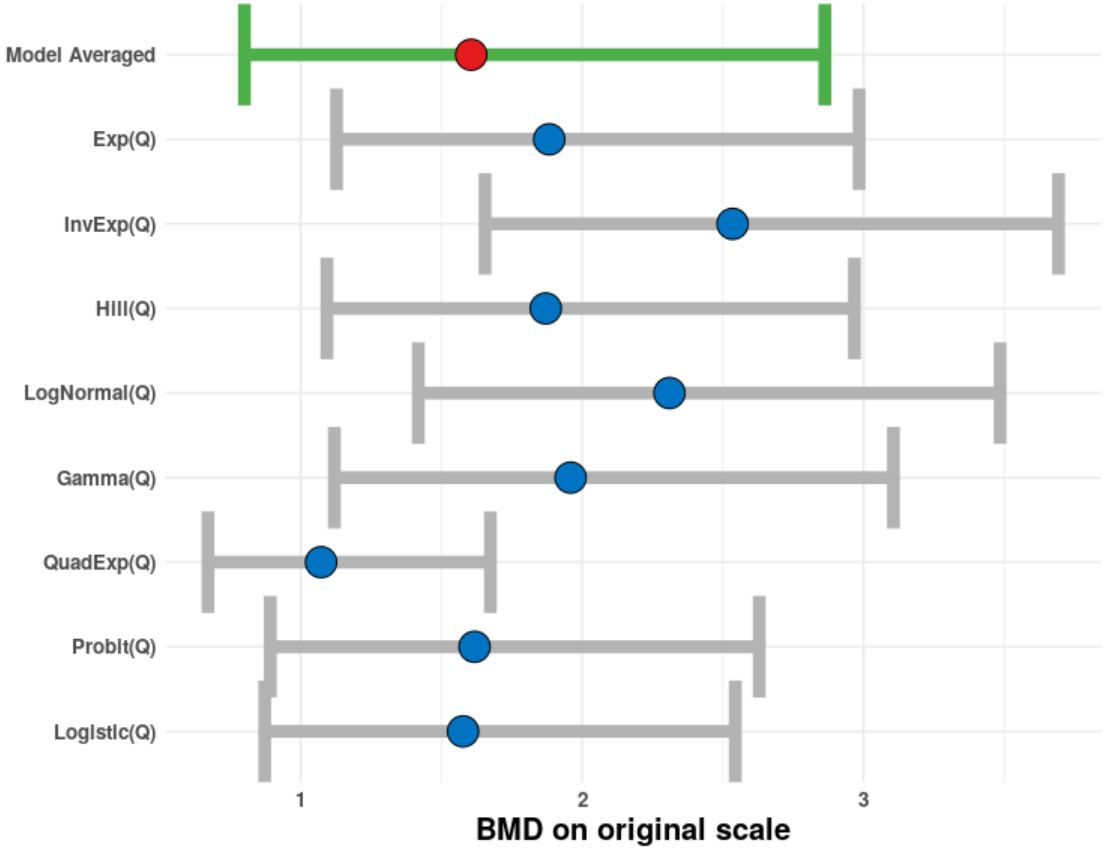
Model Averaged BMD

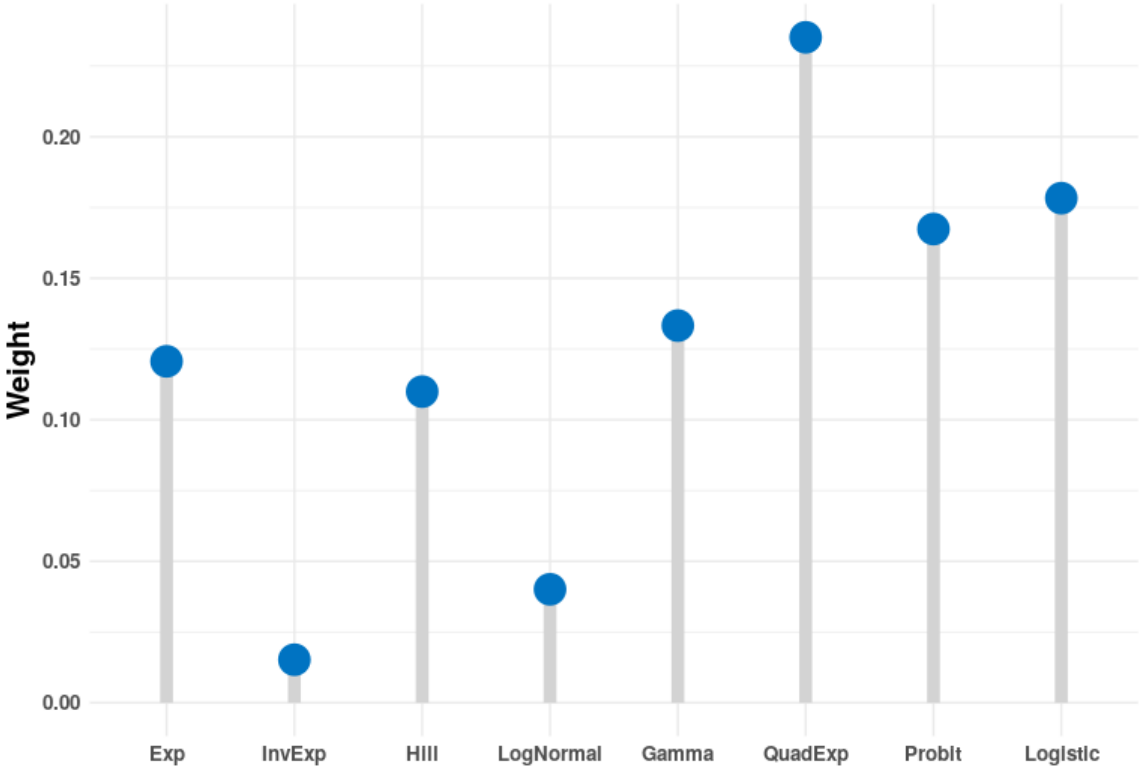
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.8	1.606	2.862

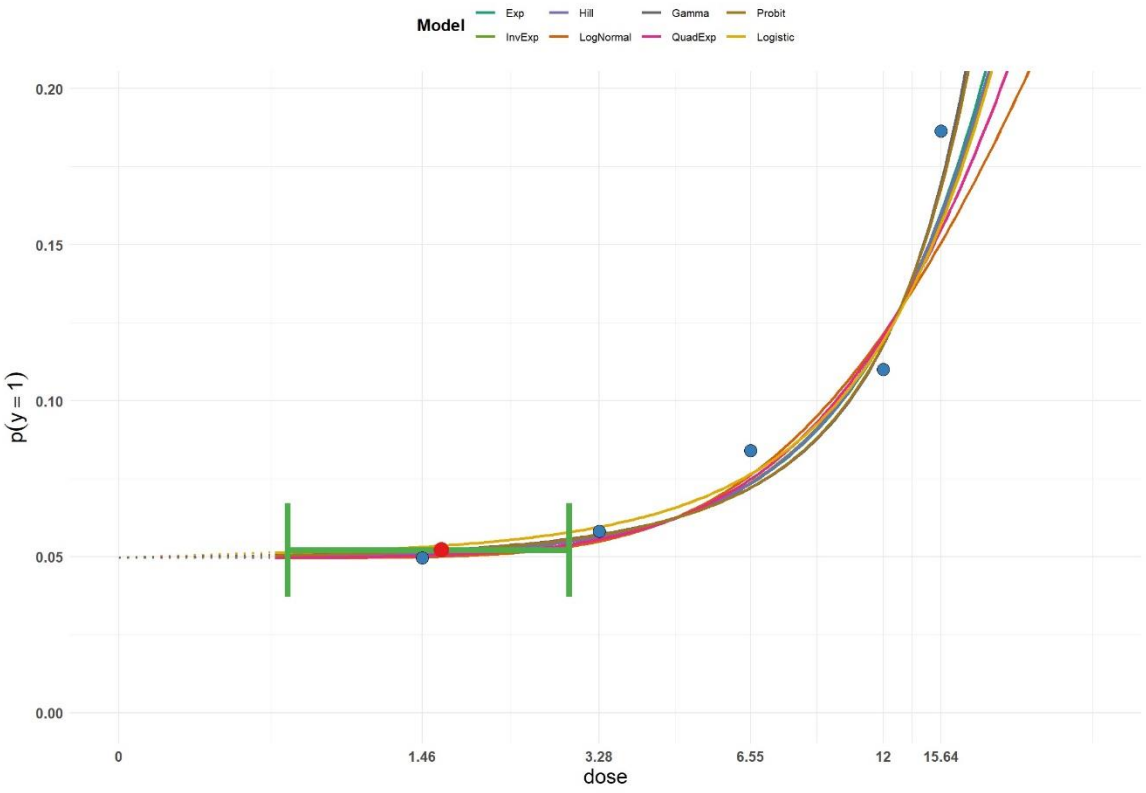
Estimated BMDs per model

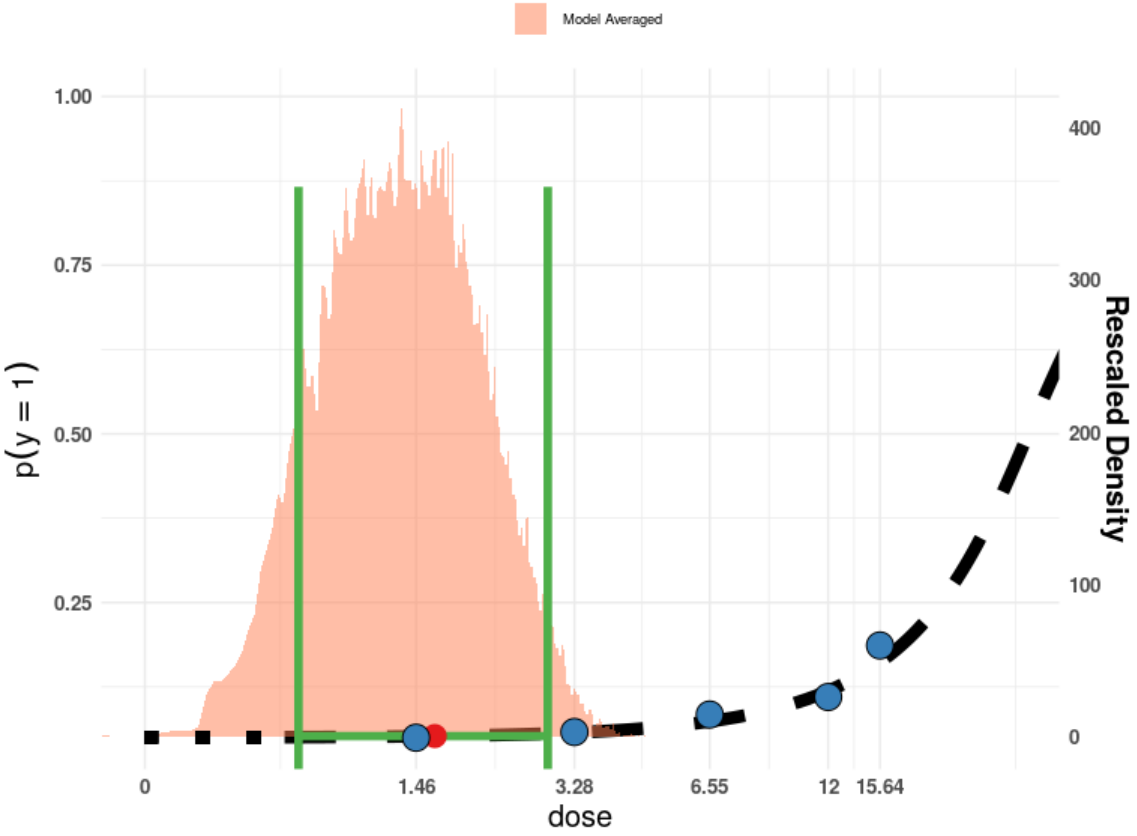
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	1.128	1.883	2.984	0.121	1
IE4_Q	1.655	2.535	3.693	0.015	1
H4_Q	1.093	1.871	2.967	0.110	1
LN4_Q	1.418	2.310	3.485	0.040	1
G4_Q	1.120	1.959	3.106	0.133	1
QE4_Q	0.671	1.073	1.674	0.235	1
P4_Q	0.892	1.618	2.629	0.167	1
L4_Q	0.872	1.577	2.544	0.178	1

Plots of Fitted Models




Weight
0.20
0.15
0.10
0.05
0.00
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic
p(y = 1)
0.20
0.15
0.10
0.05
0.00
0
1.46
3.28
6.55
12
15.64
dose


Model Averaged
1.00
0.75
0.50
0.25
p(y = 1)
400
300
200
100
0
Rescaled Density
0
1.46
3.28
6.55
12
15.64
dose

Powers et al. (2019) airflow obstruction, relative BMR 5%

Data Description

The endpoint to be analyzed is: Adj.cases for airflow obstruction

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	N
0.073	174	757
0.220	160	636
0.280	124	432

The 'Value for CES' is set to 0.01492281.

Extended dose range is not applied.

Informative background prior: min: 0.22755614; the most likely; 0.22985469; max: 0.23215324. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 2.15e+00).

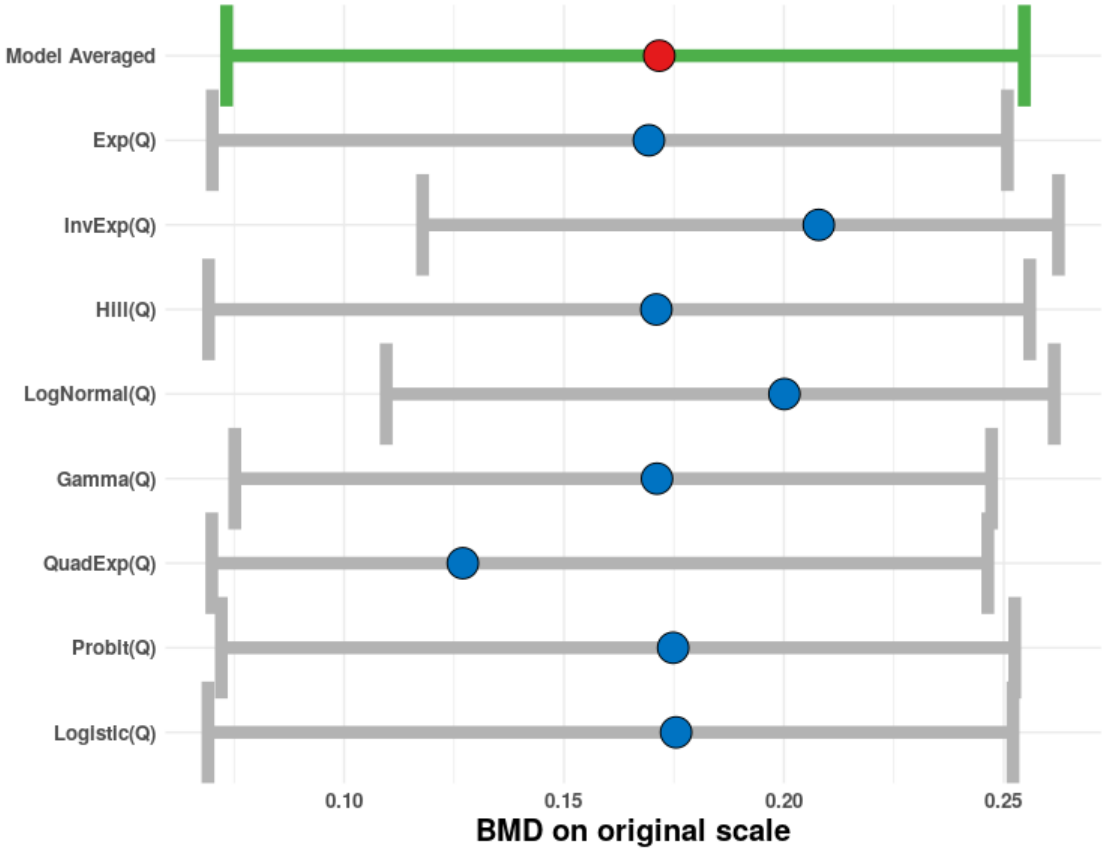
Model Averaged BMD

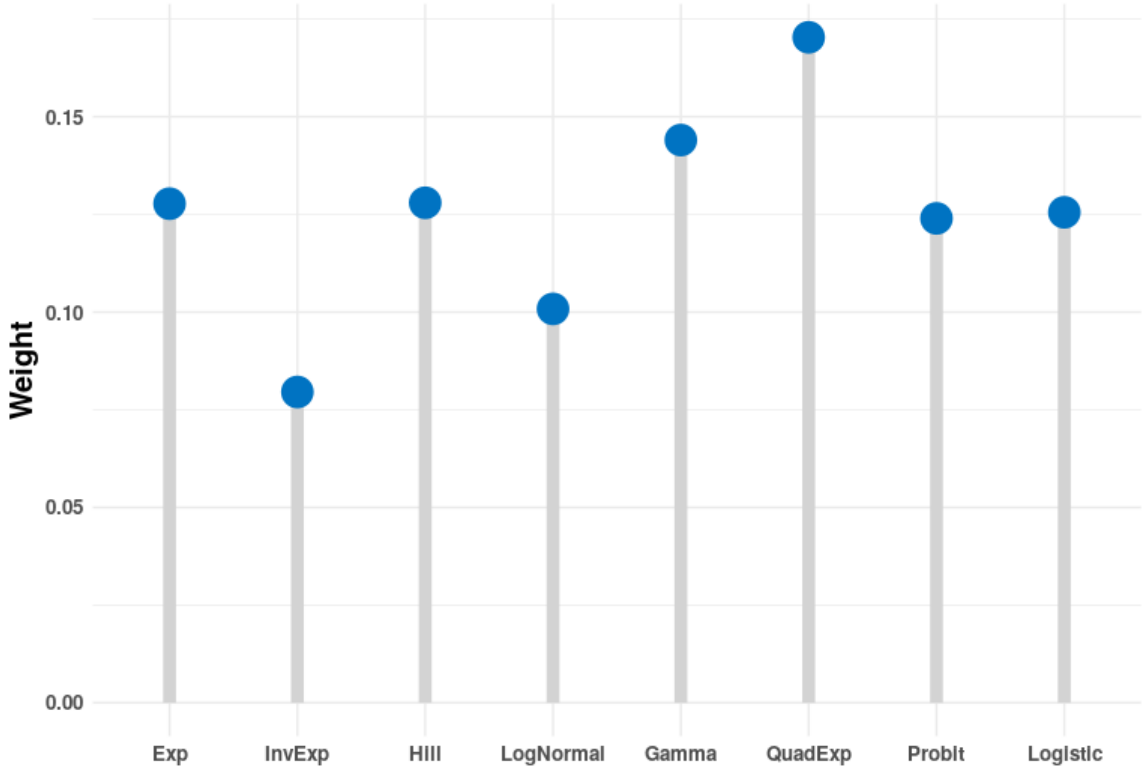
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.073	0.172	0.255

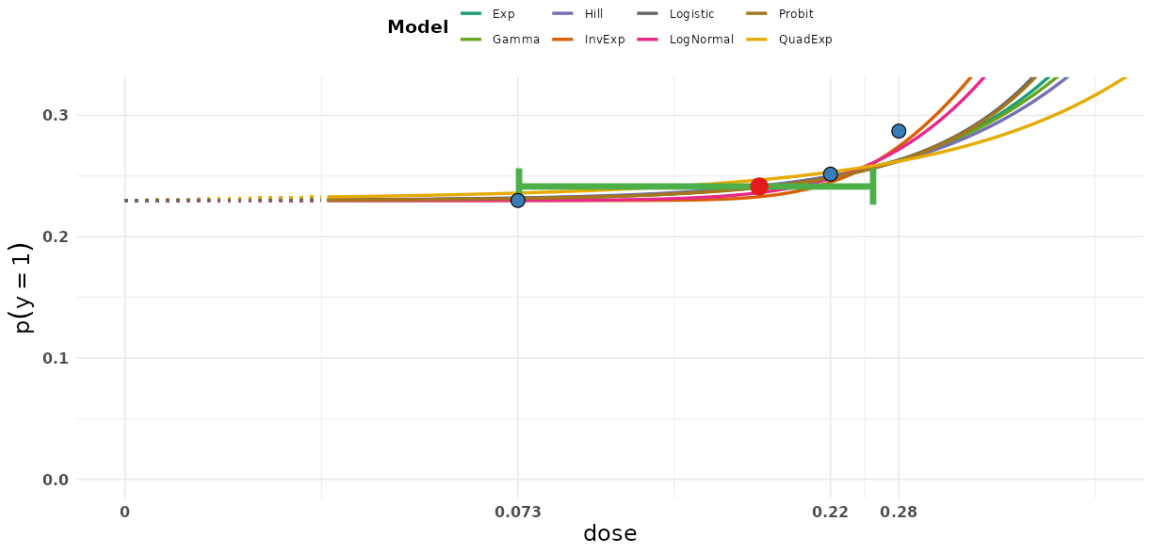
Estimated BMDs per model

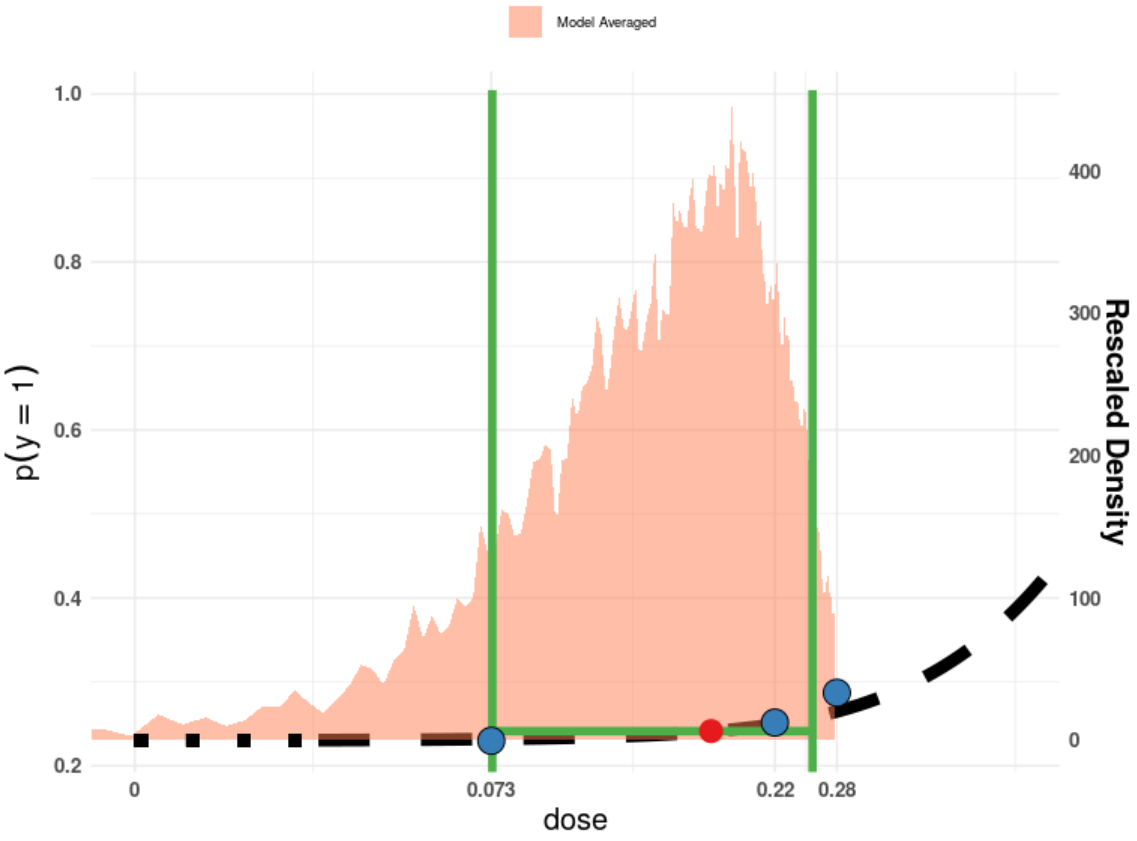
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.070	0.169	0.251	0.128	1
IE4_Q	0.118	0.208	0.262	0.080	1
H4_Q	0.069	0.171	0.256	0.128	1
LN4_Q	0.110	0.200	0.261	0.101	1
G4_Q	0.075	0.171	0.247	0.144	1
QE4_Q	0.070	0.127	0.246	0.170	1
P4_Q	0.072	0.175	0.252	0.124	1
L4_Q	0.069	0.175	0.252	0.126	1

Plots of Fitted Models




Weight
0.15
0.10
0.05
0.00
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
p(y = 1)
0.3
0.2
0.1
0.0
0
0.073
0.22
0.28
dose


Model Averaged
1.0
0.8
0.6
0.4
0.2
p(y = 1)
400
300
200
100
0
Rescaled Density
0
0.073
0.22
0.28
dose

Powers et al. (2019) emphysema, relative BMR 5%

Data Description

The endpoint to be analyzed is: Adj.cases for emphysema

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	N
0.073	26	880
0.220	25	718
0.280	27	518

The 'Value for CES' is set to 0.00152225.

Extended dose range is not applied.

Informative background prior: min: 0.02925000; the most likely: 0.02954545; max: 0.02984091. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 2.44e+00).

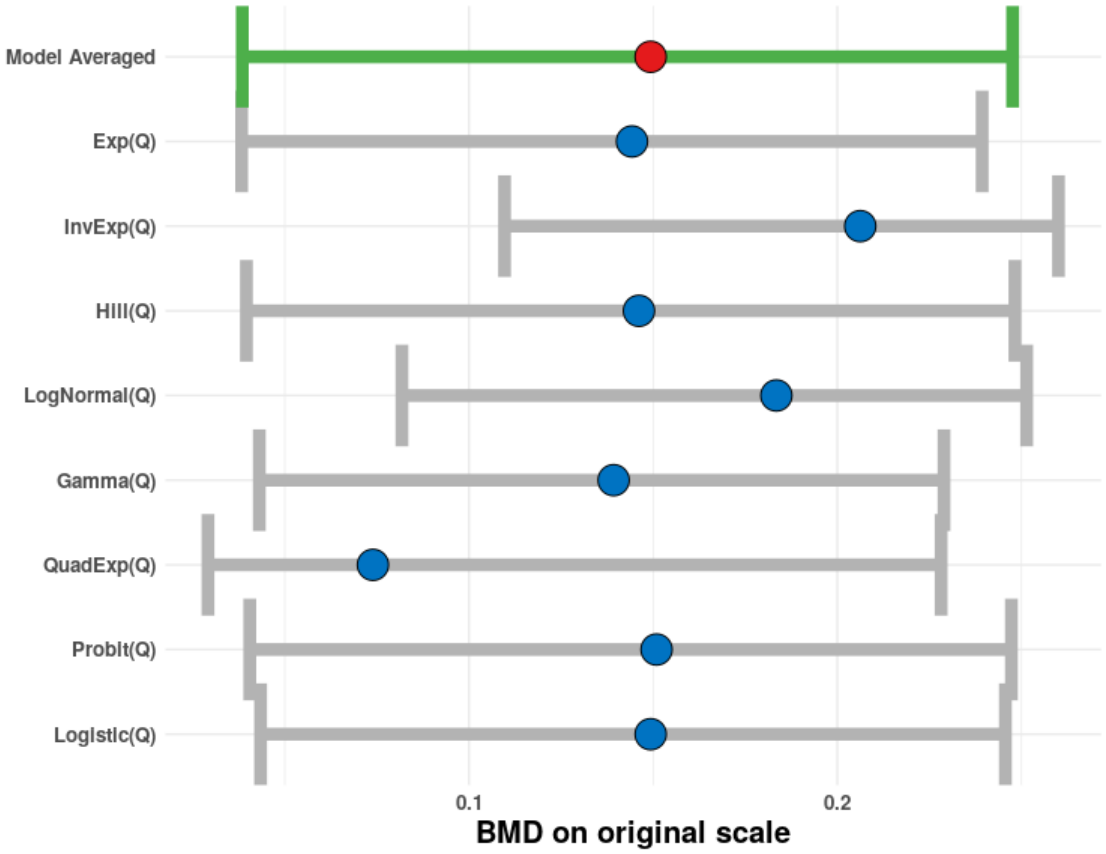
Model Averaged BMD

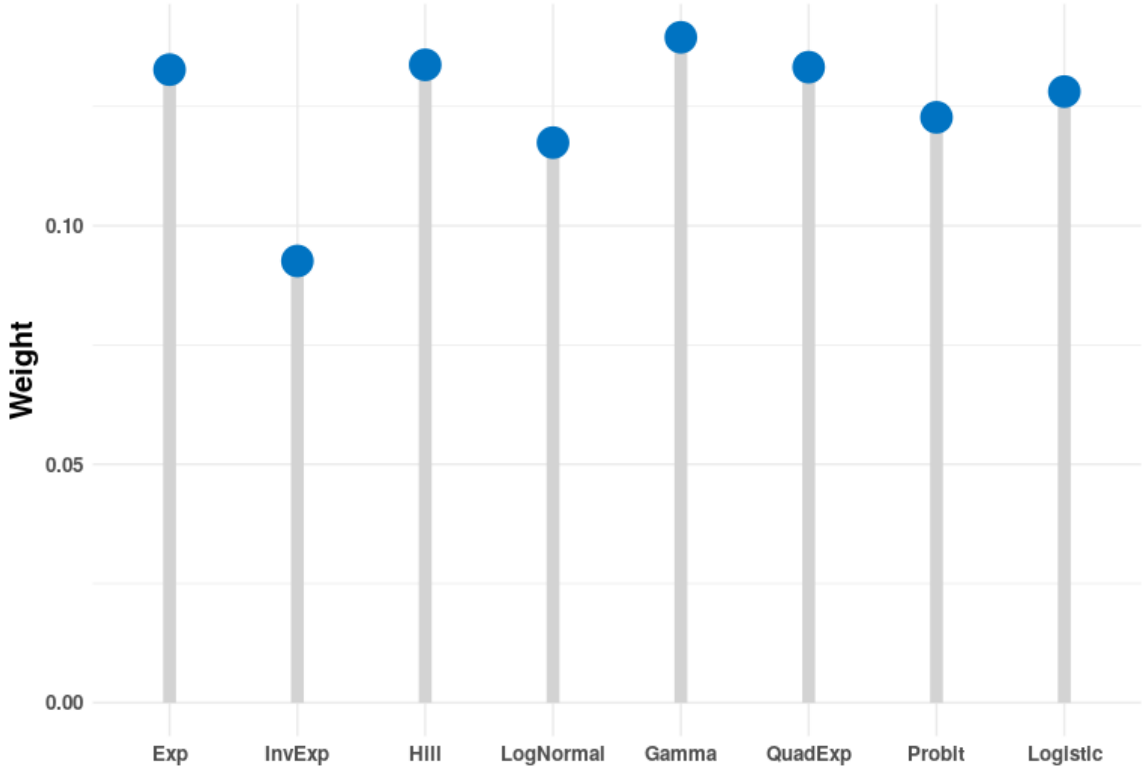
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.038	0.149	0.248

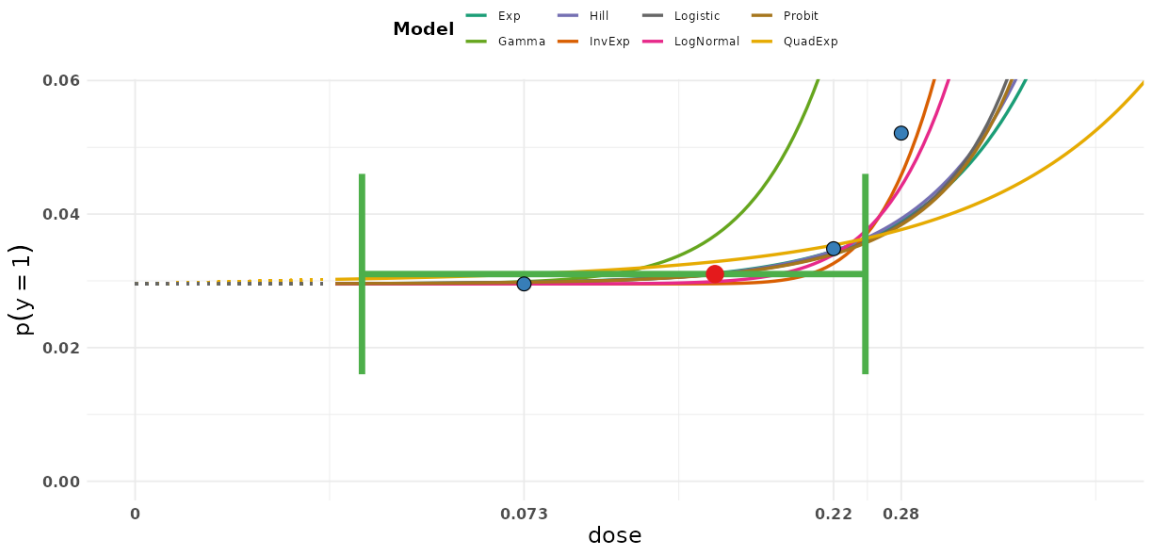
Estimated BMDs per model

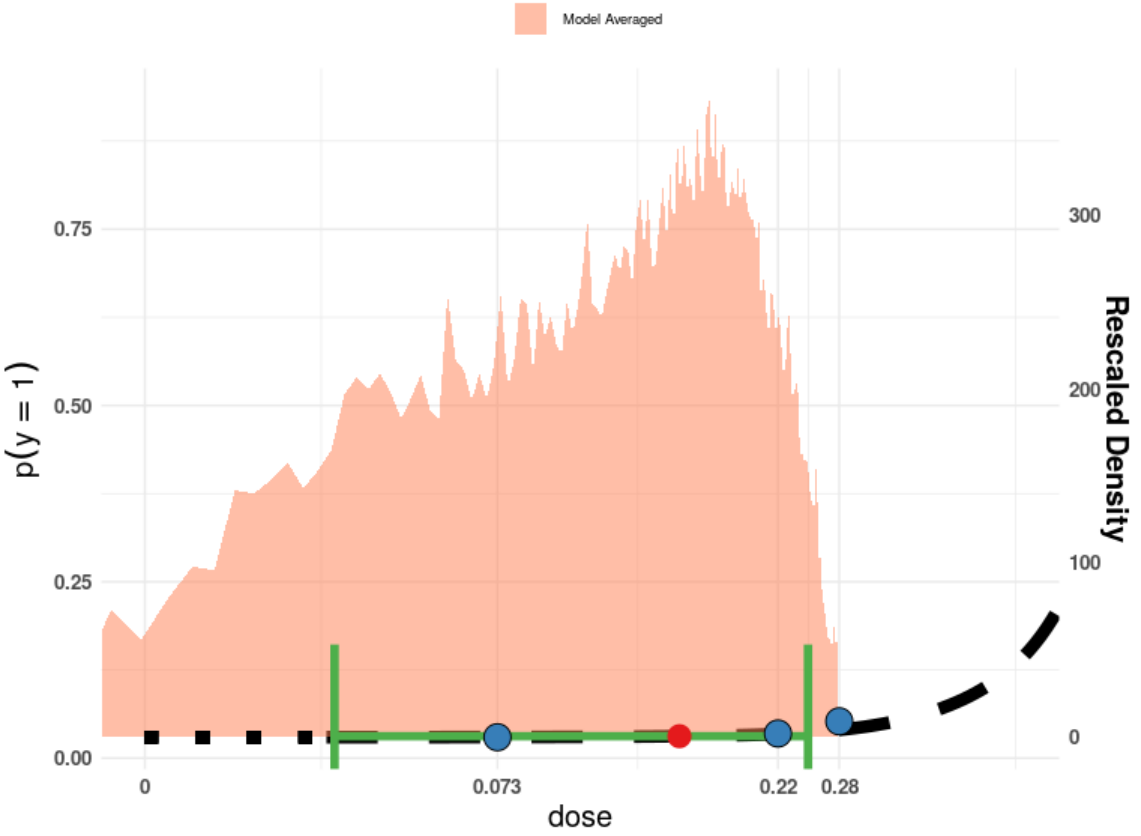
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.038	0.144	0.239	0.133	1
IE4_Q	0.110	0.206	0.260	0.093	1
H4_Q	0.040	0.146	0.248	0.134	1
LN4_Q	0.082	0.183	0.251	0.117	1
G4_Q	0.043	0.139	0.229	0.139	1
QE4_Q	0.029	0.074	0.228	0.133	1
P4_Q	0.040	0.151	0.247	0.123	1
L4_Q	0.043	0.149	0.246	0.128	1

Plots of Fitted Models




Weight
0.10
0.05
0.00
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
0.06
0.04
0.02
0.00
p(y = 1)
0
0.073
0.22
0.28
dose


Model Averaged
p(y = 1)
0.75
0.50
0.25
0.00
300
200
100
0
Rescaled Density
0
0.073
0.22
0.28
dose

Powers et al. (2019) restrictive pattern, relative BMR 5%

Data Description

The endpoint to be analyzed is: Adj.cases for restrictive pattern

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	N
0.073	133	725
0.220	92	558
0.280	81	391

The 'Value for CES' is set to 0.01123311.

Extended dose range is not applied.

Informative background prior: min: 0.14675862; the most likely; 0.18344828; max: 0.22013793. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 3.63e+00).

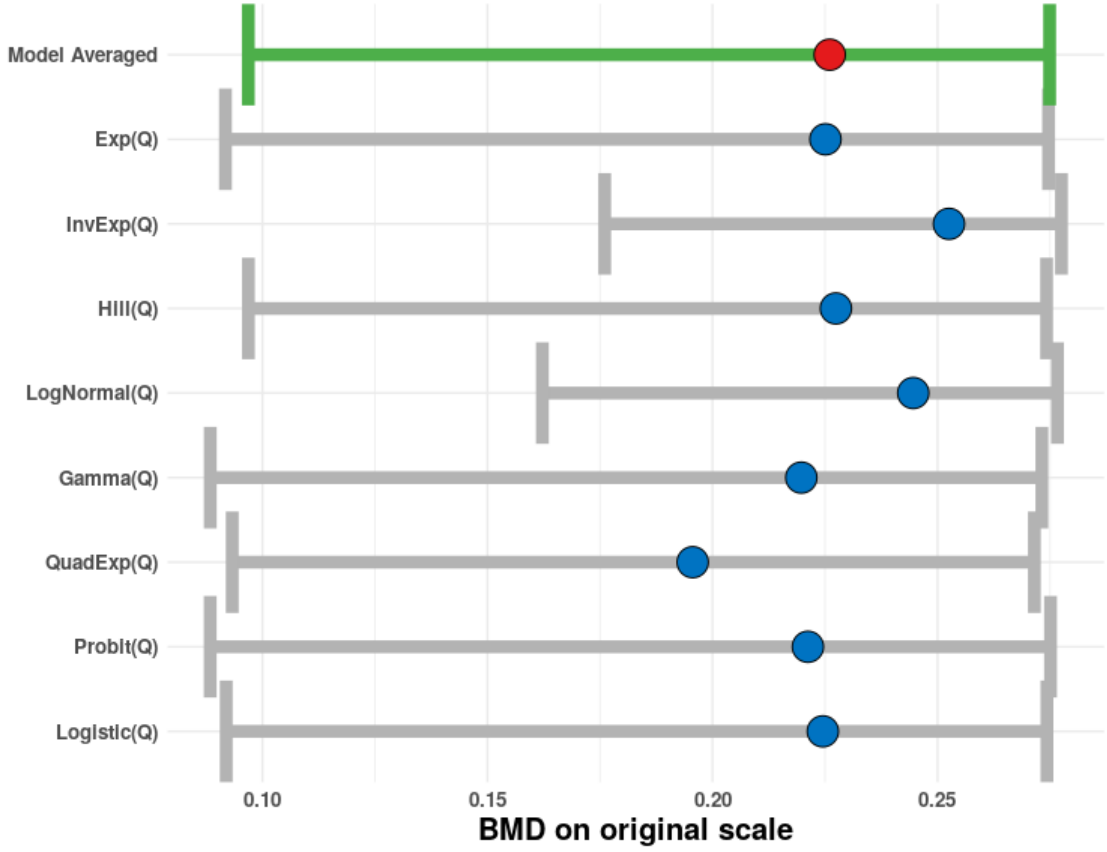
Model Averaged BMD

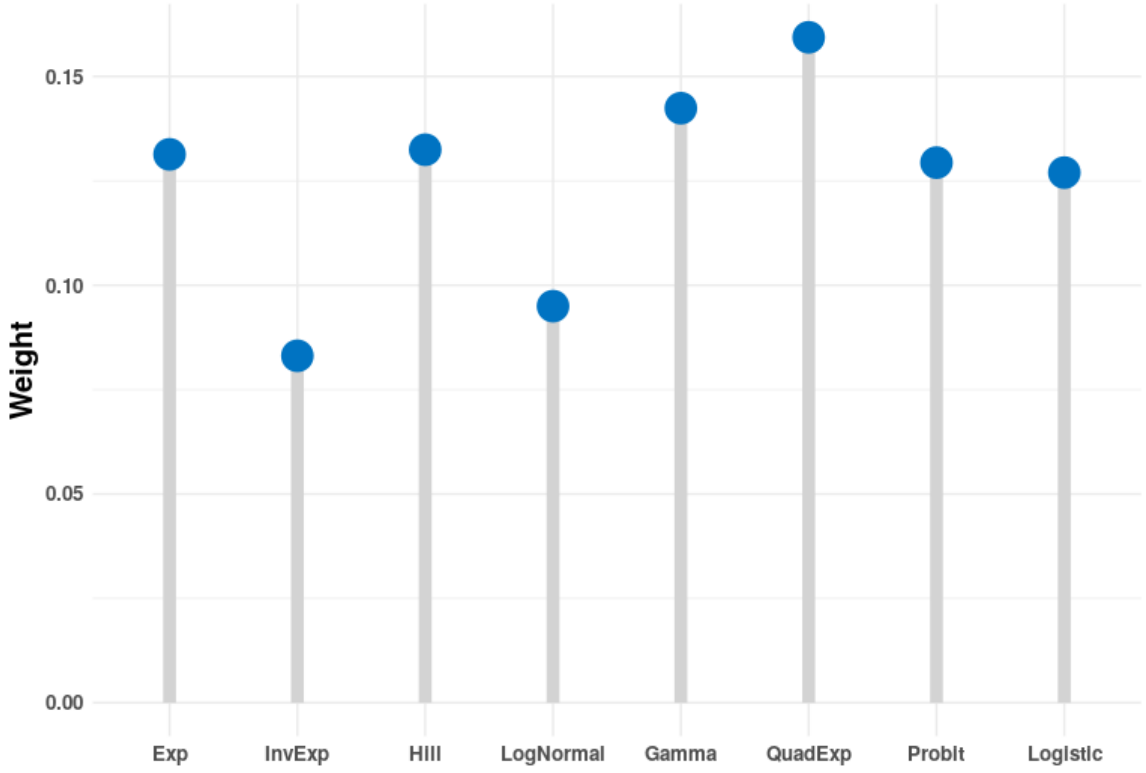
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.097	0.226	0.275

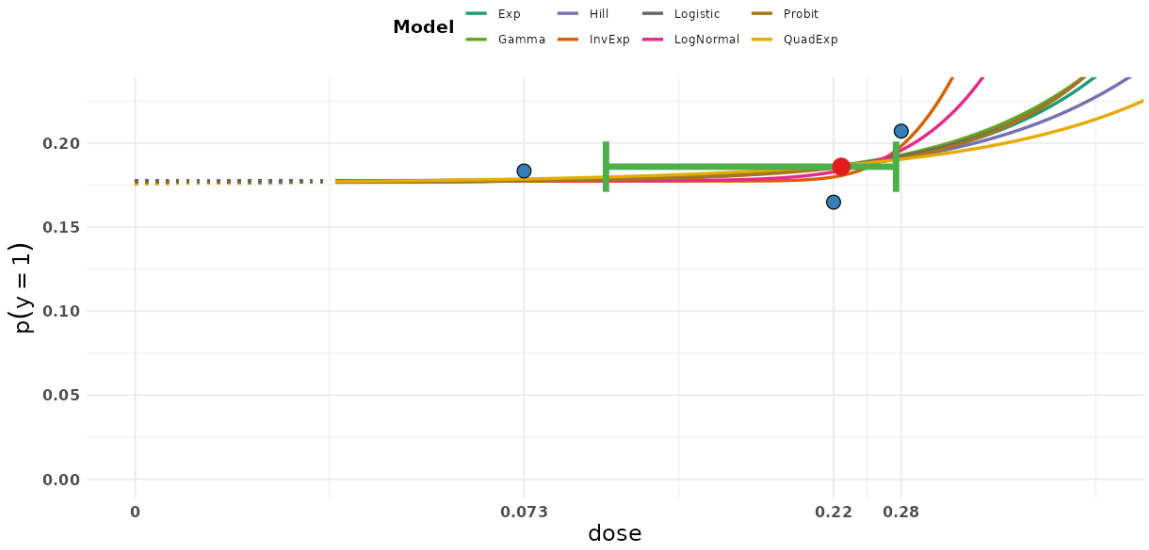
Estimated BMDs per model

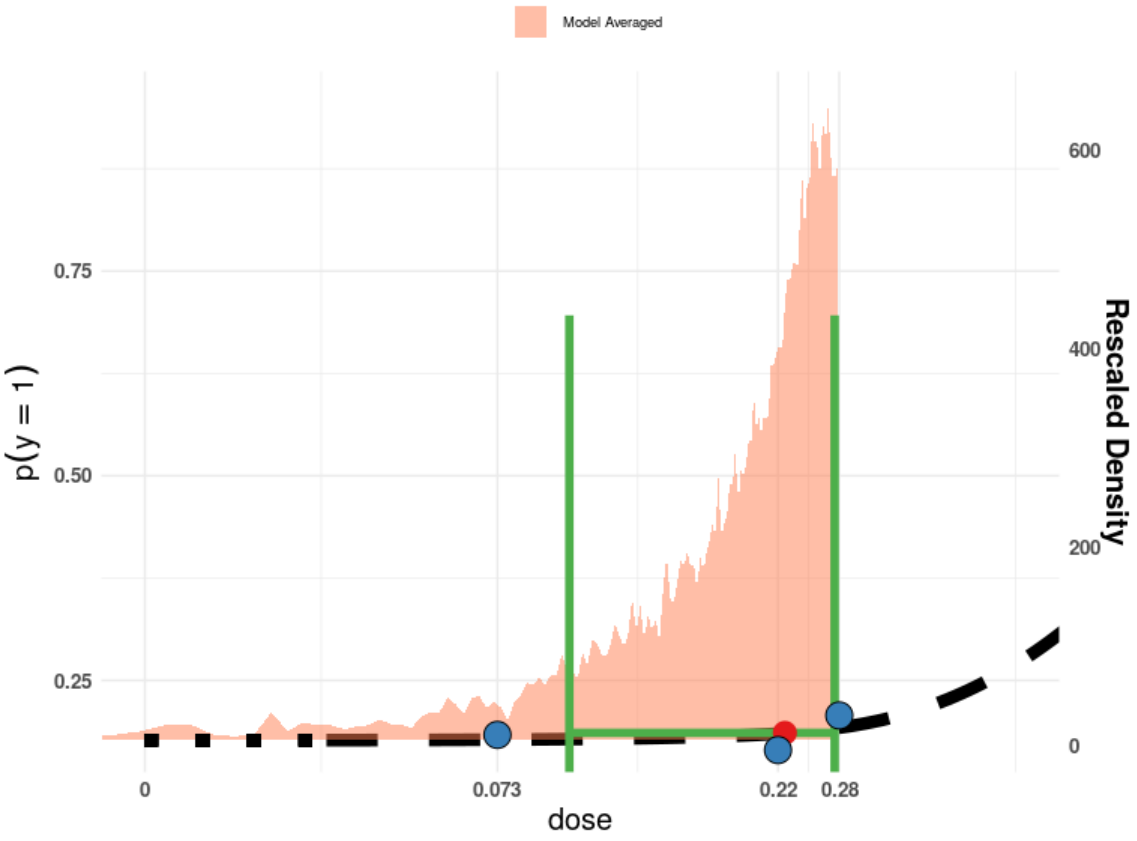
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.092	0.225	0.275	0.131	1
IE4_Q	0.176	0.253	0.278	0.083	1
H4_Q	0.097	0.227	0.274	0.132	1
LN4_Q	0.162	0.245	0.277	0.095	1
G4_Q	0.088	0.220	0.273	0.142	0
QE4_Q	0.093	0.196	0.272	0.159	1
P4_Q	0.088	0.221	0.275	0.129	1
L4_Q	0.092	0.225	0.274	0.127	1

Plots of Fitted Models




Weight
0.15
0.10
0.05
0.00
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
p(y = 1)
0.20
0.15
0.10
0.05
0.00
0
0.073
0.22
0.28
dose


Model Averaged
p(y = 1)
0.75
0.50
0.25
0
0.073
0.22
0.28
dose
600
400
200
0
Rescaled Density

Rahman et al. (2007) infant death, relative BMR 5%

Data Description

The endpoint to be analyzed is: Adj.cases for infant death

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	N
1.13	237	5119
6.47	267	5113
17.38	282	5122
25.75	306	5131
38.55	281	5109

The 'Value for CES' is set to 0.00242728.

Extended dose range is not applied.

Informative background prior: min: 0.04583512; the most likely: 0.04629811; max: 0.04676109. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 1.40e-03).

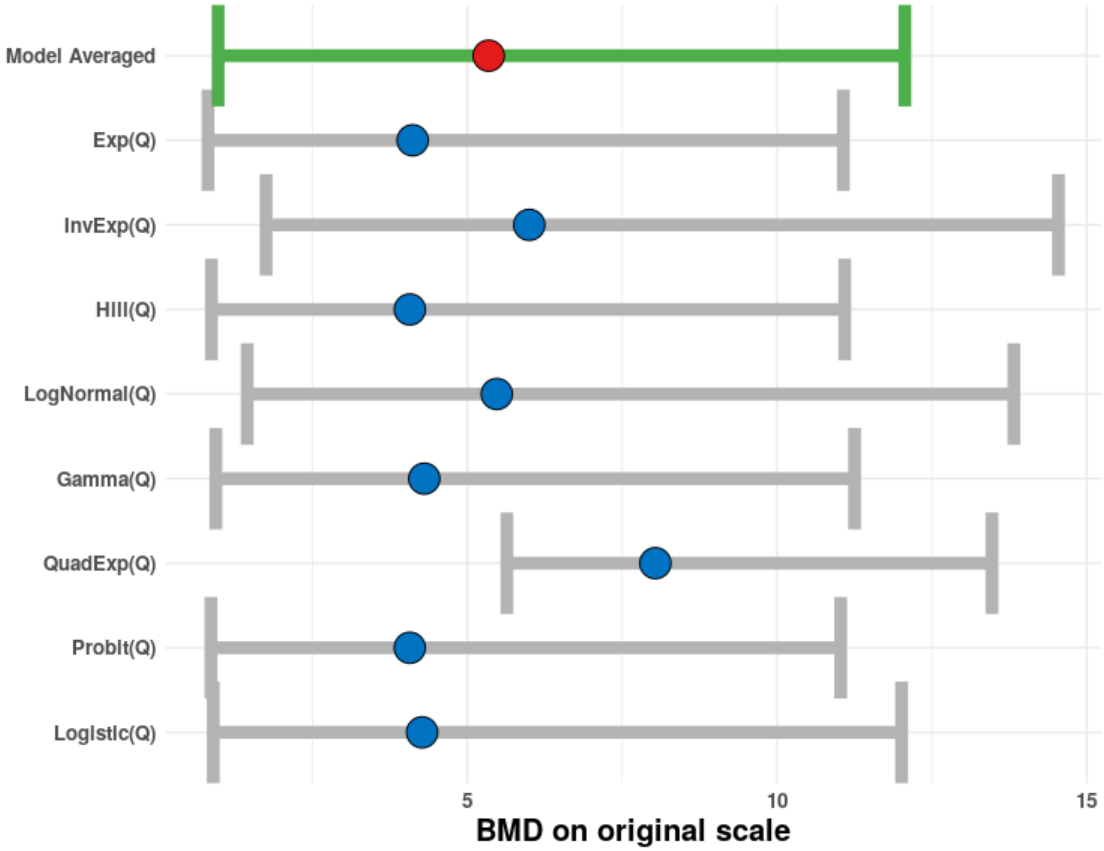
Model Averaged BMD

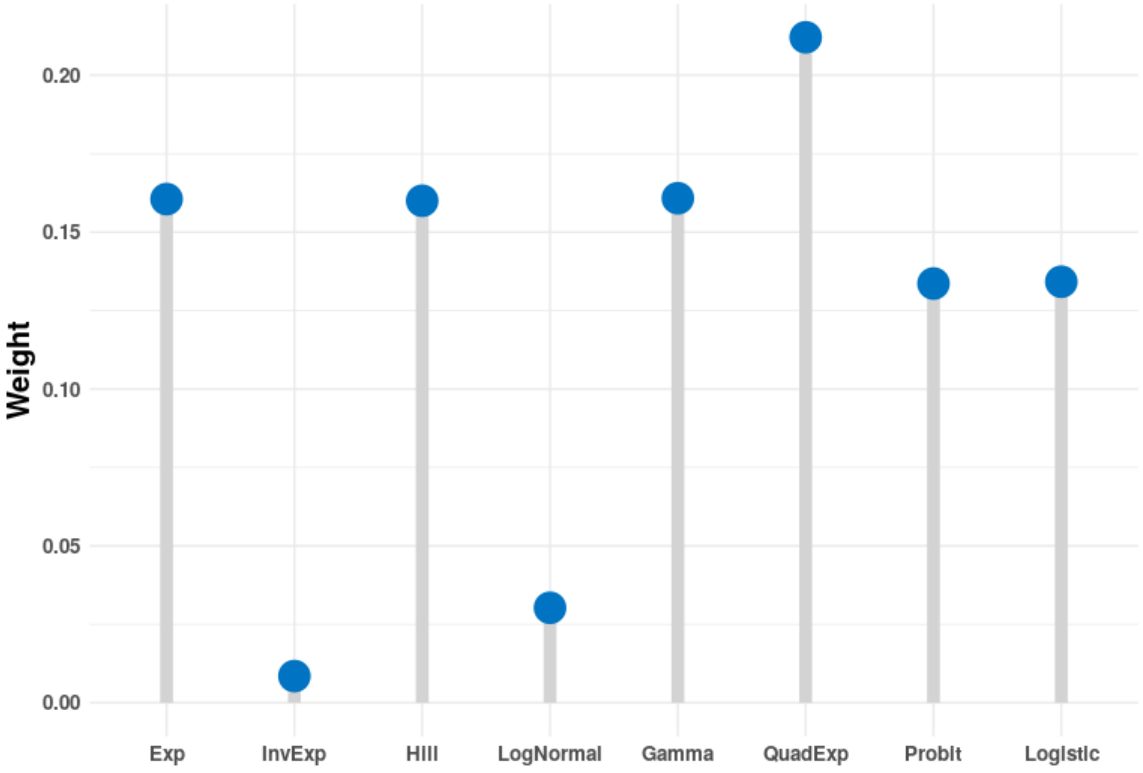
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.975	5.343	12.063

Estimated BMDs per model

Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.811	4.116	11.069	0.161	1
IE4_Q	1.749	5.998	14.543	0.008	1
H4_Q	0.866	4.071	11.093	0.160	1
LN4_Q	1.444	5.474	13.823	0.030	1
G4_Q	0.939	4.303	11.251	0.161	1
QE4_Q	5.638	8.034	13.470	0.212	1
P4_Q	0.858	4.070	11.026	0.134	1
L4_Q	0.896	4.268	12.011	0.134	1

Plots of Fitted Models




Weight
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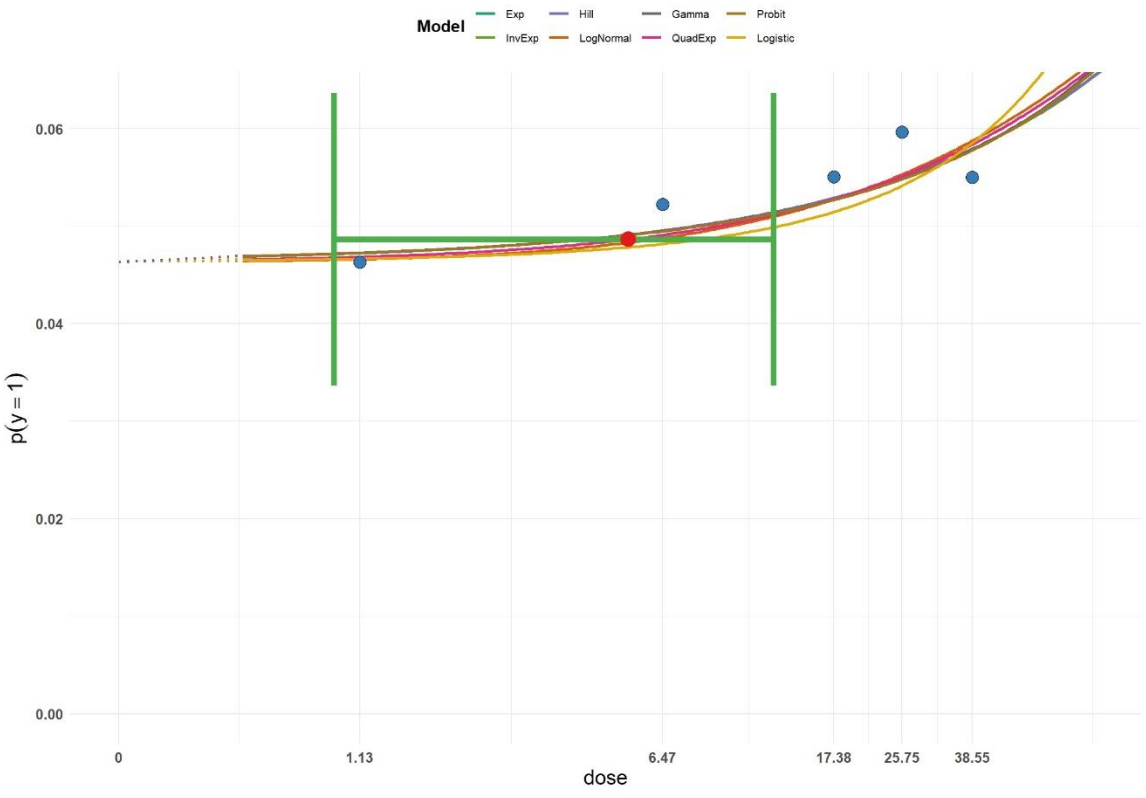
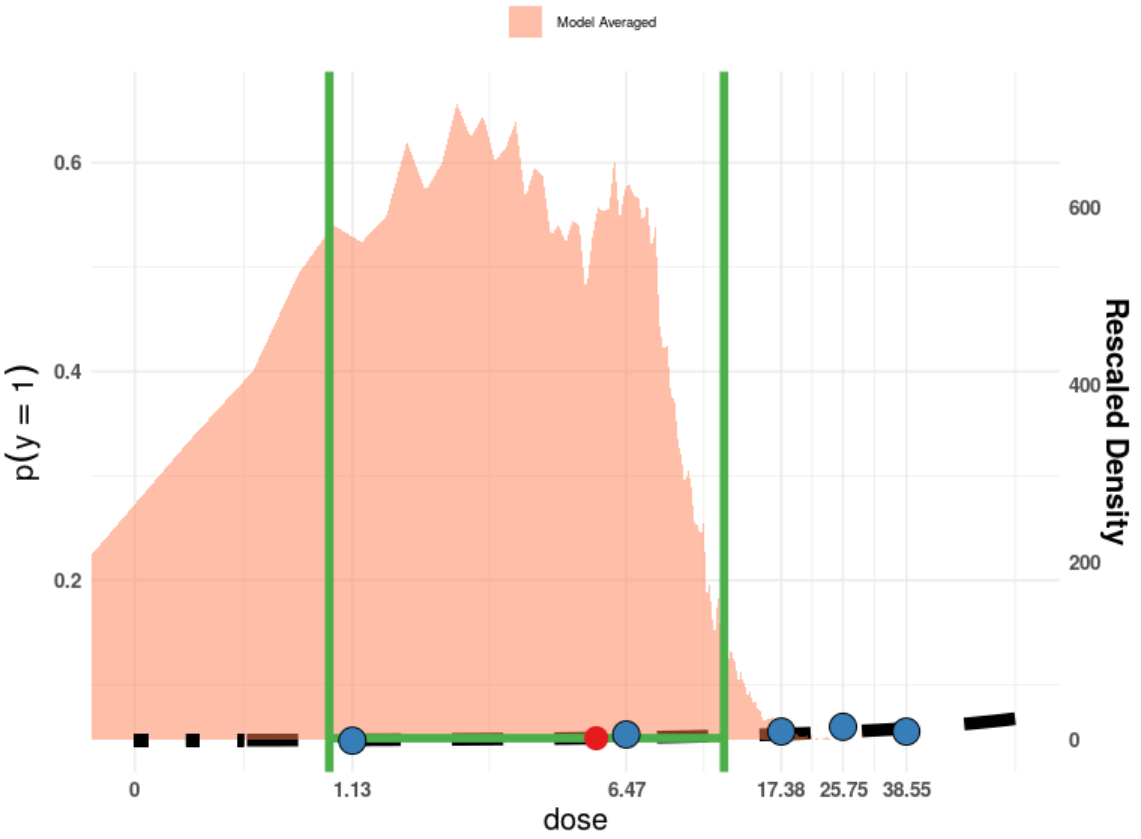
0.15
0.10
0.05
0.00
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic
p(y = 1)
0.06
0.04
0.02
0.00
0
1.13
6.47
17.38
25.75
38.55
dose


Model Averaged
p(y = 1)
0.6
0.4
0.2
600
400
200
0
Rescaled Density
0
1.13
6.47
17.38
25.75
38.55
dose

Rahman et al. (2010) infant mortality, relative BMR 5%

Data Description

The endpoint to be analyzed is: Adj.cases for infant mortality

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	N
1.09	3	338
1.82	5	342
3.42	6	339
6.87	7	335
14.18	15	339

The 'Value for CES' is set to 0.000447761.

Extended dose range is not applied.

Informative background prior: min: 0.008786982; the most likely: 0.00887574; max: 0.008964497. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

The results do not fulfill the EFSA BMD guidance (EFSA Scientific Committee, 2022) recommendations since BMDU/BMDL > 50.

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 8.13e-04).

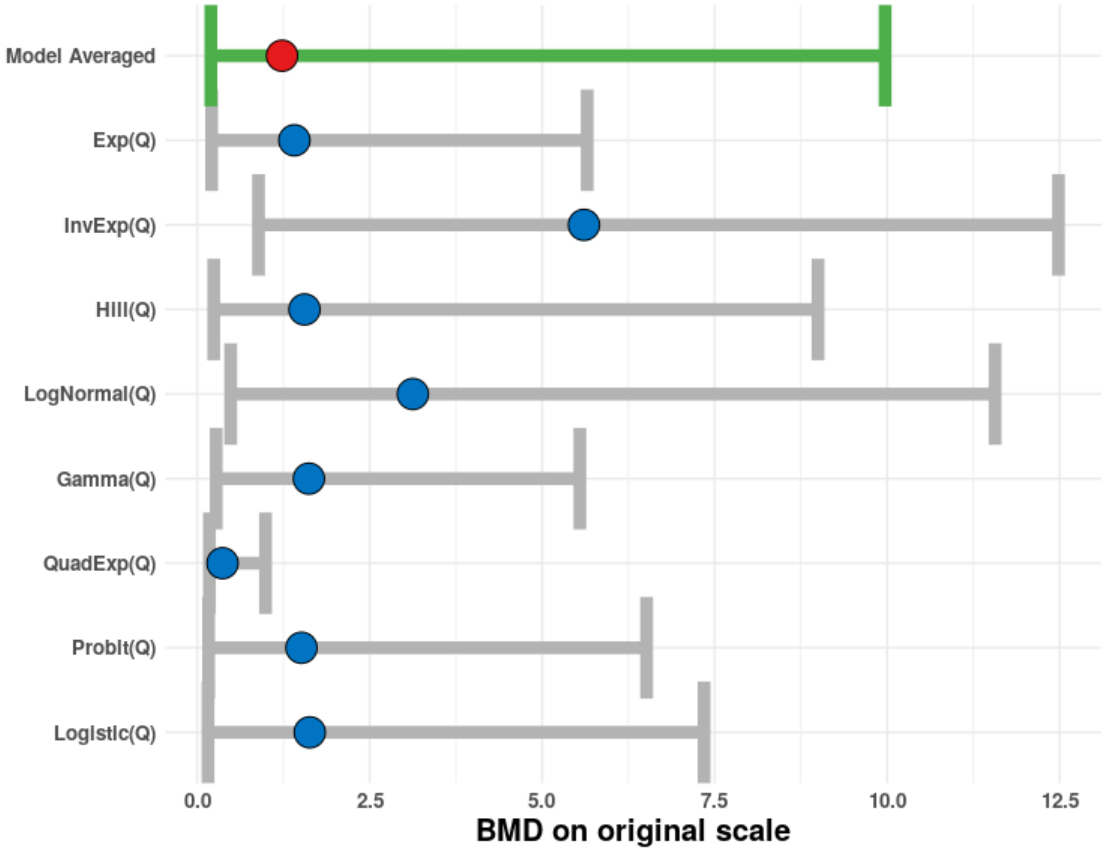
Model Averaged BMD

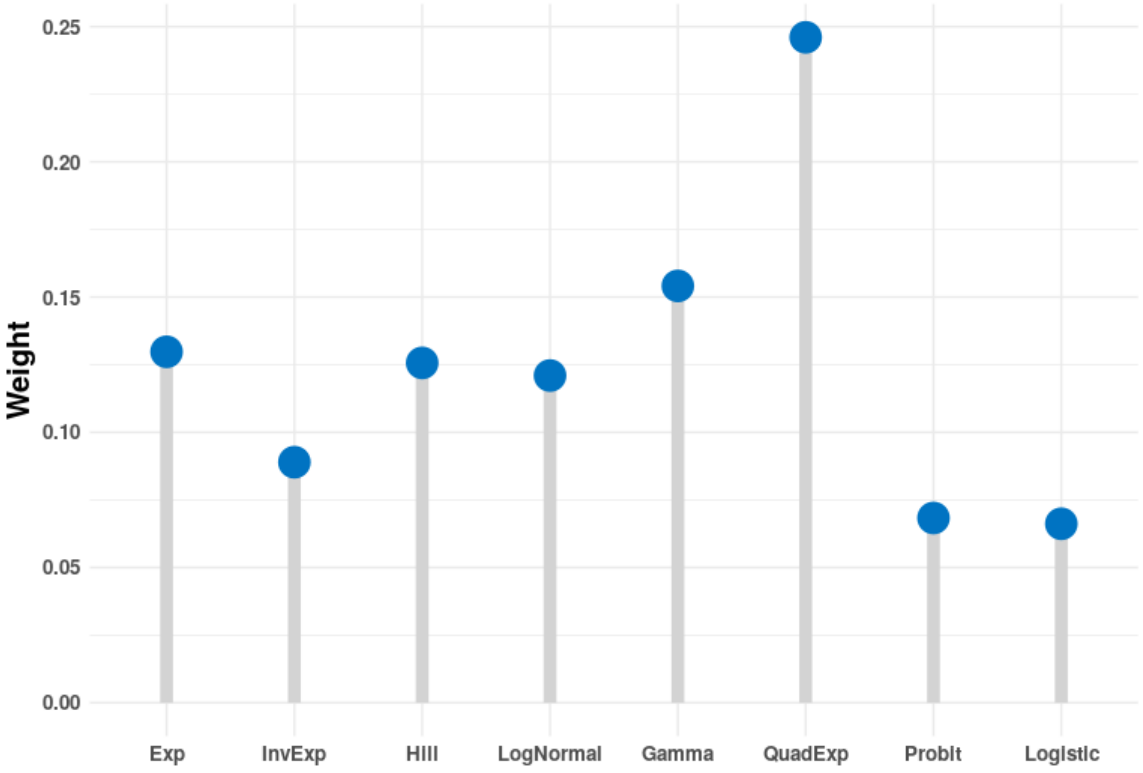
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.198	1.23	9.97

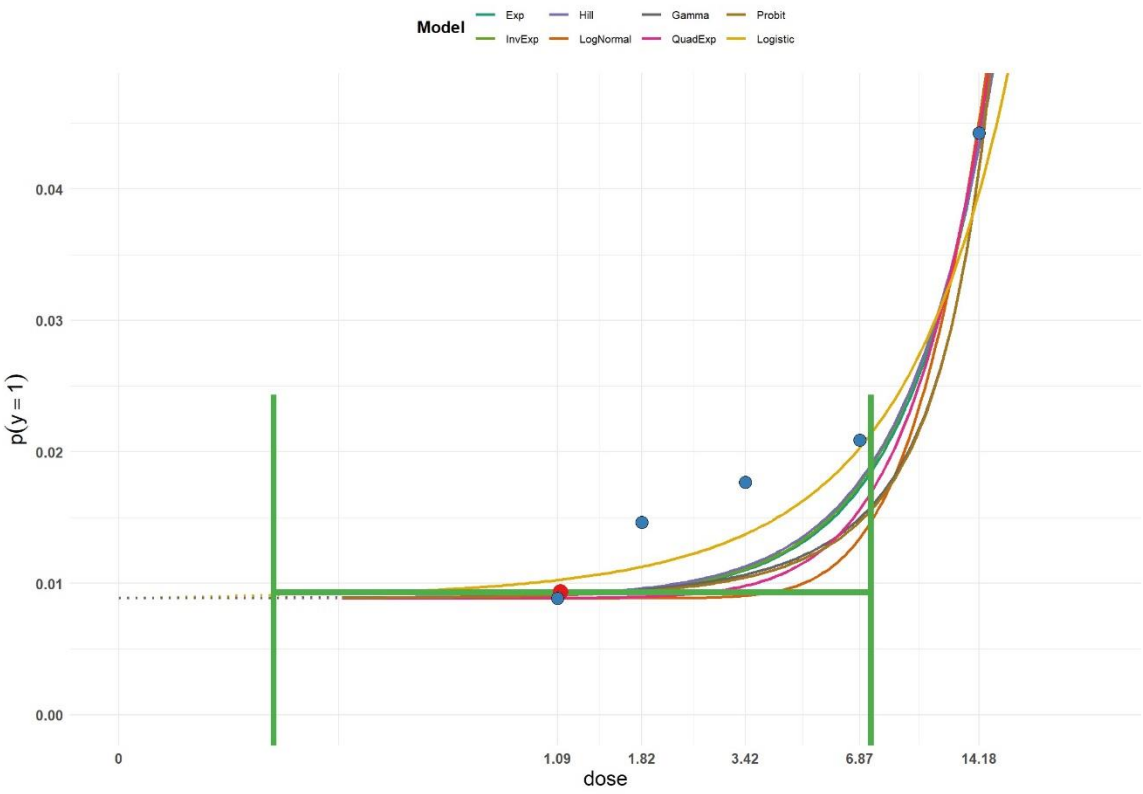
Estimated BMDs per model

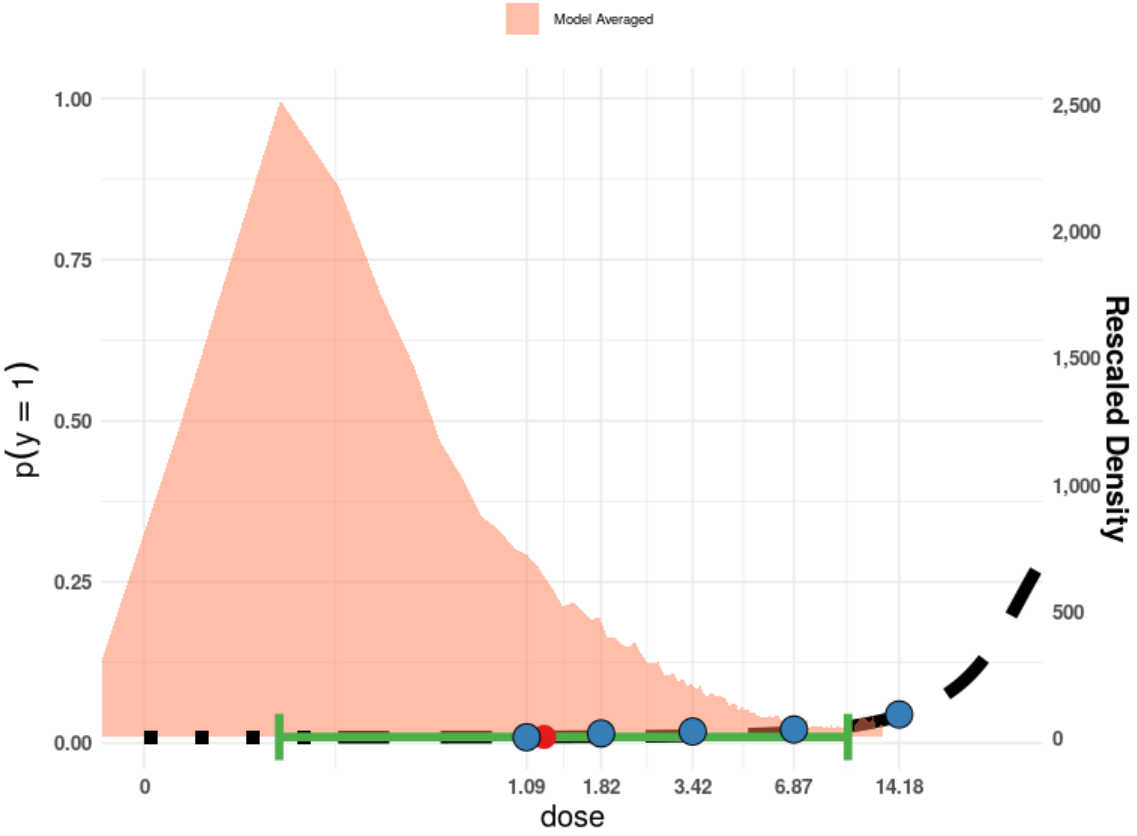
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.209	1.409	5.652	0.130	1
IE4_Q	0.889	5.605	12.483	0.089	0
H4_Q	0.240	1.556	8.998	0.126	0
LN4_Q	0.486	3.126	11.564	0.121	1
G4_Q	0.276	1.619	5.546	0.154	1
QE4_Q	0.177	0.367	0.990	0.246	1
P4_Q	0.165	1.511	6.513	0.068	1
L4_Q	0.156	1.631	7.346	0.066	1

Plots of Fitted Models




Weight
0.25
0.20
0.15
0.10
0.05
0.00
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic
p(y = 1)
0.04
0.03
0.02
0.01
0.00
0
1.09
1.82
3.42
6.87
14.18
dose


Model Averaged
1.00
0.75
0.50
0.25
0.00
p(y = 1)
2,500
2,000
1,500
1,000
500
0
Rescaled Density
0
1.09
1.82
3.42
6.87
14.18
dose

Rahman et al. (2010) spontaneous abortion, relative BMR 5%

Data Description

The endpoint to be analyzed is: Adj.cases for spontaneous abortion

Exposure.µg.kg.bw.per.day	Adj.cases	N
0.84	45	553
1.53	57	558
2.91	63	567
6.44	47	549
13.89	63	557

The 'Value for CES' is set to 0.004429134.

Extended dose range is not applied.

Informative background prior: min: 0.080560579; the most likely: 0.081374322; max: 0.082188065. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

The study was rejected following visual screening due to the non-monotonic dose-response seen.

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 1.81e-02).

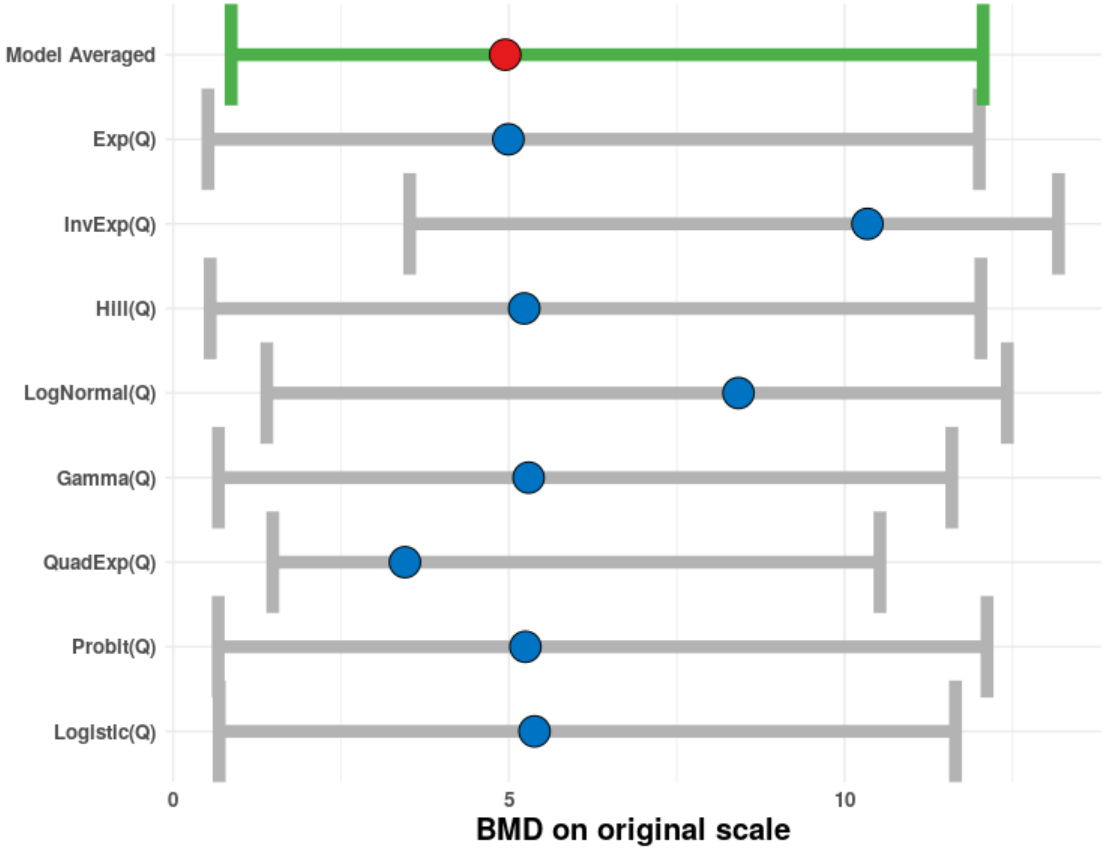
Model Averaged BMD

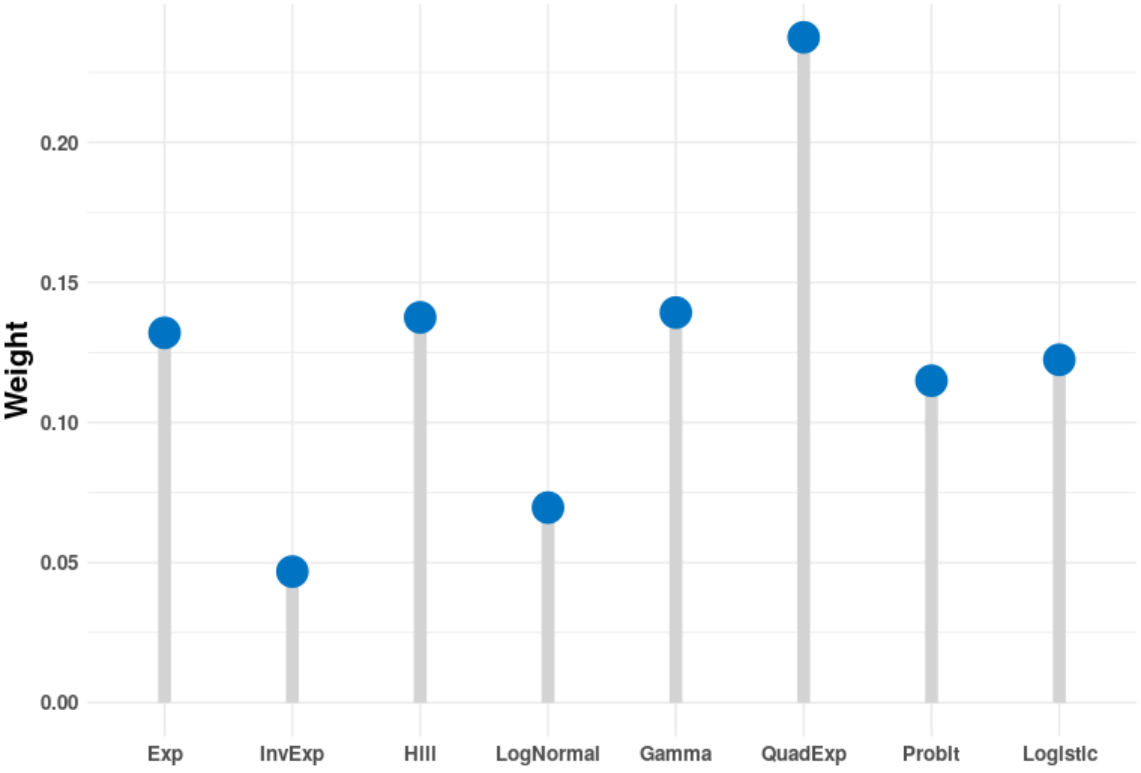
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.864	4.946	12.064

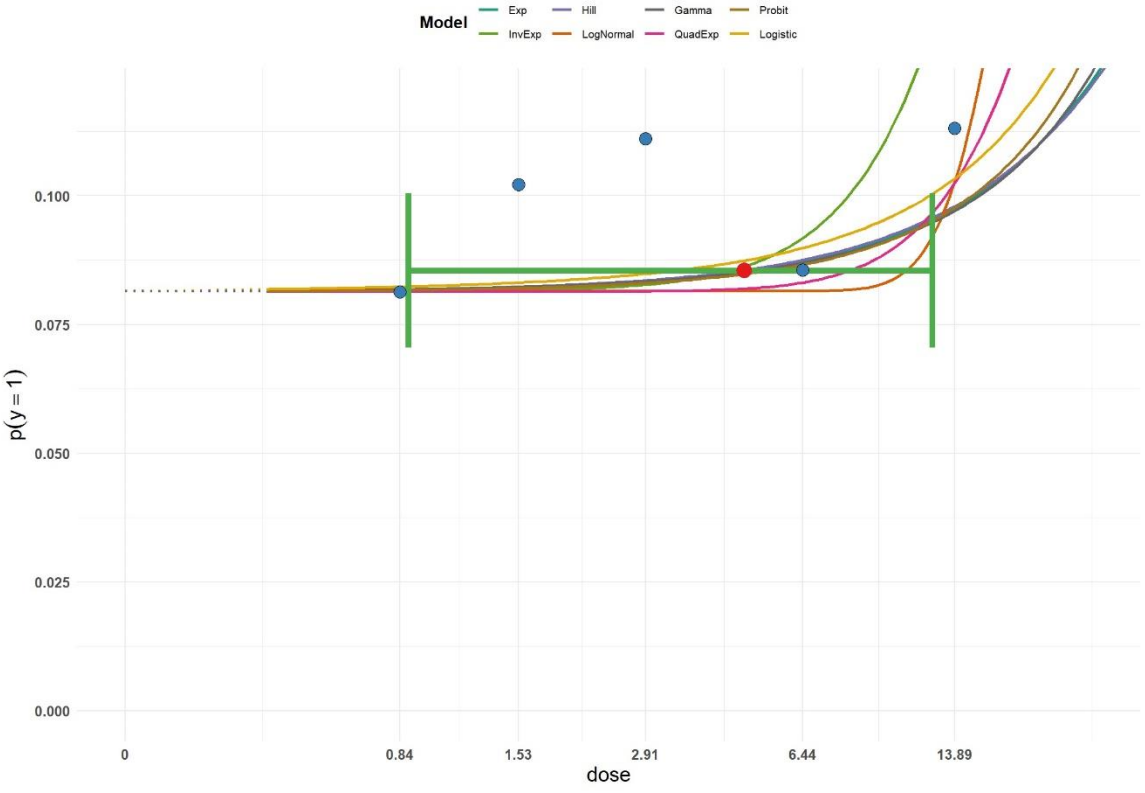
Estimated BMDs per model

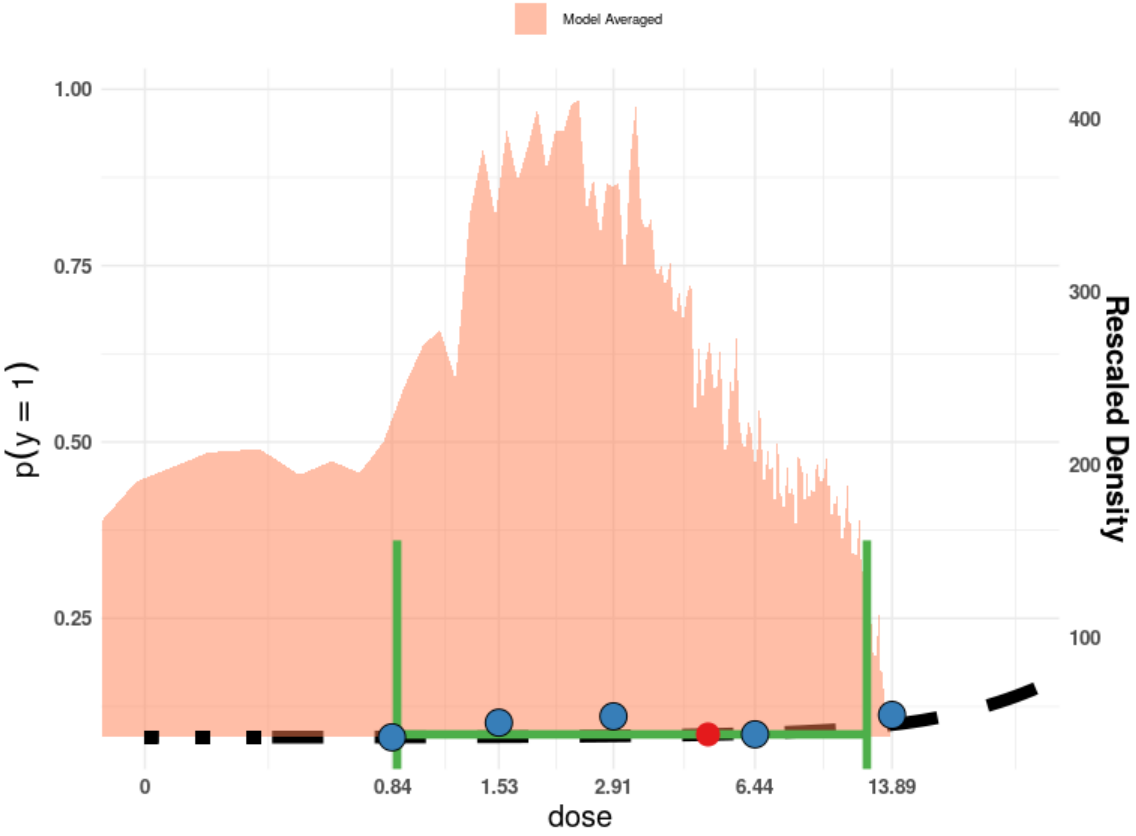
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.519	4.993	12.007	0.132	1
IE4_Q	3.523	10.341	13.186	0.047	1
H4_Q	0.552	5.229	12.030	0.138	1
LN4_Q	1.396	8.420	12.424	0.070	1
G4_Q	0.675	5.295	11.598	0.139	1
QE4_Q	1.484	3.452	10.527	0.237	1
P4_Q	0.672	5.246	12.122	0.115	1
L4_Q	0.686	5.383	11.652	0.122	1

Plots of Fitted Models




Weight
0.20
0.15
0.10
0.05
0.00
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic
p(y = 1)
0.100
0.075
0.050
0.025
0.000
0
0.84
1.53
2.91
6.44
13.89
dose


Model Averaged
1.00
0.75
0.50
0.25
p(y = 1)
400
300
200
100
Rescaled Density
0
0.84
1.53
2.91
6.44
13.89
dose

Rahman et al. (2010) stillbirth, relative BMR 5%

Data Description

The endpoint to be analyzed is: Adj.cases for stillbirth

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	N
1.09	3	341
1.82	6	348
3.42	7	346
6.87	10	345
14.18	6	345

The 'Value for CES' is set to 0.000443787.

Extended dose range is not applied.

Informative background prior: min: 0.008709677; the most likely; 0.008797654; max: 0.00888563. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

The results do not fulfill the EFSA BMD guidance (2022) recommendations since BMDU/BMDL > 50.

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 3.38e-02).

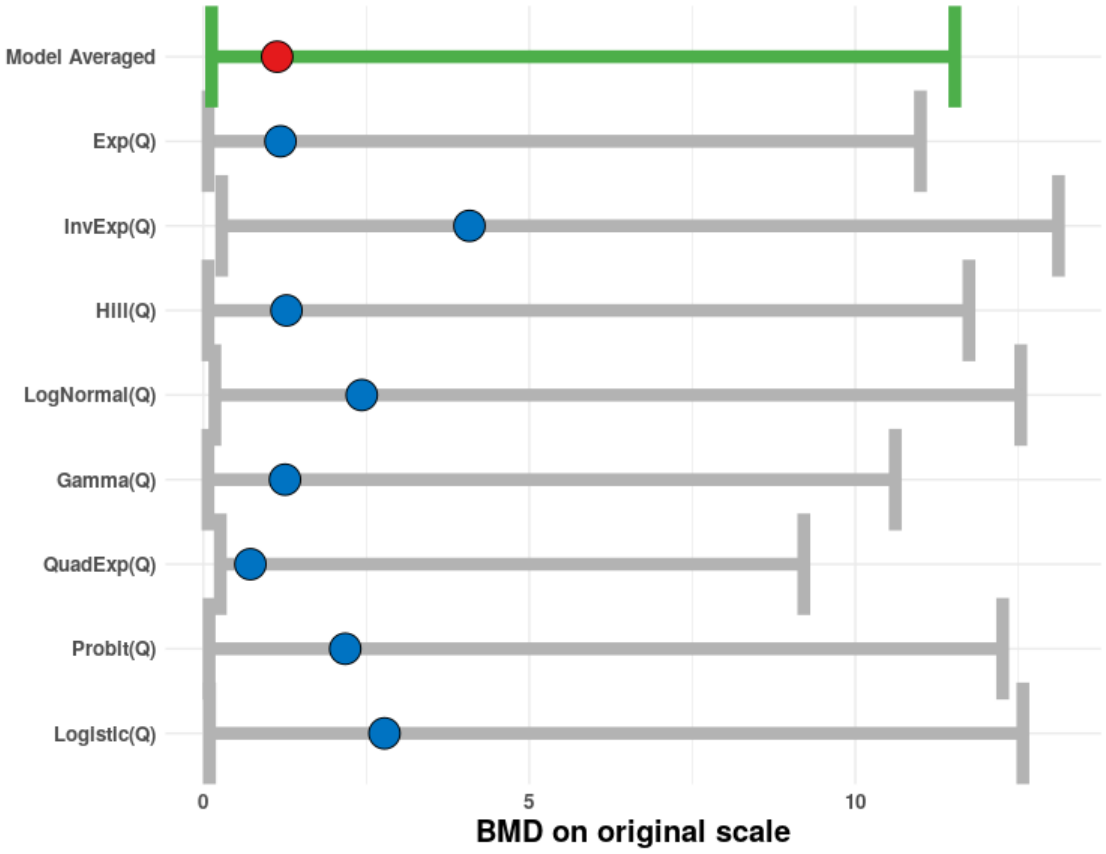
Model Averaged BMD

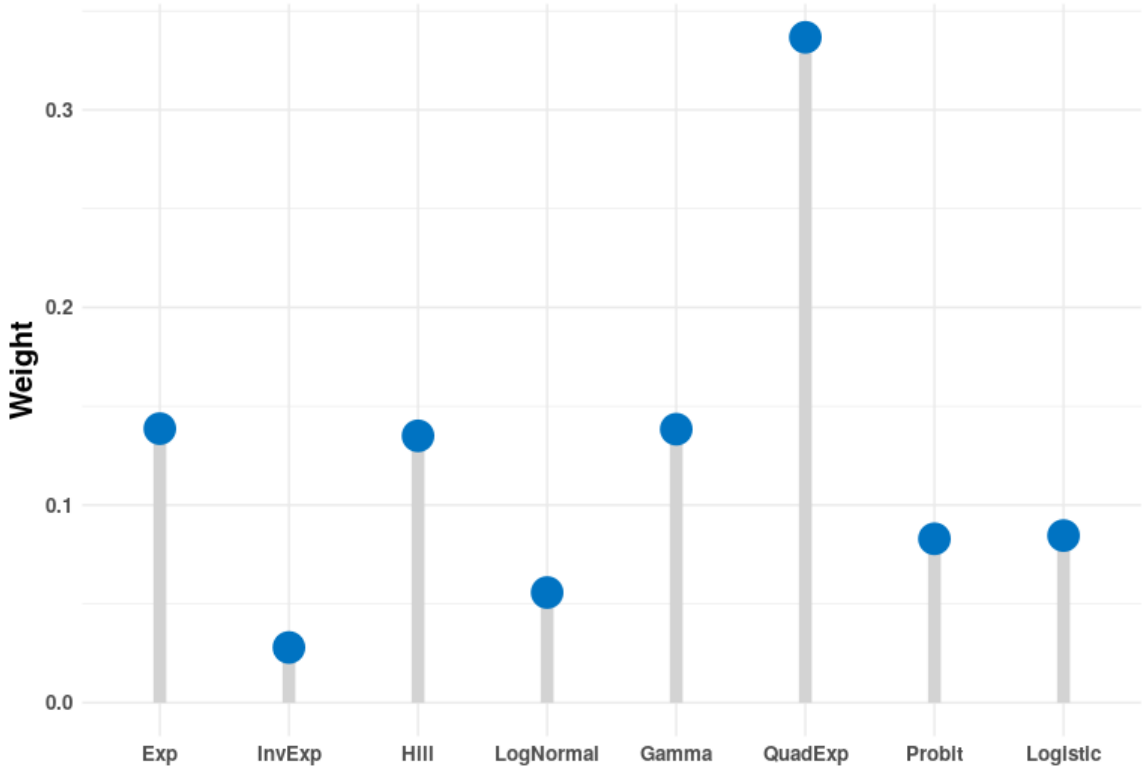
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.126	1.132	11.527

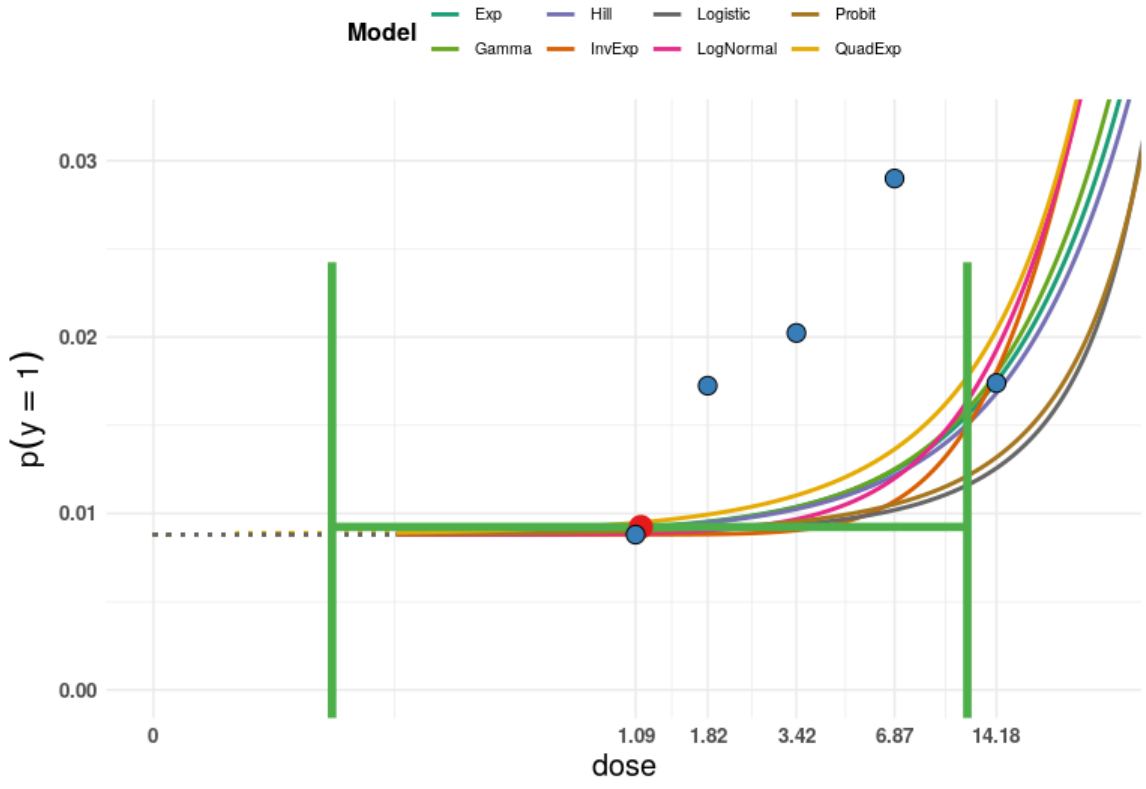
Estimated BMDs per model

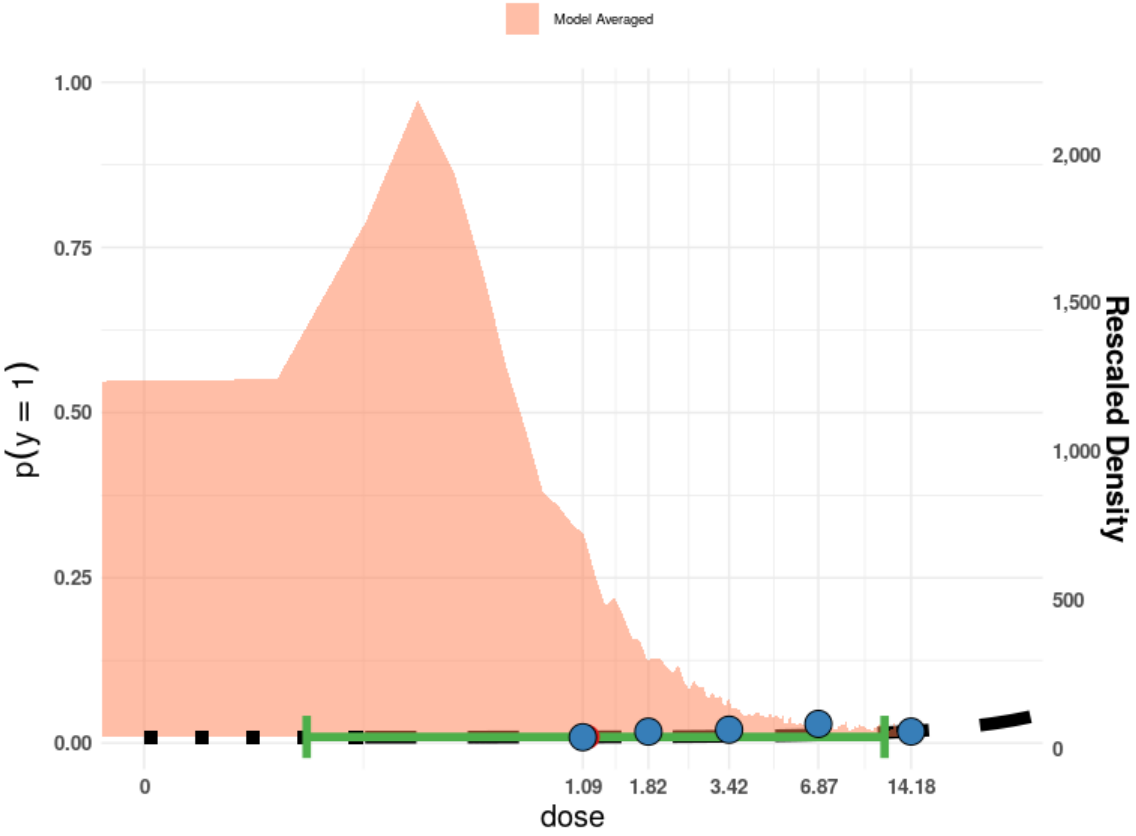
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.072	1.183	10.999	0.139	1
IE4_Q	0.281	4.081	13.116	0.028	0
H4_Q	0.072	1.275	11.743	0.135	1
LN4_Q	0.177	2.430	12.537	0.056	1
G4_Q	0.071	1.252	10.613	0.138	1
QE4_Q	0.260	0.721	9.210	0.337	1
P4_Q	0.088	2.176	12.260	0.083	1
L4_Q	0.095	2.778	12.570	0.085	1

Plots of Fitted Models




Weight
0.3
0.2
0.1
0.0
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
p(y = 1)
0.03
0.02
0.01
0.00
0
1.09
1.82
3.42
6.87
14.18
dose


Model Averaged
1.00
0.75
0.50
0.25
0.00
p(y = 1)
2,000
1,500
1,000
500
0
Rescaled Density
0
1.09
1.82
3.42
6.87
14.18
dose

Richter et al. (2022) congenital heart disease, relative BMR 5%

Data Description

The endpoint to be analyzed is: Adj.cases for congenital heart disease

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	N
0.12	4453	495970
0.13	2413	235630
0.17	3522	292222
0.22	239	18591

The 'Value for CES' is set to 0.000452985.

Extended dose range is not applied.

Informative background prior: min: 0.008888582; the most likely: 0.008978366; max: 0.009068149. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

The results do not fulfill the EFSA BMD guidance (2022) recommendations since none of the candidate models fit the data sufficiently well.

Goodness of Fit

None of the models provide an adequate fit do the data (Bayes factor is 8.00e+04).

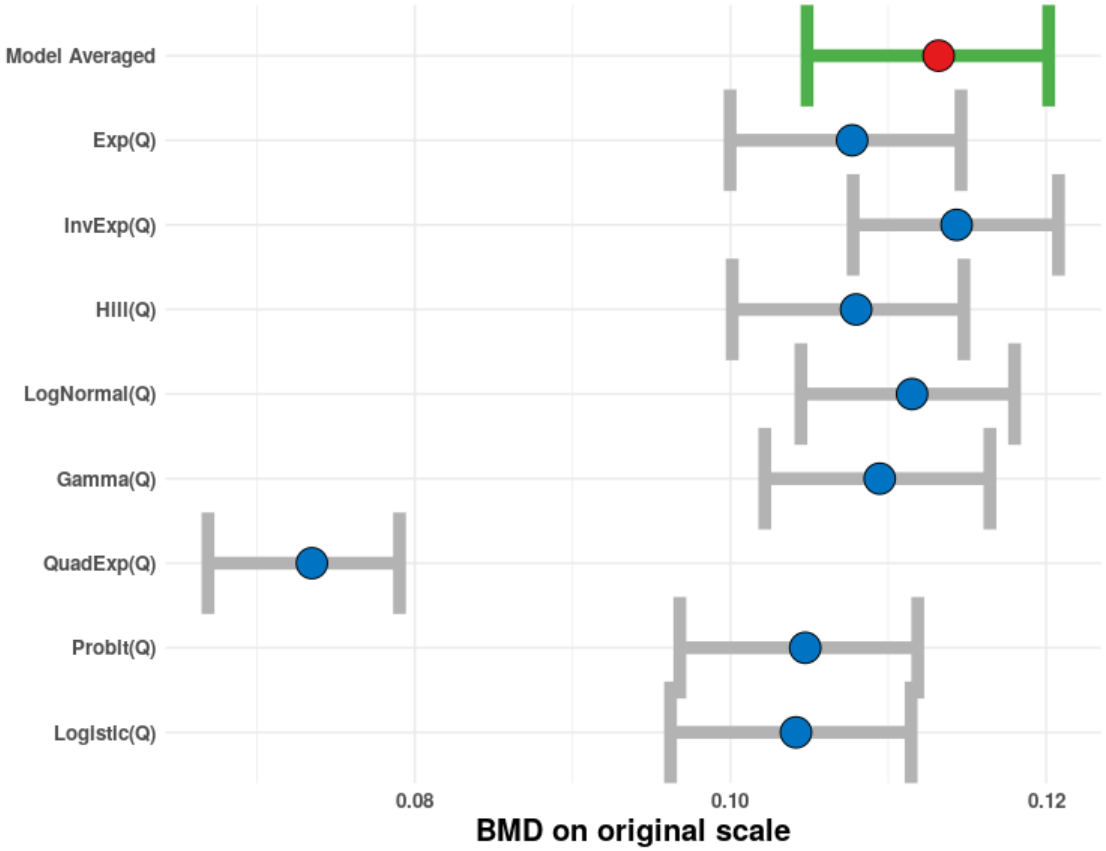
Model Averaged BMD

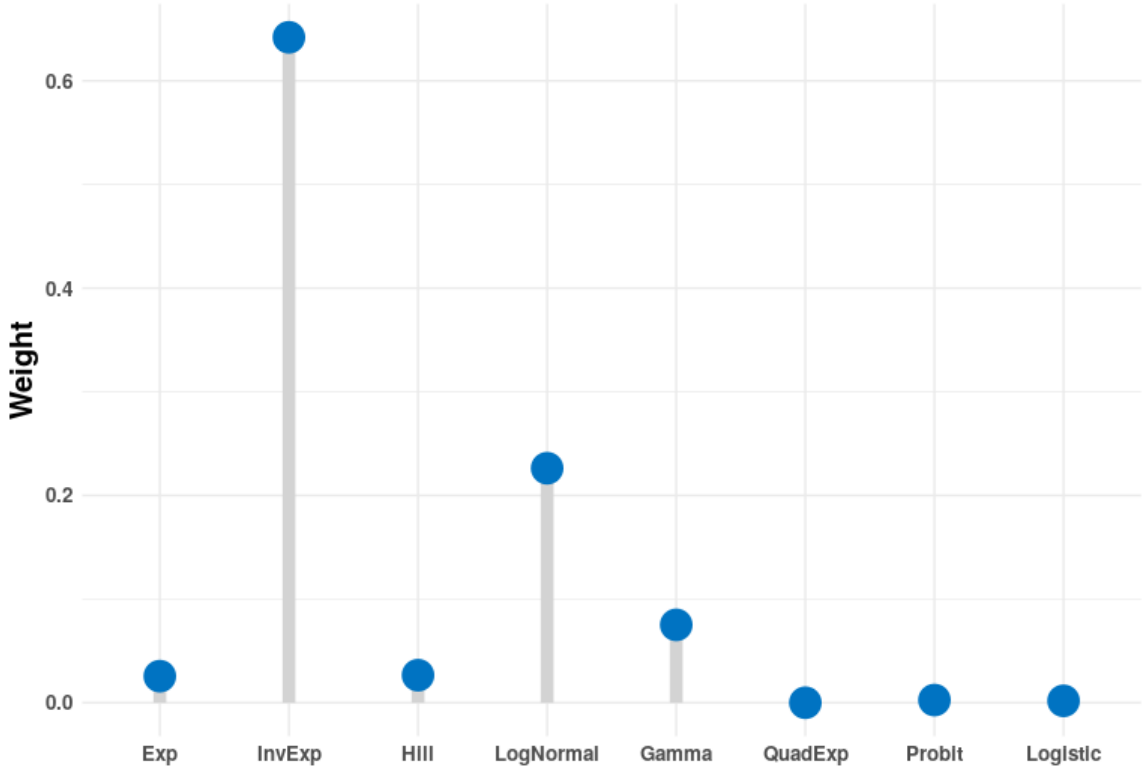
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.105	0.113	0.12

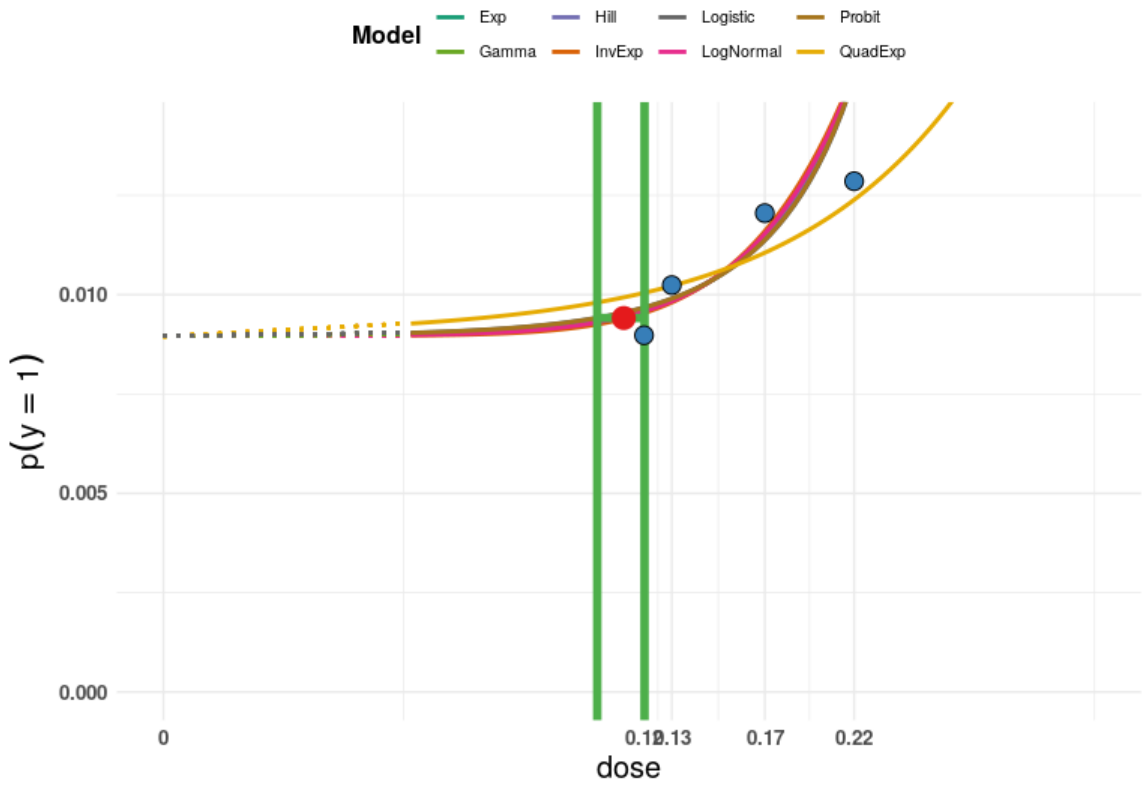
Estimated BMDs per model

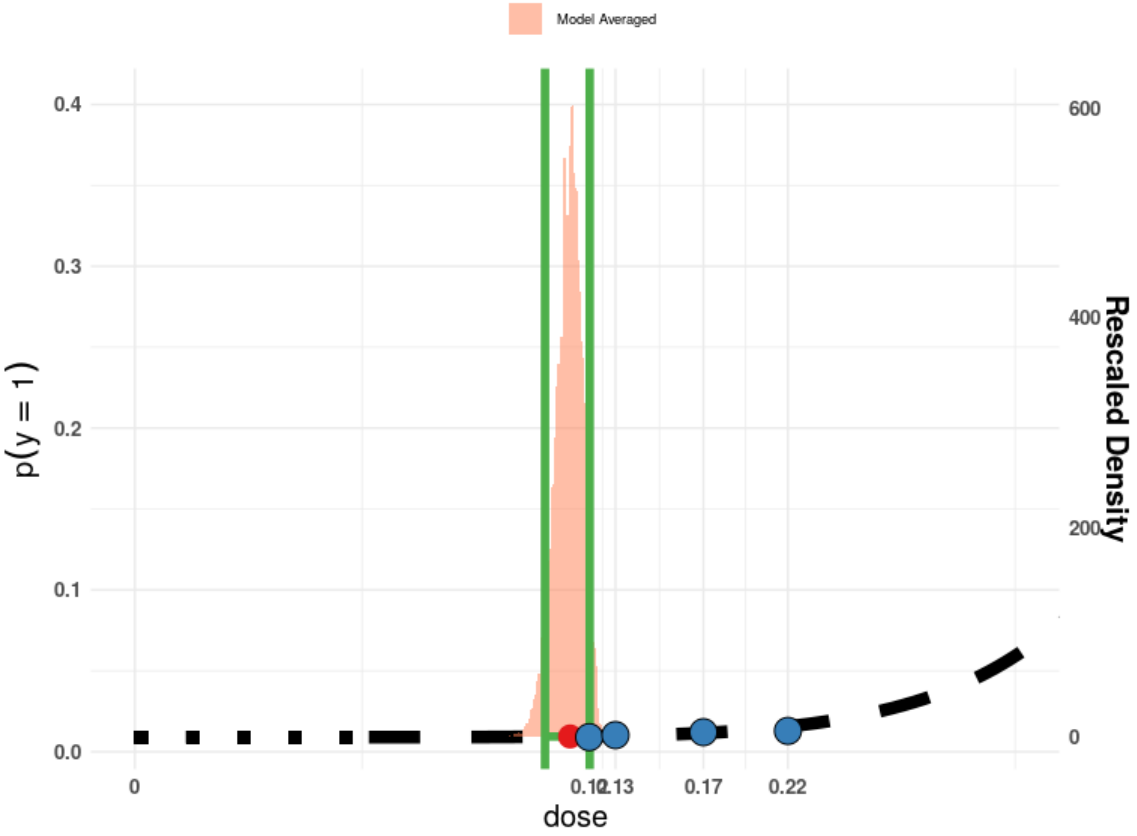
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.100	0.108	0.115	0.026	1
IE4_Q	0.108	0.114	0.121	0.642	1
H4_Q	0.100	0.108	0.115	0.027	1
LN4_Q	0.104	0.112	0.118	0.226	1
G4_Q	0.102	0.109	0.116	0.075	1
QE4_Q	0.067	0.073	0.079	0.000	1
P4_Q	0.097	0.105	0.112	0.003	1
L4_Q	0.096	0.104	0.111	0.002	1

Plots of Fitted Models




Weight
0.6
0.4
0.2
0.0
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
p(y = 1)
0.010
0.005
0.000
0
0.17
0.22
dose


Model Averaged
0.4
0.3
0.2
0.1
0.0
p(y = 1)
600
400
200
0
Rescaled Density
0
0.13
0.17
0.22
dose

Siddique et al. (2020) asthma symptoms, relative BMR 5%

Data Description

The endpoint to be analyzed is: Adj.cases for asthma symptoms

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	N
1.28	14	279
6.16	27	281
71.45	46	282

The 'Value for CES' is set to 0.002641509.

Extended dose range is not applied.

Informative background prior: min: 0.049677419; the most likely: 0.050179211; max: 0.050681004. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

The results do not fulfill the EFSA BMD guidance (EFSA Scientific Committee, 2022) recommendations since none of the candidate models fit the data sufficiently well, BMD/BMDL > 20 and BMDU/BMDL > 50.

Goodness of Fit

None of the models provide an adequate fit do the data (Bayes factor is 2.78e+01).

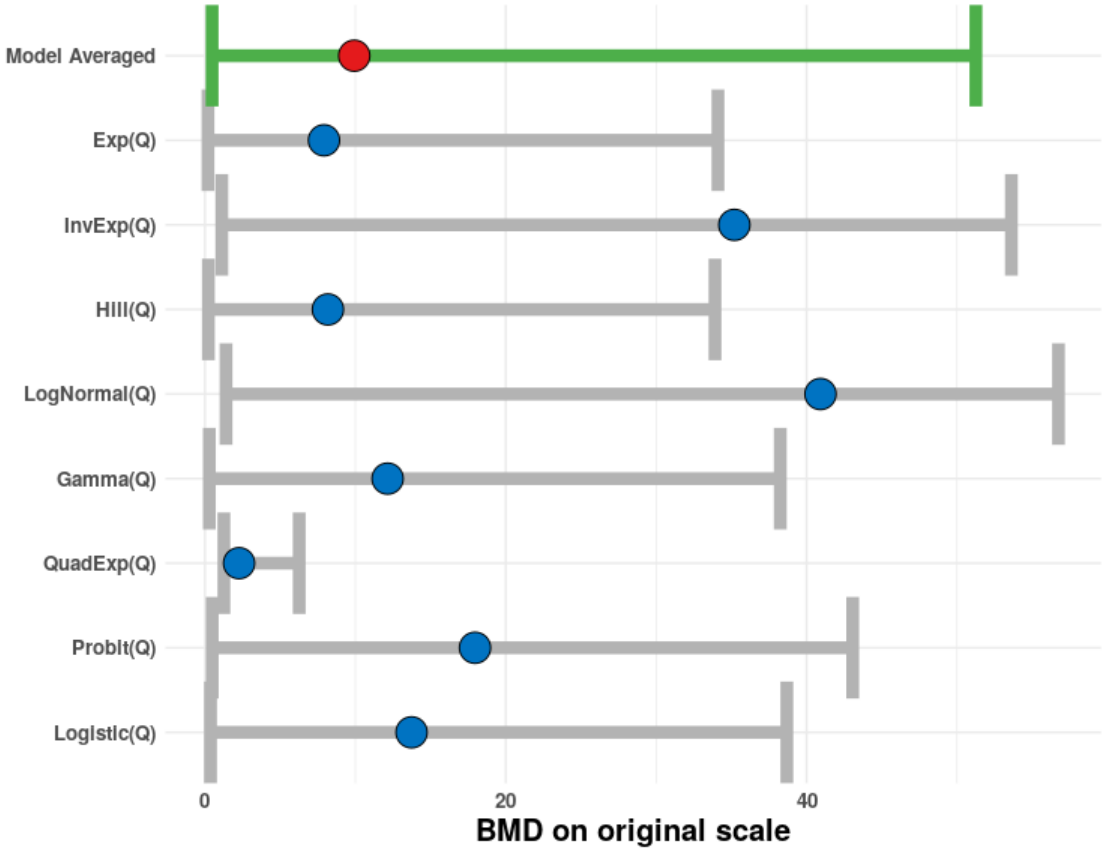
Model Averaged BMD

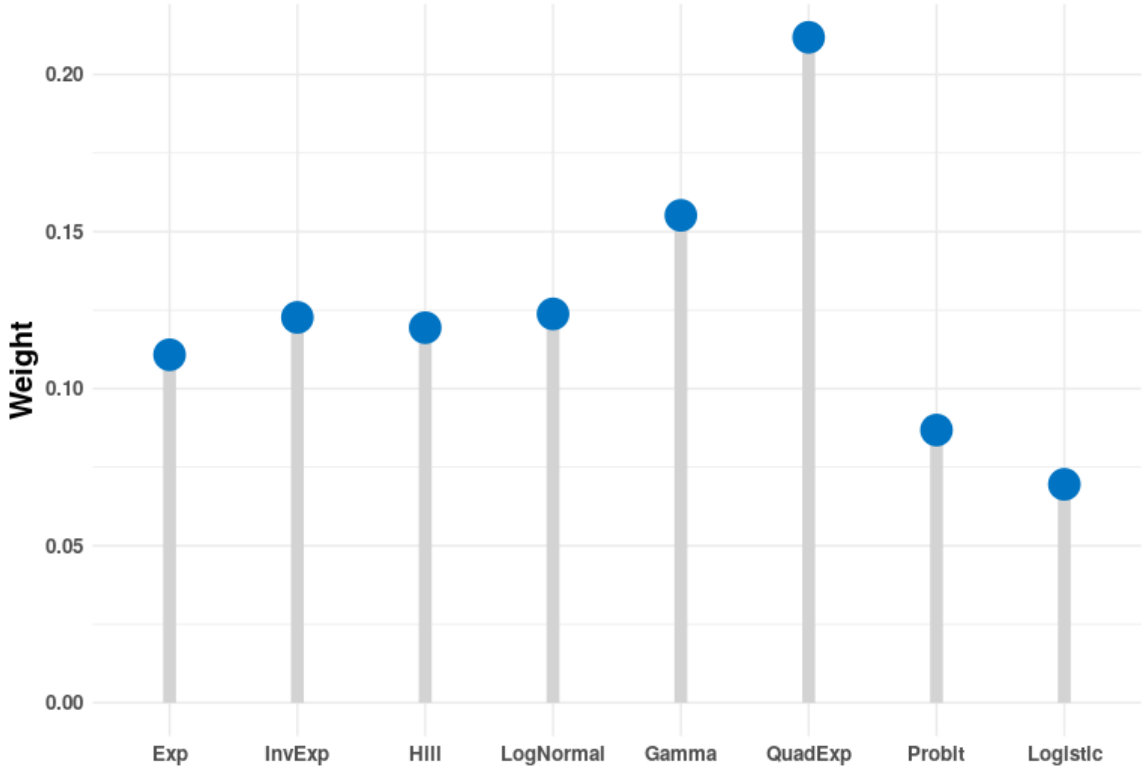
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.475	9.927	51.257

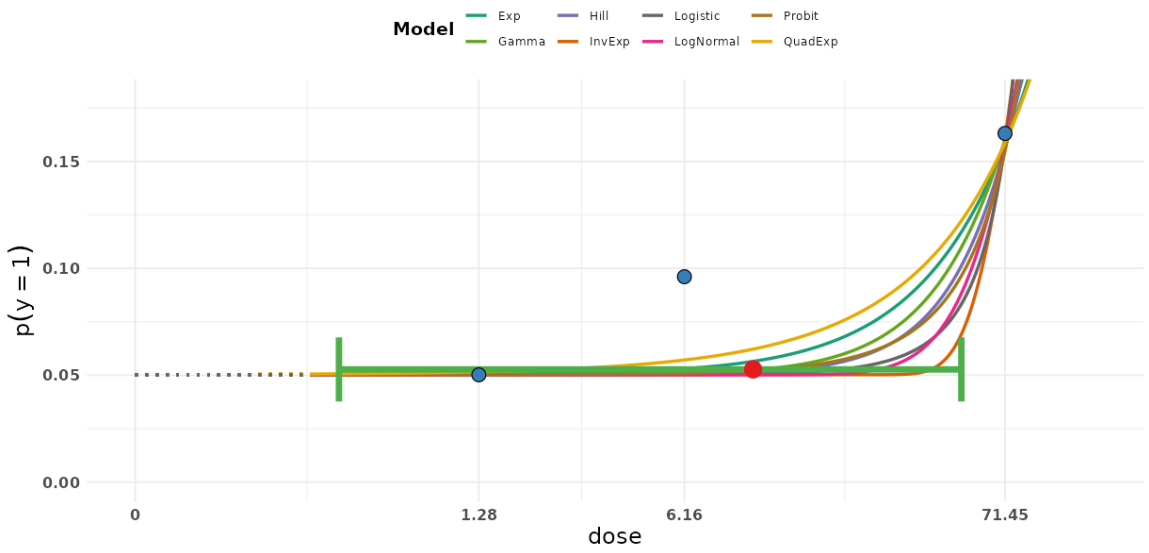
Estimated BMDs per model

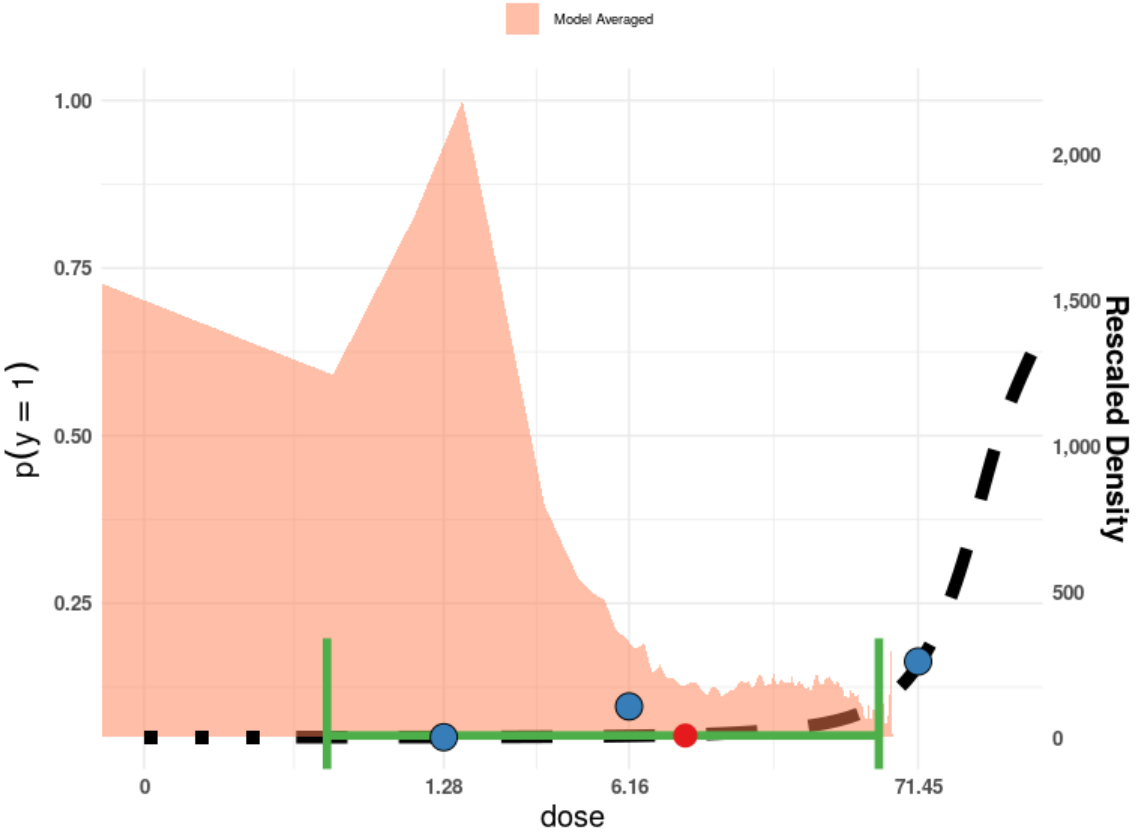
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.202	7.914	34.109	0.111	1
IE4_Q	1.119	35.197	53.617	0.123	1
H4_Q	0.228	8.175	33.911	0.119	0
LN4_Q	1.402	40.924	56.749	0.124	0
G4_Q	0.292	12.145	38.251	0.155	1
QE4_Q	1.260	2.267	6.268	0.212	1
P4_Q	0.482	17.956	43.066	0.087	1
L4_Q	0.370	13.737	38.688	0.070	1

Plots of Fitted Models




Weight
0.20
0.15
0.10
0.05
0.00
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
p(y = 1)
0.15
0.10
0.05
0.00
0
1.28
6.16
71.45
dose


Model Averaged
1.00
0.75
0.50
0.25
p(y = 1)
2,000
1,500
1,000
500
0
Rescaled Density
0
1.28
6.16
71.45
dose

Siddique et al. (2020) FEV1 (lung function), BMR 5%

Data Description

The endpoint to be analyzed is: FEV1 response

Data used for analysis:

Exposure.µg.kg.bw.per.day	Response	SD	N
1.28	1.578	0.575	279
6.16	1.455	0.578	281
71.45	1.375	0.797	282

The 'Value for CES' is set to 0.05.

Extended dose range is not applied.

Informative background prior: min: 1.4202; the most likely: 1.578; max: 1.7358. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

The results do not fulfill the EFSA BMD guidance (2022) recommendations since none of the candidate models fit the data sufficiently well.

Check for constant variance coefficient of variation

distributional assumption of constant variance for the normal distribution is not met, Bartlett test p-value is 0.0000

distributional assumption of constant variance (on log-scale) is not met, Bartlett test p-value is 0.0000

Goodness of Fit

None of the models provide an adequate fit do the data (Bayes factor is 3.46e+01).

Model Averaged BMD

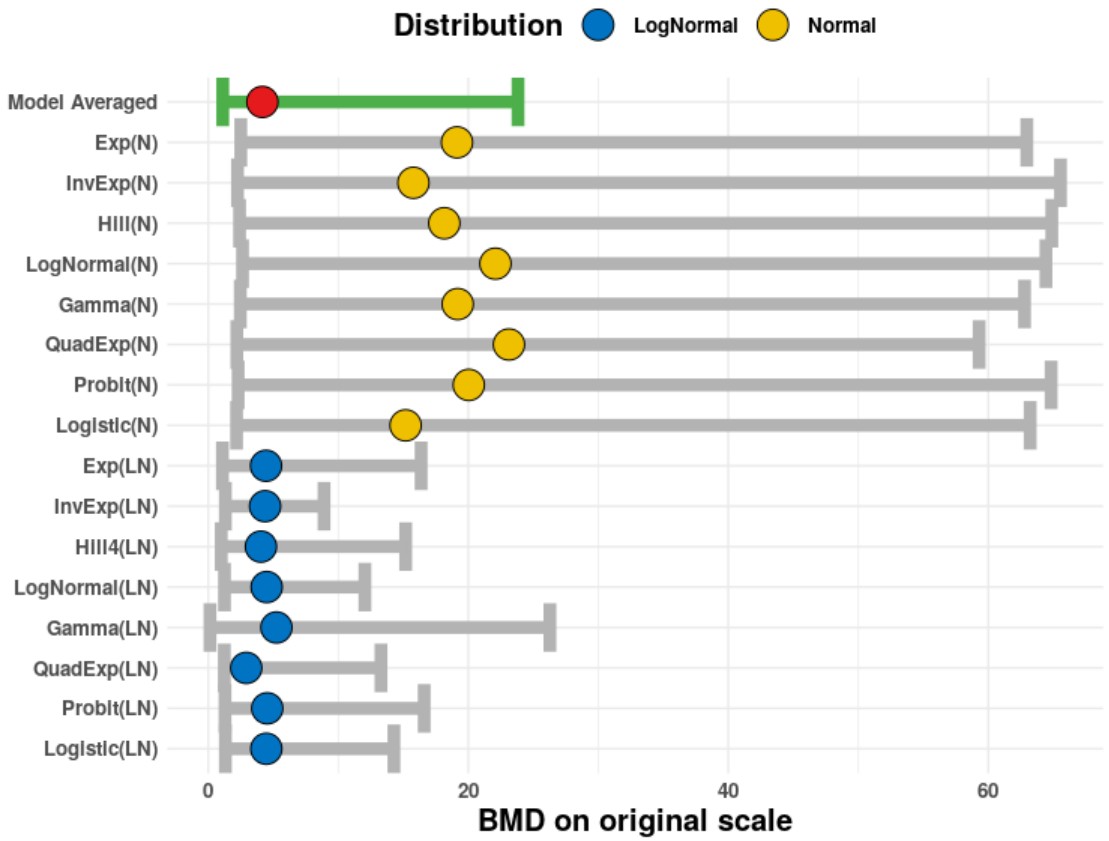
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	1.115	4.163	23.827
Model Averaged	BS	2.193	10.390	60.440
Model Averaged	BS	2.705	28.216	66.152
Model Averaged	BS	1.256	3.735	7.077

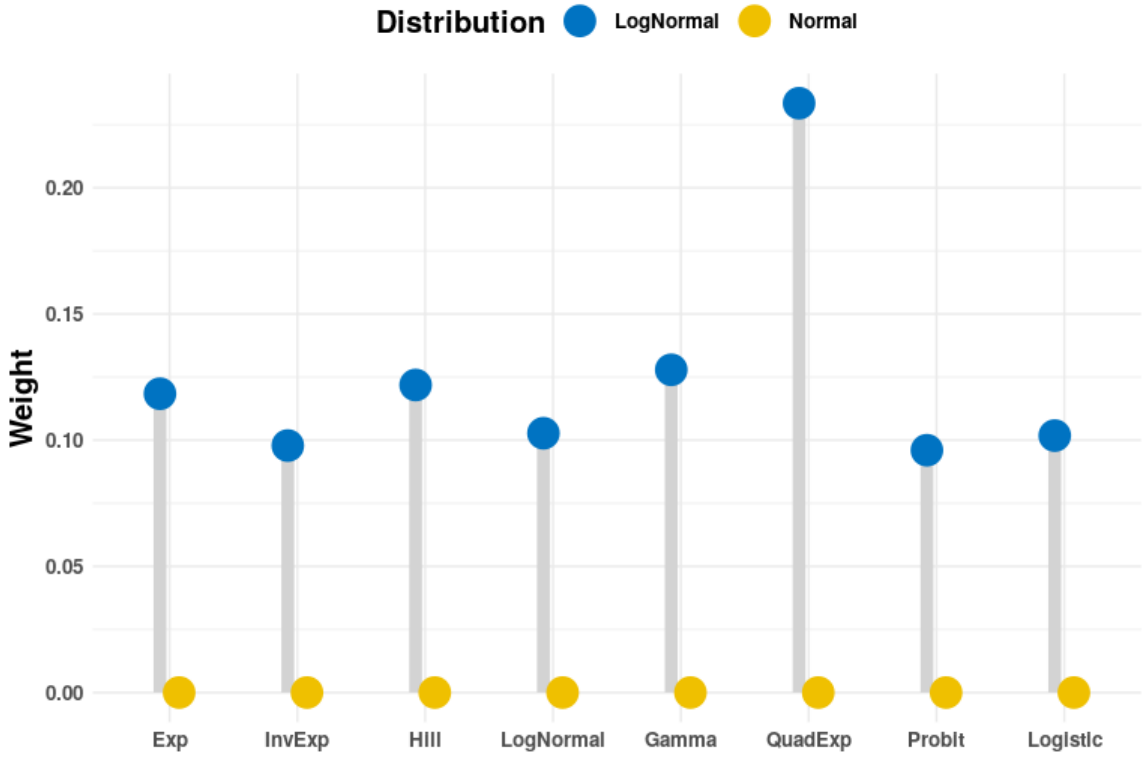
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	1.314	4.749	40.021

Estimated BMDs per model

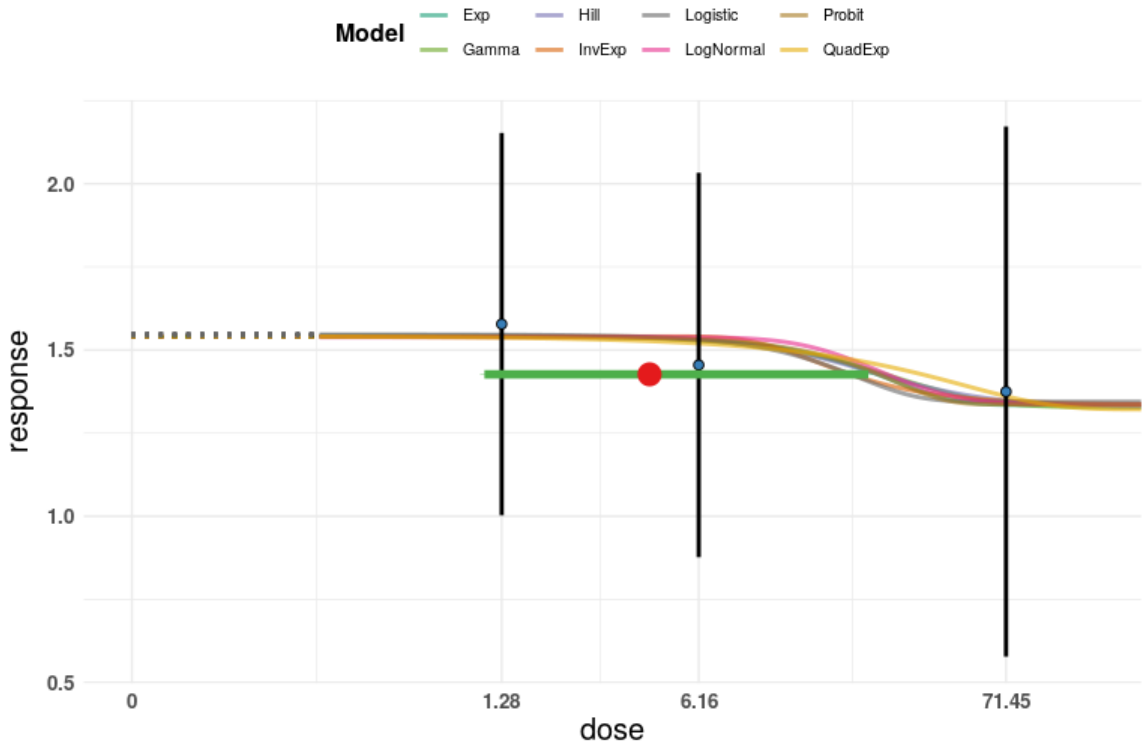
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_N	2.502	19.134	62.961	0.000	1
IE4_N	2.251	15.782	65.551	0.000	1
H4_N	2.410	18.157	64.883	0.000	1
LN4_N	2.637	22.090	64.432	0.000	1
G4_N	2.465	19.188	62.784	0.000	1
QE4_N	2.200	23.129	59.294	0.000	1
P4_N	2.301	20.039	64.830	0.000	1
L4_N	2.180	15.180	63.218	0.000	1
E4_LN	1.091	4.444	16.373	0.118	1
IE4_LN	1.316	4.371	8.907	0.098	1
H4_LN	1.001	4.053	15.185	0.122	1
LN4_LN	1.249	4.494	12.050	0.103	1
G4_LN	0.134	5.245	26.279	0.128	0
QE4_LN	1.239	2.924	13.286	0.233	1
P4_LN	1.289	4.539	16.611	0.096	1
L4_LN	1.318	4.466	14.283	0.102	1

Plots of Fitted Models

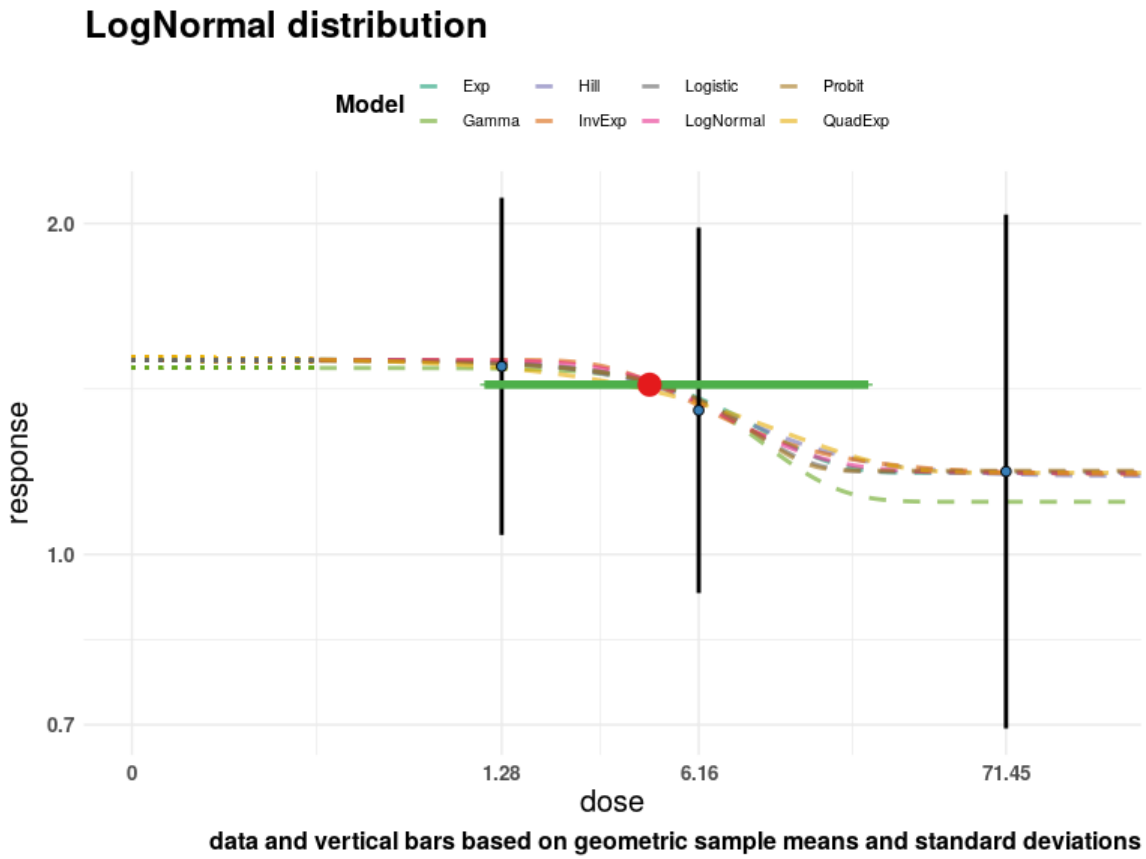


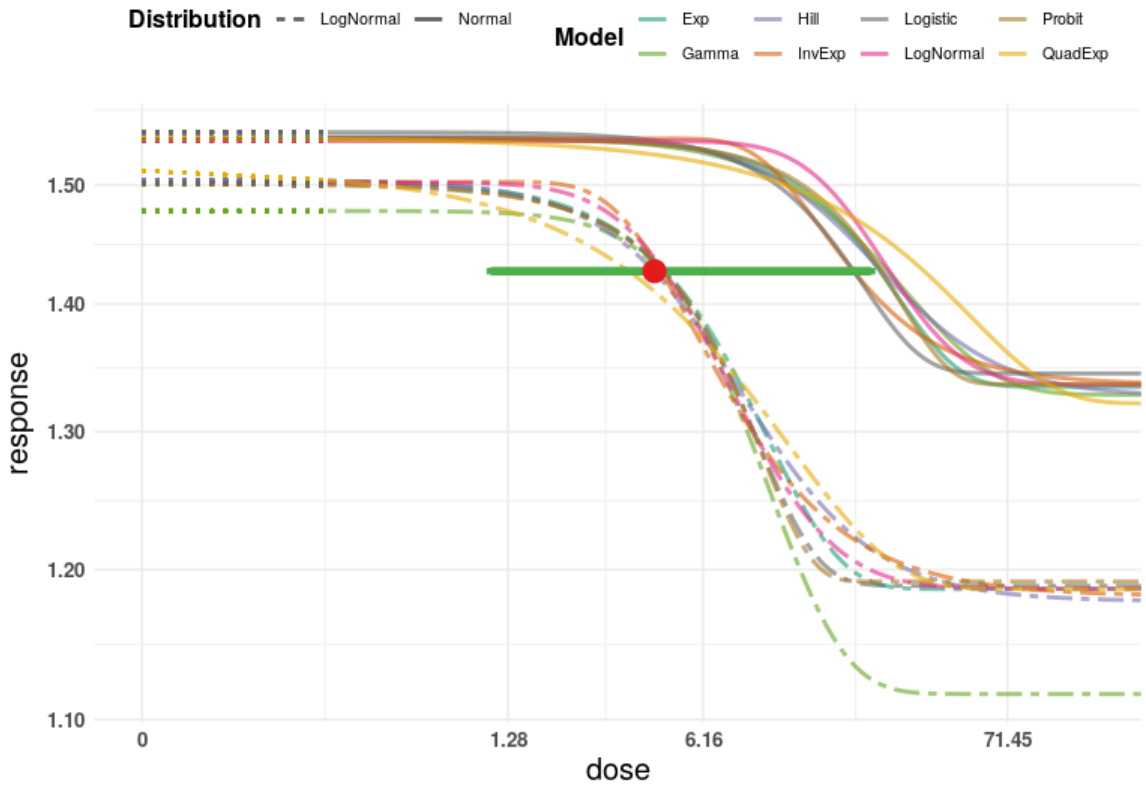


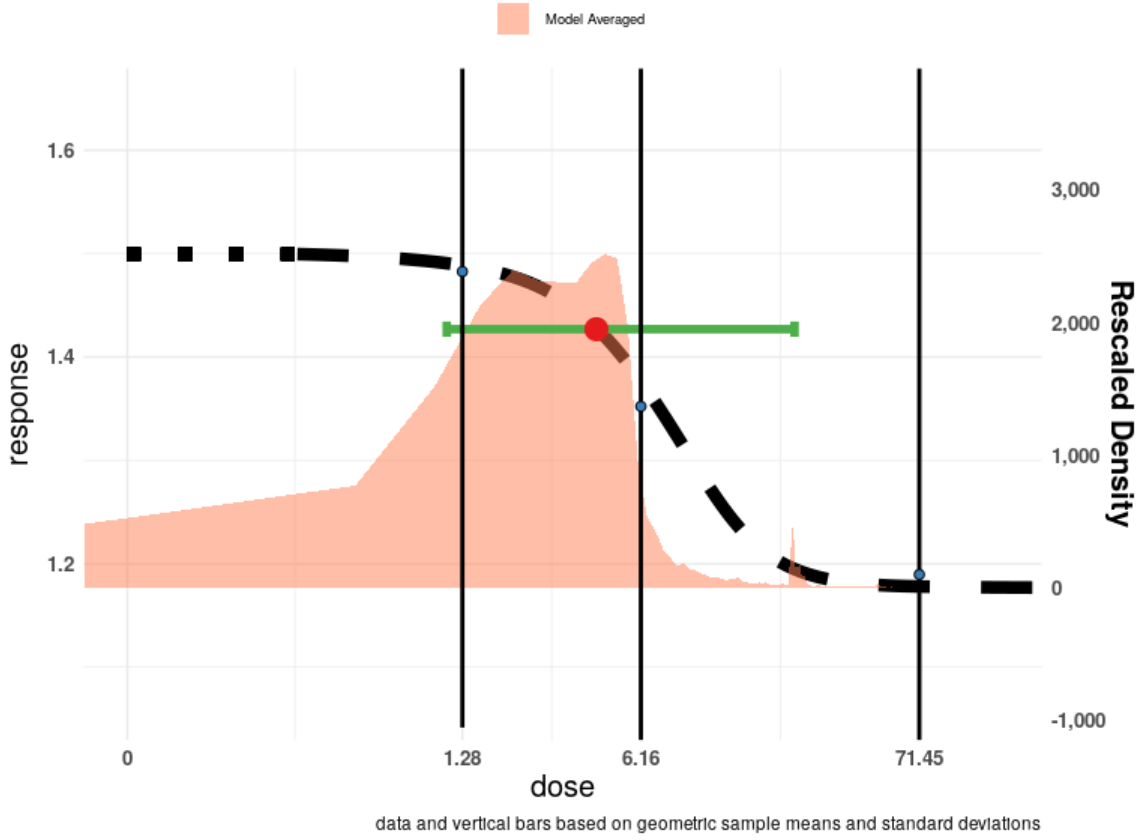
Normal distribution



data and vertical bars based on arithmetic sample means and standard deviations


LogNormal distribution
Model
Exp
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
2.0
1.0
0.7
response
0
1.28
6.16
71.45
dose
data and vertical bars based on geometric sample means and standard deviations


Distribution
LogNormal
Normal
Model
Exp
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
1.50
1.40
1.30
1.20
1.10
response
0
1.28
6.16
71.45
dose


Model Averaged
response
1.6
1.4
1.2
3,000
2,000
1,000
0
-1,000
Rescaled Density
0
1.28
6.16
71.45
dose
data and vertical bars based on geometric sample means and standard deviations

Siddique et al. (2020) FEV6 (lung function), BMR 5%

Data Description

The endpoint to be analyzed is: FEV6 response

Data used for analysis:

Exposure.µg.kg.bw.per.day	Response	SD	N
1.28	1.669	0.536	279
6.16	1.547	0.538	281
71.45	1.500	0.851	282

The 'Value for CES' is set to 0.05.

Extended dose range is not applied.

Informative background prior: min: 1.5021; the most likely: 1.669; max: 1.8359. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

The results do not fulfill the EFSA BMD guidance (EFSA Scientific Committee, 2022) recommendations since none of the candidate models fit the data sufficiently well.

Check for constant variance coefficient of variation

Distributional assumption of constant variance for the normal distribution is not met, Bartlett test p-value is 0

Distributional assumption of constant variance (on log-scale) are not met, Bartlett test p-value is 0

Check for constant variance coefficient of variation

distributional assumption of constant variance for the normal distribution is not met, Bartlett test p-value is 0.0000

distributional assumption of constant variance (on log-scale) is not met, Bartlett test p-value is 0.0000

Goodness of Fit

None of the models provide an adequate fit do the data (Bayes factor is 4.67e+01).

Model Averaged BMD

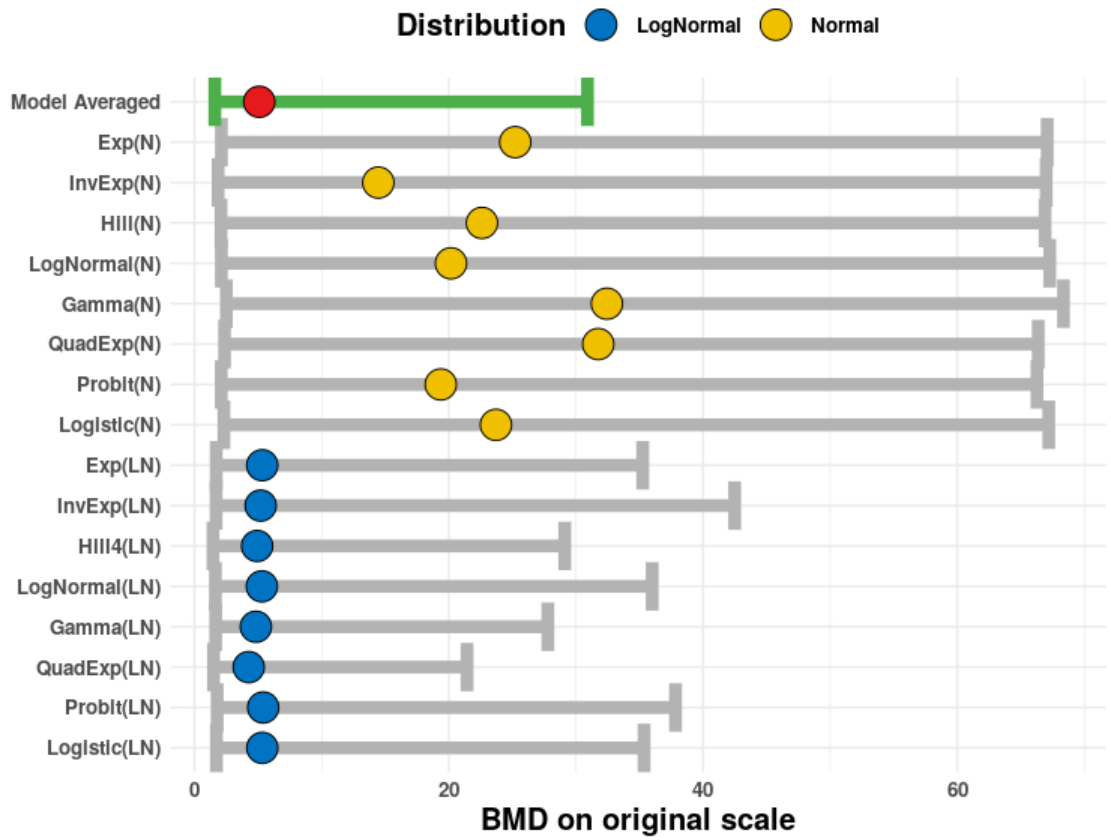
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	1.600	5.091	30.913

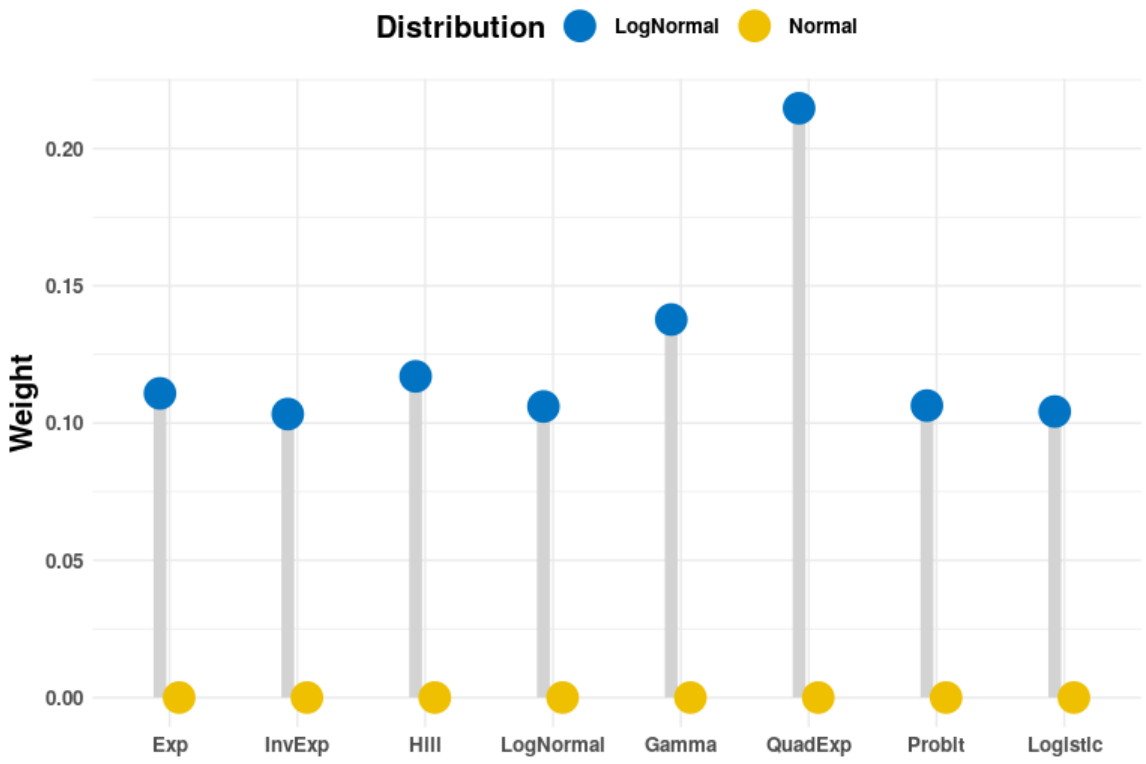
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	1.829	8.088	64.527
Model Averaged	BS	2.842	36.619	68.215
Model Averaged	BS	1.525	4.400	10.449
Model Averaged	BS	1.662	6.403	45.149

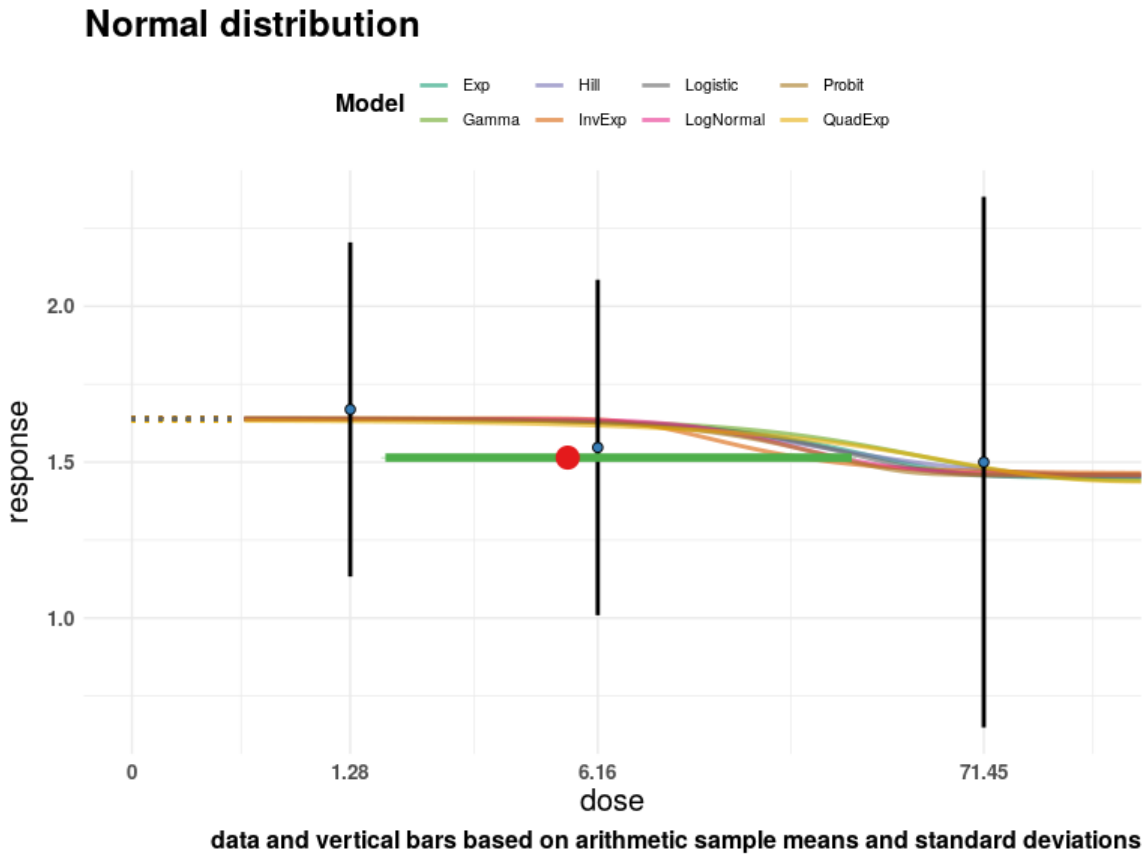
Estimated BMDs per model

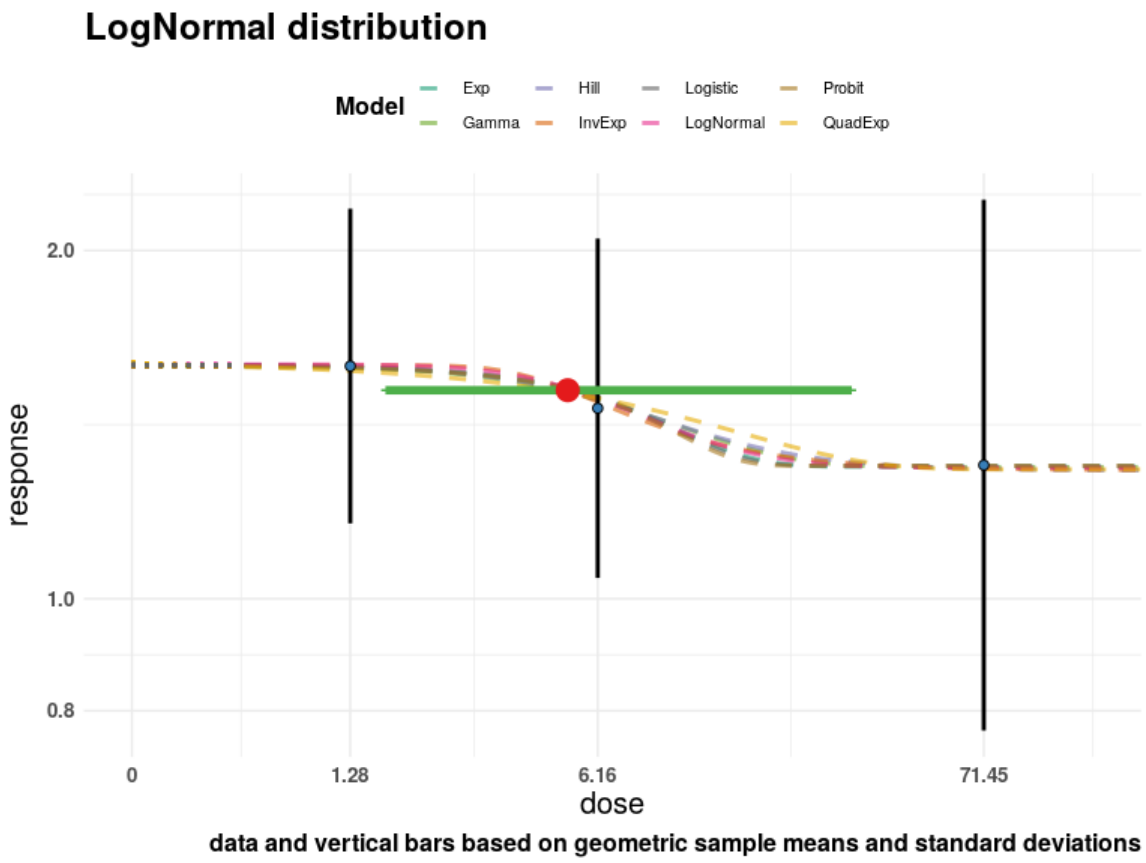
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_N	2.115	25.229	67.076	0.000	1
IE4_N	1.855	14.460	66.995	0.000	1
H4_N	2.081	22.610	66.904	0.000	0
LN4_N	2.114	20.174	67.273	0.000	1
G4_N	2.509	32.442	68.355	0.000	0
QE4_N	2.360	31.756	66.370	0.000	1
P4_N	2.105	19.371	66.272	0.000	1
L4_N	2.312	23.713	67.197	0.000	1
E4_LN	1.707	5.326	35.255	0.111	1
IE4_LN	1.696	5.204	42.489	0.103	1
H4_LN	1.453	4.924	29.124	0.117	1
LN4_LN	1.643	5.298	35.999	0.106	1
G4_LN	1.664	4.829	27.794	0.138	1
QE4_LN	1.495	4.263	21.436	0.215	1
P4_LN	1.780	5.400	37.838	0.106	1
L4_LN	1.723	5.331	35.362	0.104	1

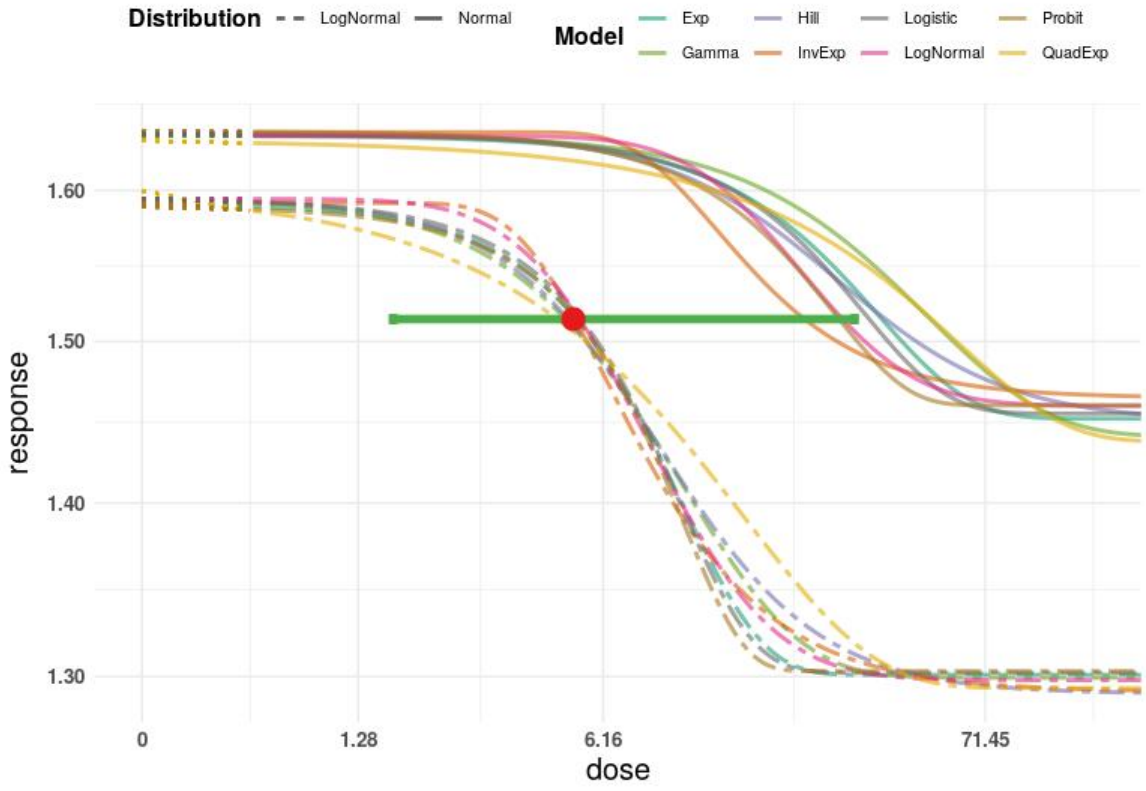
Plots of Fitted Models

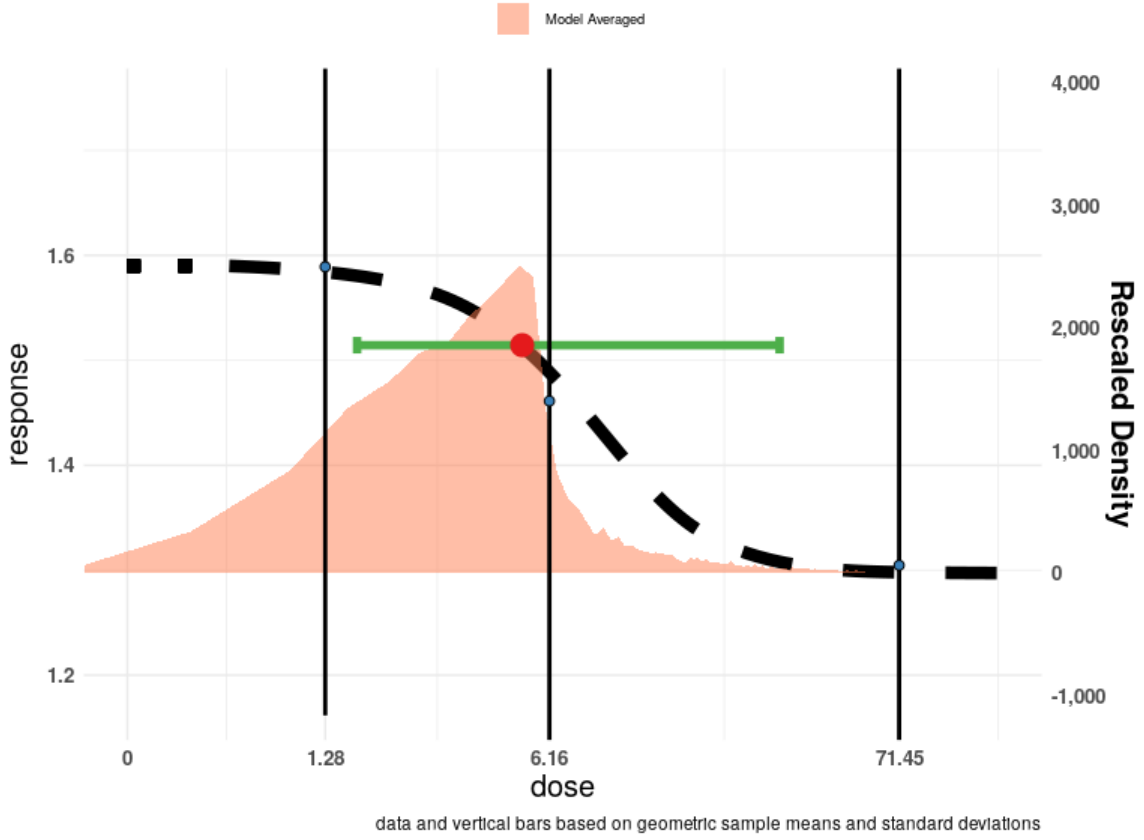



Distribution
LogNormal
Normal
Weight
0.20
0.15
0.10
0.05
0.00
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Normal distribution
Model
Exp
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
response
2.0
1.5
1.0
0
1.28
6.16
71.45
dose
data and vertical bars based on arithmetic sample means and standard deviations


LogNormal distribution
Model
Exp
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
2.0
1.0
0.8
response
0
1.28
6.16
71.45
dose
data and vertical bars based on geometric sample means and standard deviations


Distribution
LogNormal
Normal
Model
Exp
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
1.60
1.50
1.40
1.30
response
0
1.28
6.16
71.45
dose


Model Averaged
response
1.6
1.4
1.2
4,000
3,000
2,000
1,000
0
-1,000
Rescaled Density
0
1.28
6.16
71.45
dose
data and vertical bars based on geometric sample means and standard deviations

Siddique et al. (2020) obstruction (lung function), relative BMR 5%

Data Description

The endpoint to be analyzed is: Adj.cases for obstruction

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	N
1.28	16	279
6.16	30	281
71.45	52	282

The 'Value for CES' is set to 0.003041825.

Extended dose range is not applied.

Informative background prior: min: 0.056774194; the most likely: 0.05734767; max: 0.057921147. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

The results do not fulfill the EFSA BMD guidance (2022) recommendations since none of the candidate models fit the data sufficiently well and BMDU/BMDL > 50.

Goodness of Fit

None of the models provide an adequate fit do the data (Bayes factor is 2.78e+01).

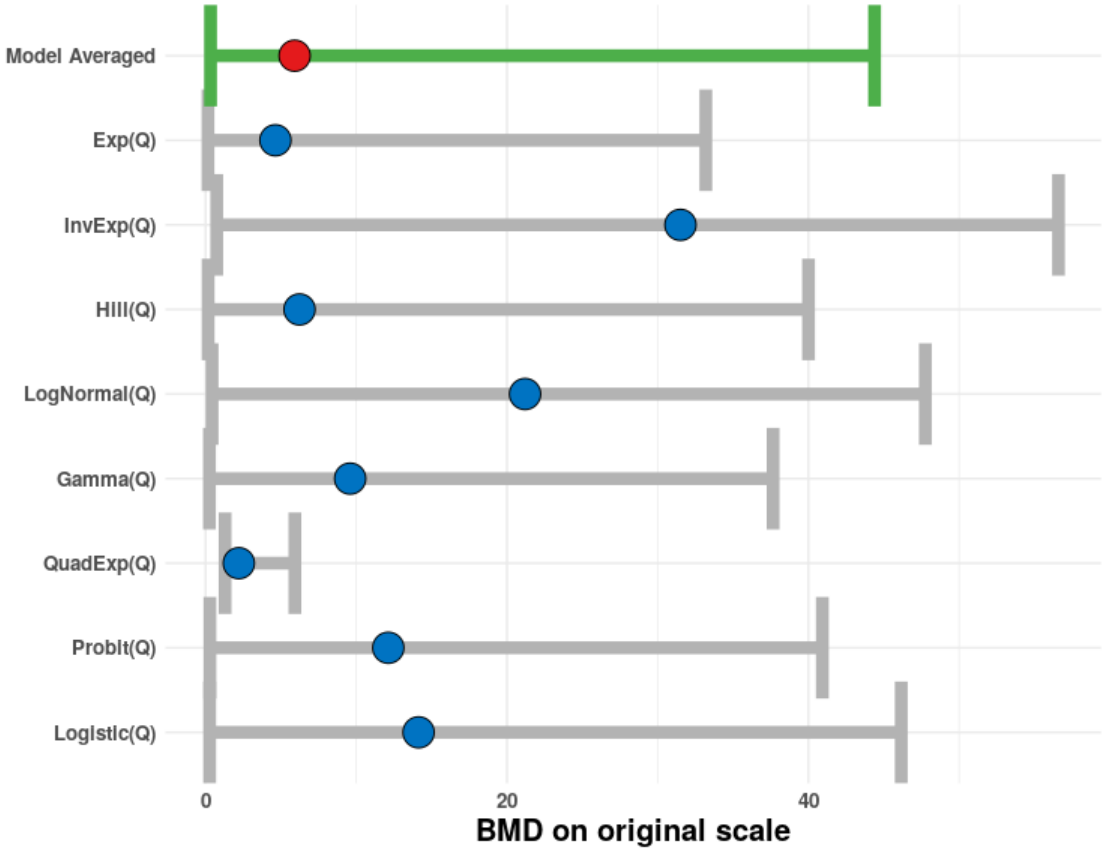
Model Averaged BMD

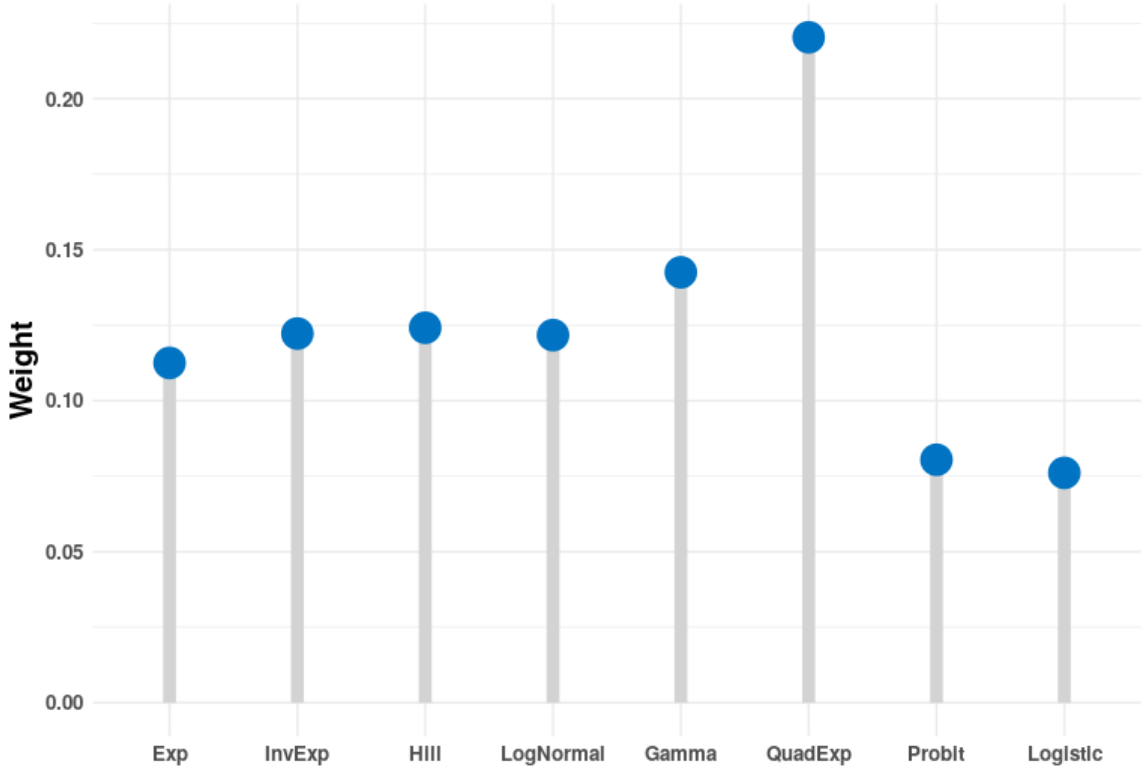
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.327	5.908	44.394

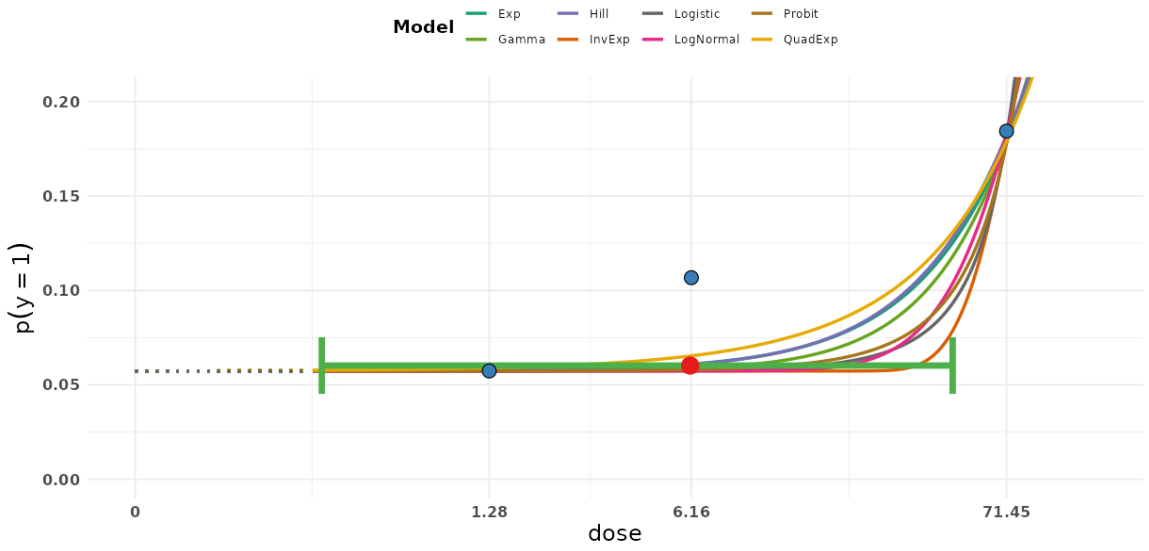
Estimated BMDs per model

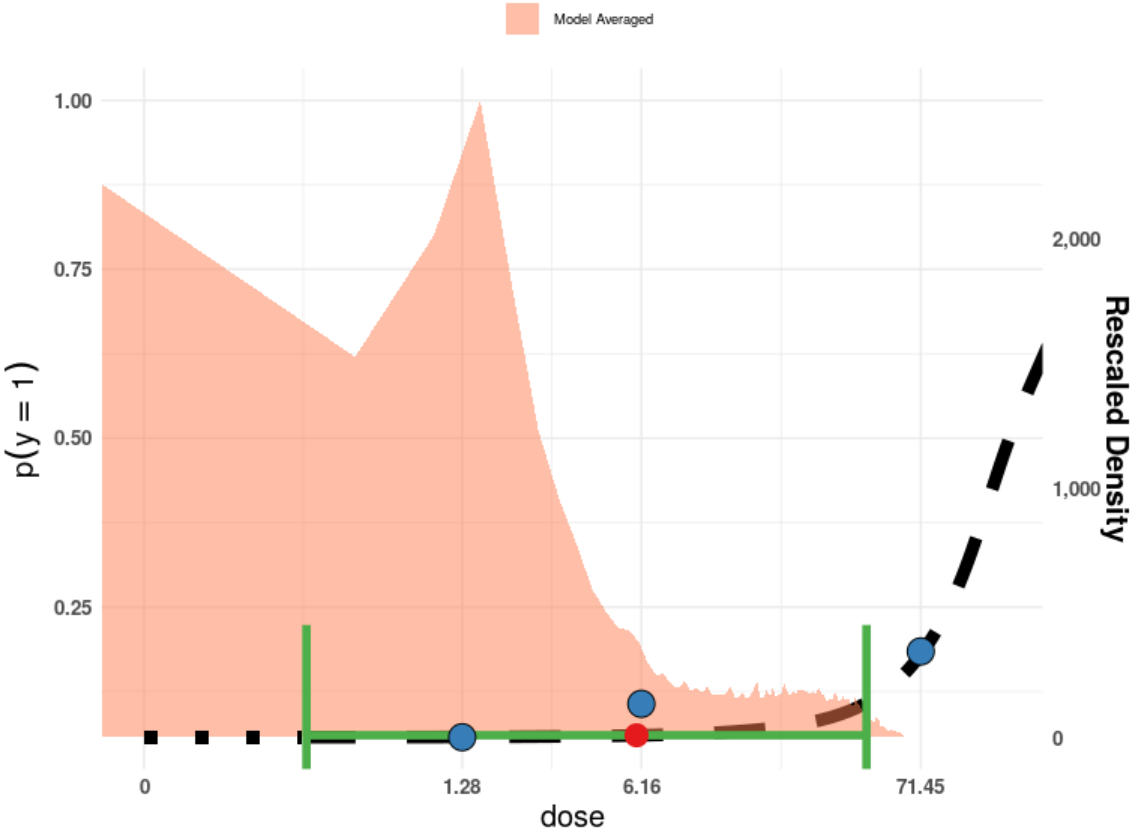
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.157	4.632	33.194	0.113	1
IE4_Q	0.736	31.510	56.598	0.122	0
H4_Q	0.167	6.230	40.009	0.124	1
LN4_Q	0.429	21.199	47.763	0.122	0
G4_Q	0.253	9.591	37.659	0.143	1
QE4_Q	1.291	2.204	5.925	0.220	1
P4_Q	0.283	12.123	40.928	0.080	0
L4_Q	0.267	14.132	46.164	0.076	0

Plots of Fitted Models




Weight
0.20
0.15
0.10
0.05
0.00
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
p(y = 1)
0.20
0.15
0.10
0.05
0.00
0
1.28
6.16
71.45
dose


Model Averaged
1.00
0.75
0.50
0.25
p(y = 1)
2,000
1,000
0
Rescaled Density
0
1.28
6.16
71.45
dose

Siddique et al. (2020) reversible obstruction (lung function), relative BMR 5%

Data Description

The endpoint to be analyzed is: Adj.cases for reversible obstruction

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	N
1.28	11	279
6.16	19	281
71.45	39	282

The 'Value for CES' is set to 0.002052239.

Extended dose range is not applied.

Informative background prior: min: 0.039032258; the most likely: 0.039426523; max: 0.039820789. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

The results do not fulfill the EFSA BMD guidance (EFSA Scientific Committee, 2022) recommendations since none of the candidate models fit the data sufficiently well.

Goodness of Fit

None of the models provide an adequate fit do the data (Bayes factor is 1.14e+01).

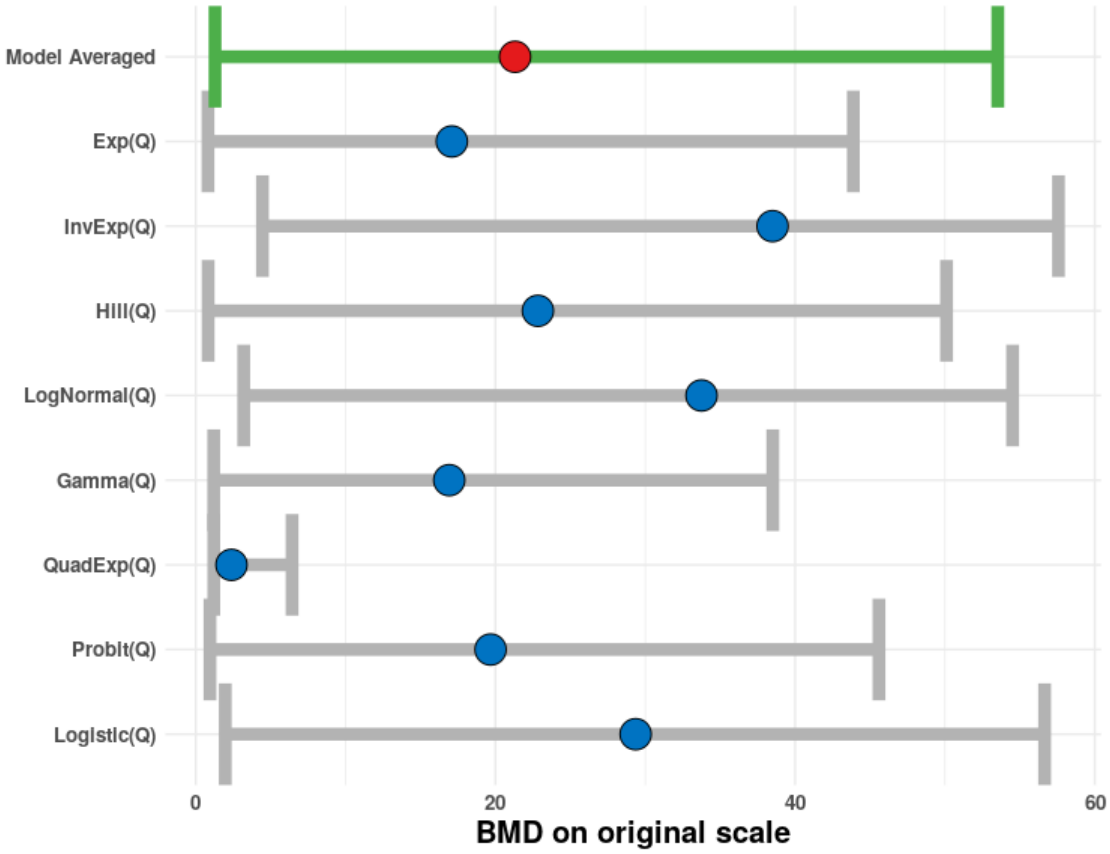
Model Averaged BMD

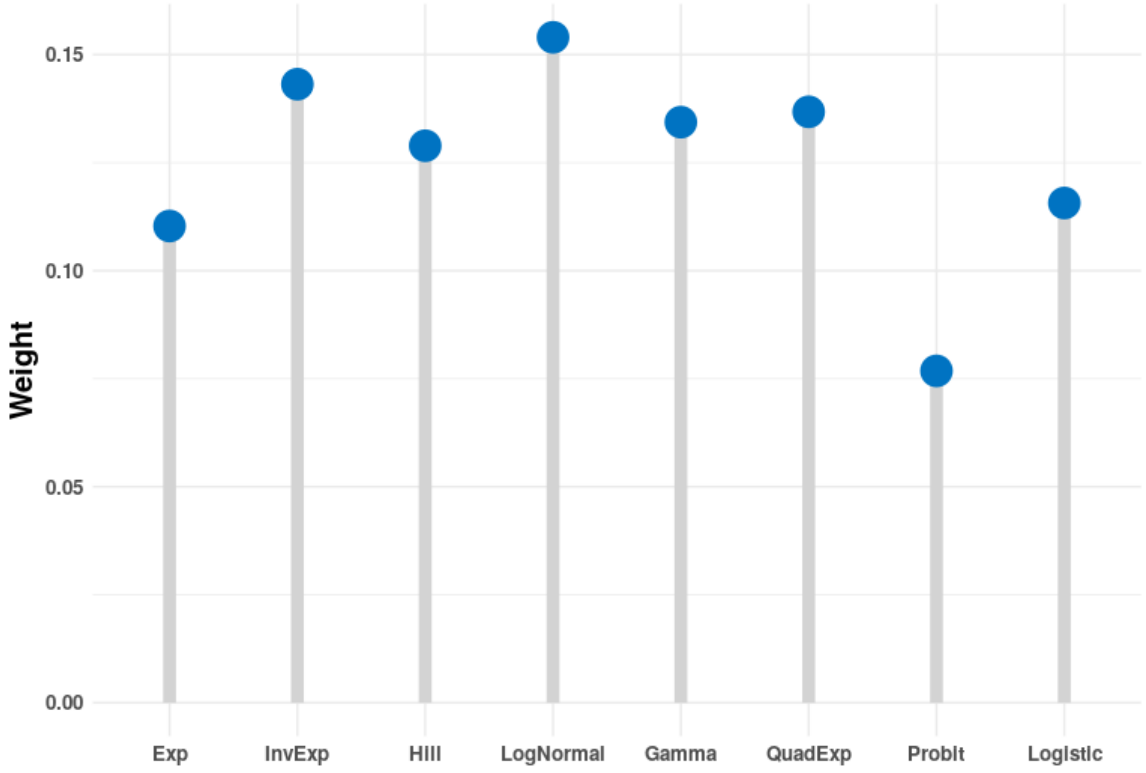
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	1.287	21.31	53.526

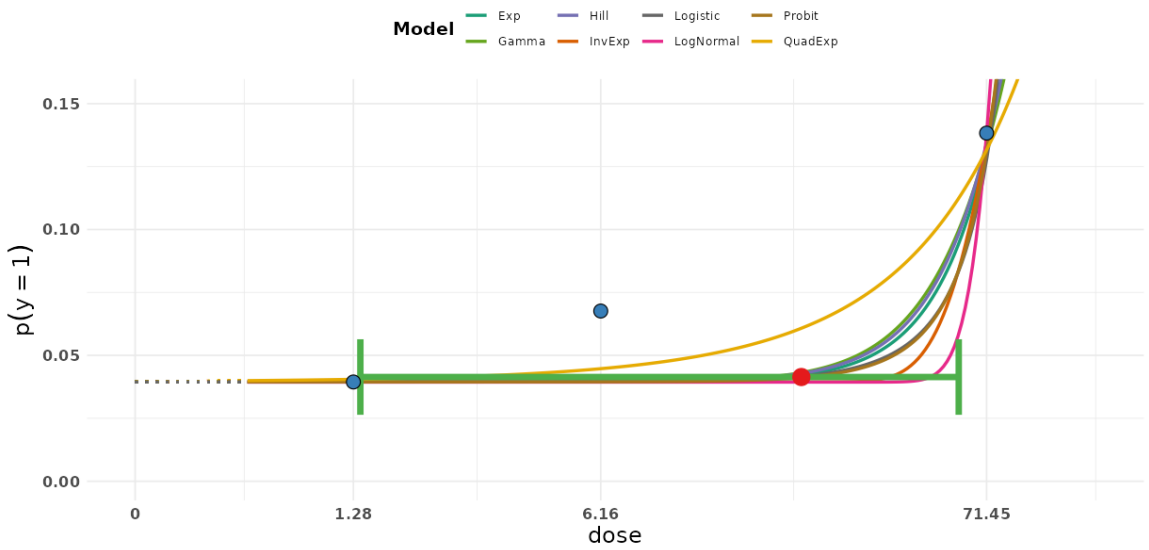
Estimated BMDs per model

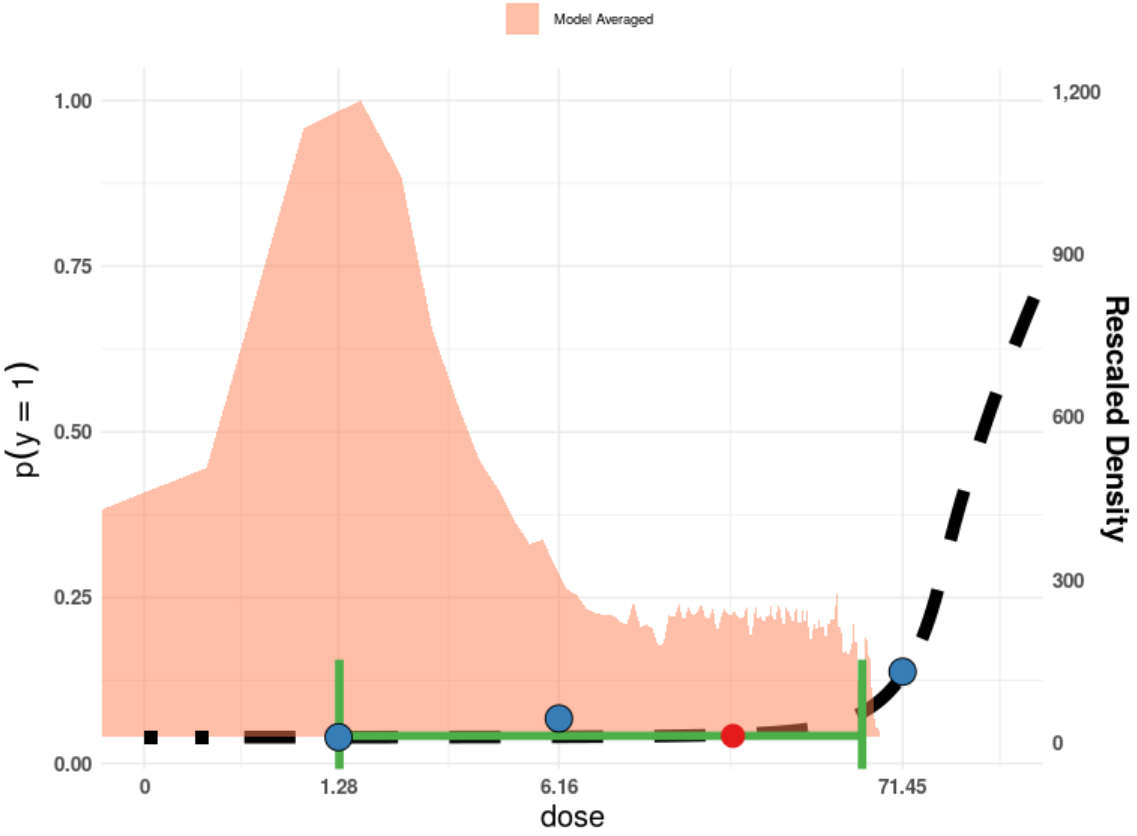
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.817	17.090	43.884	0.110	1
IE4_Q	4.452	38.492	57.576	0.143	1
H4_Q	0.828	22.834	50.105	0.129	0
LN4_Q	3.201	33.752	54.515	0.154	1
G4_Q	1.199	16.916	38.509	0.134	1
QE4_Q	1.204	2.384	6.430	0.137	1
P4_Q	0.947	19.674	45.596	0.077	1
L4_Q	1.971	29.357	56.652	0.116	0

Plots of Fitted Models




Weight
0.15
0.10
0.05
0.00
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
p(y = 1)
0.15
0.10
0.05
0.00
0
1.28
6.16
71.45
dose


Model Averaged
1.00
0.75
0.50
0.25
0.00
p(y = 1)
1,200
900
600
300
0
Rescaled Density
0
1.28
6.16
71.45
dose

Steinmaus et al. (2013) bladder cancer, relative BMR 5%

Exposure: lifetime average, all years, based on arsenic water concentrations and water intake of 1.9L (included only in the uncertainty analysis)

Data Description

The endpoint to be analyzed is: Adj.cases. for bladder cancer

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	N
0.64	34	142031
1.71	29	132891
4.05	62	99844
5.63	107	75234

The 'Value for CES' is set to 1.197e-05.

Extended dose range is applied.

Informative background prior: min: 0.00022742; the most likely: 0.00023938; max: 0.00025135. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 2.38e-03).

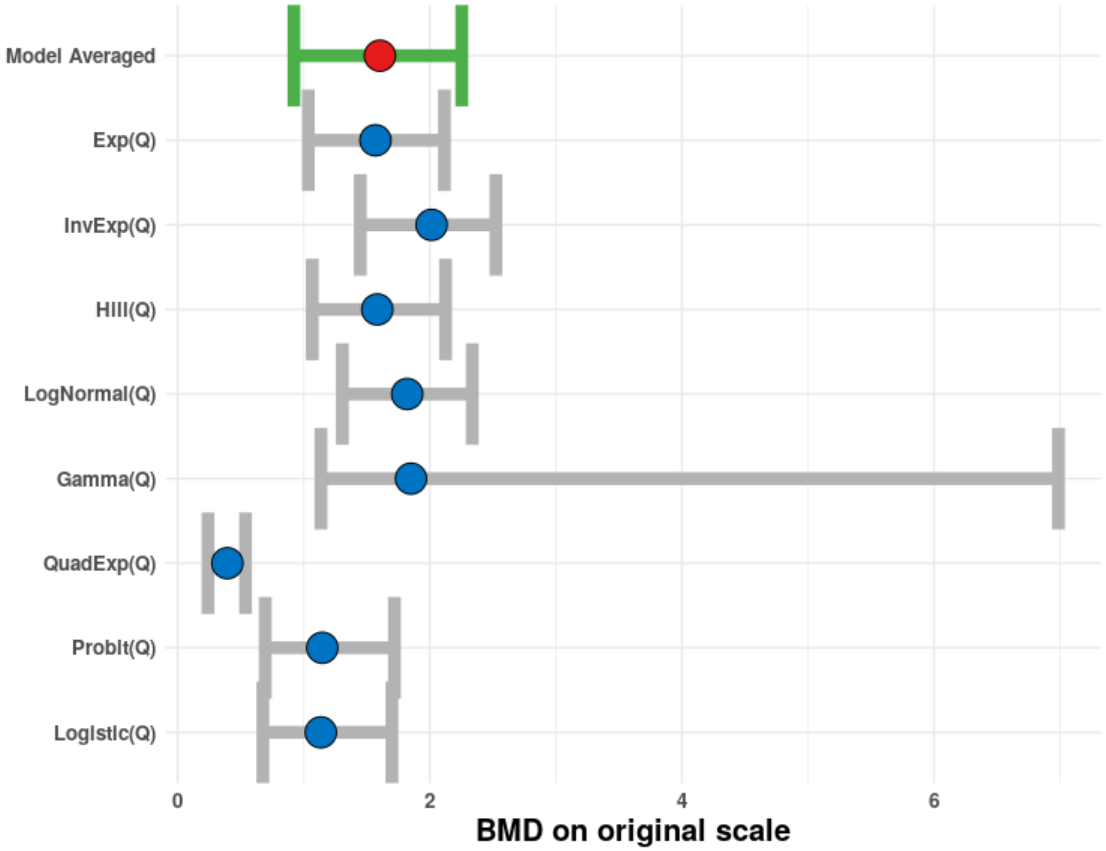
Model Averaged BMD

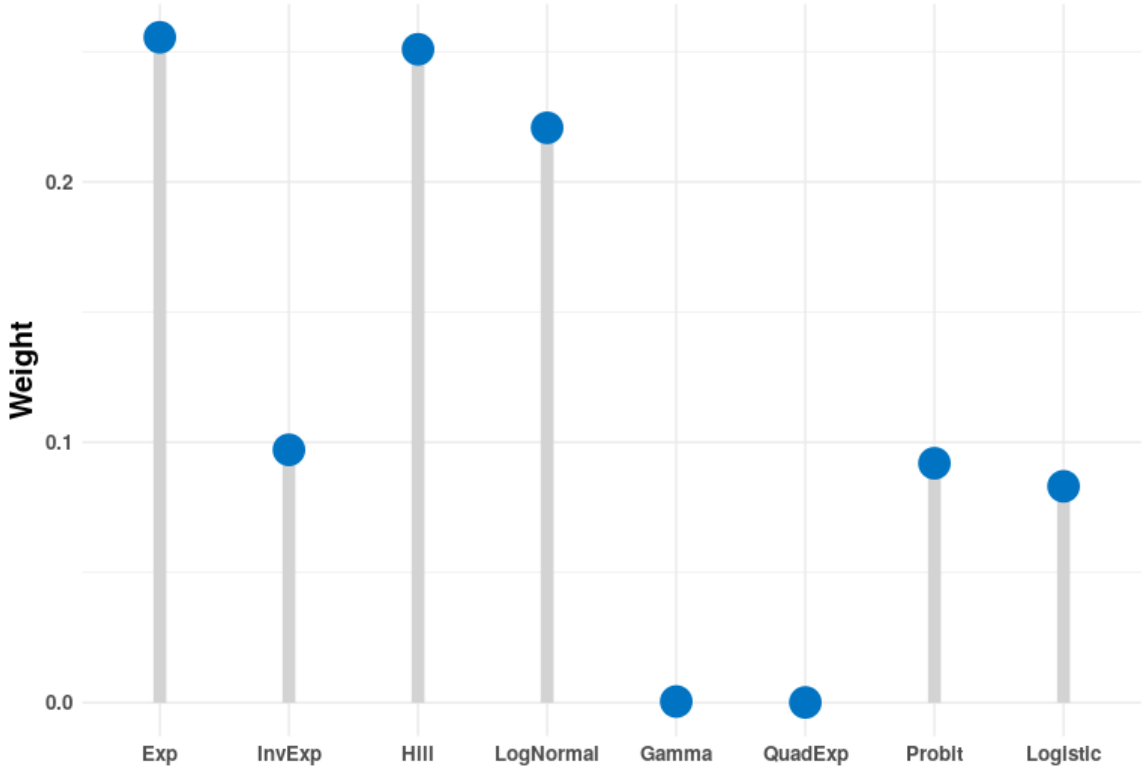
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.922	1.605	2.254

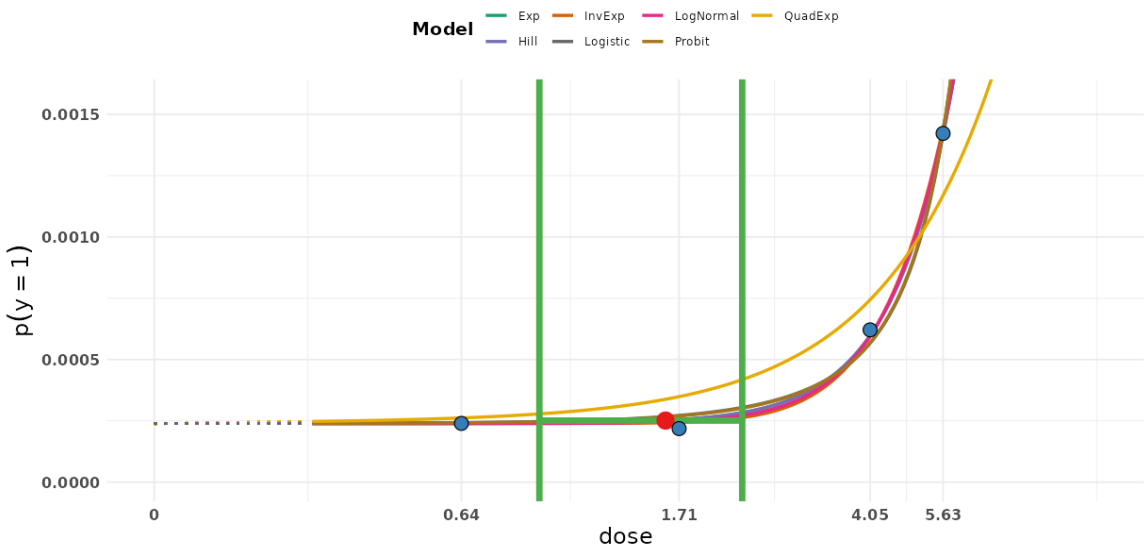
Estimated BMDs per model

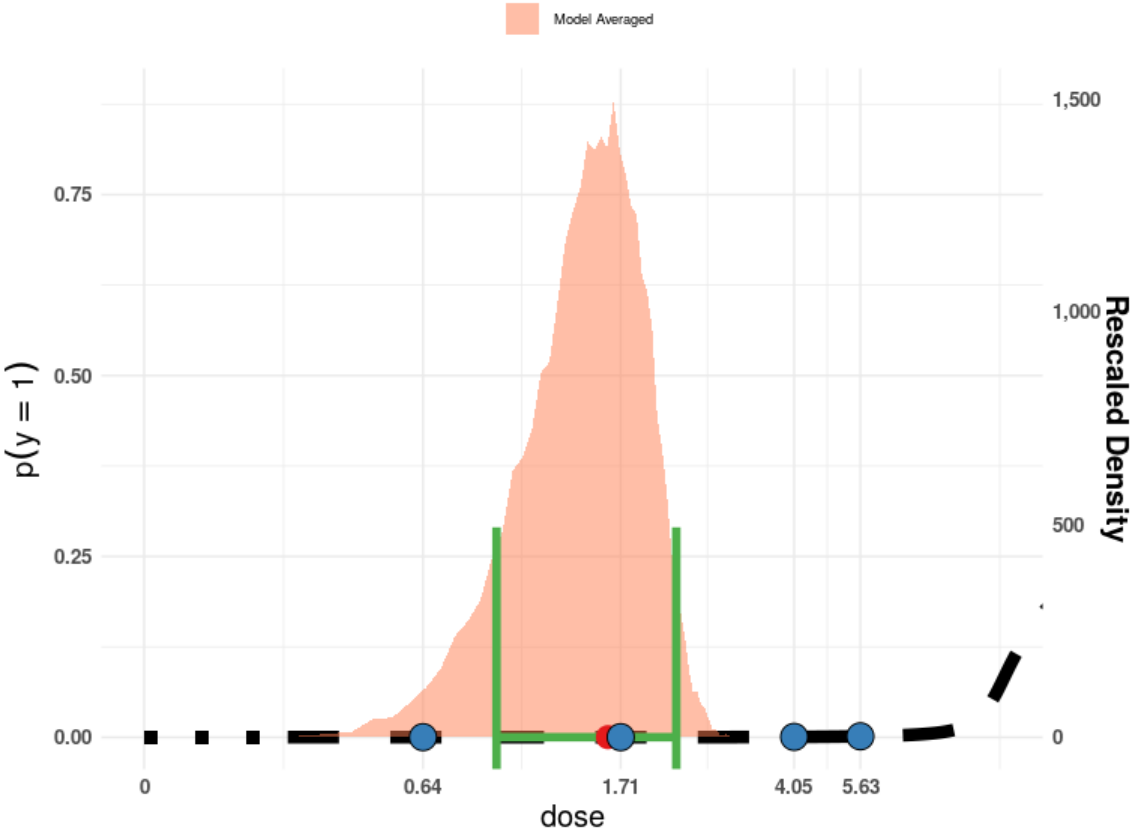
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	1.037	1.569	2.116	0.256	1
IE4_Q	1.449	2.015	2.525	0.097	1
H4_Q	1.068	1.583	2.125	0.251	1
LN4_Q	1.306	1.821	2.337	0.221	1
G4_Q	1.137	1.851	6.988	0.000	0
QE4_Q	0.241	0.394	0.539	0.000	1
P4_Q	0.695	1.148	1.720	0.092	1
L4_Q	0.676	1.136	1.700	0.083	1

Plots of Fitted Models




Weight
0.2
0.1
0.0
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
InvExp
LogNormal
QuadExp
Hill
Logistic
Probit
p(y = 1)
0.0015
0.0010
0.0005
0.0000
0
0.64
1.71
4.05
5.63
dose


Model Averaged
p(y = 1)
0.75
0.50
0.25
0.00
1,500
1,000
500
0
Rescaled Density
0
0.64
1.71
4.05
5.63
dose

Steinmaus et al. (2013) bladder cancer, relative BMR 5%

Exposure: lifetime average, all years, based on arsenic daily intakes (the preferred exposure estimate for the study)

Data Description

The endpoint to be analyzed is: Adj.cases for bladder cancer

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	N
0.58	32	138516
1.55	34	136406
3.46	76	108281
4.67	90	66797

The 'Value for CES' is set to 1.155e-05.

Extended dose range is applied.

Informative background prior: min: 0.00022871; the most likely: 0.00023102; max: 0.00023333. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 1.70e-03).

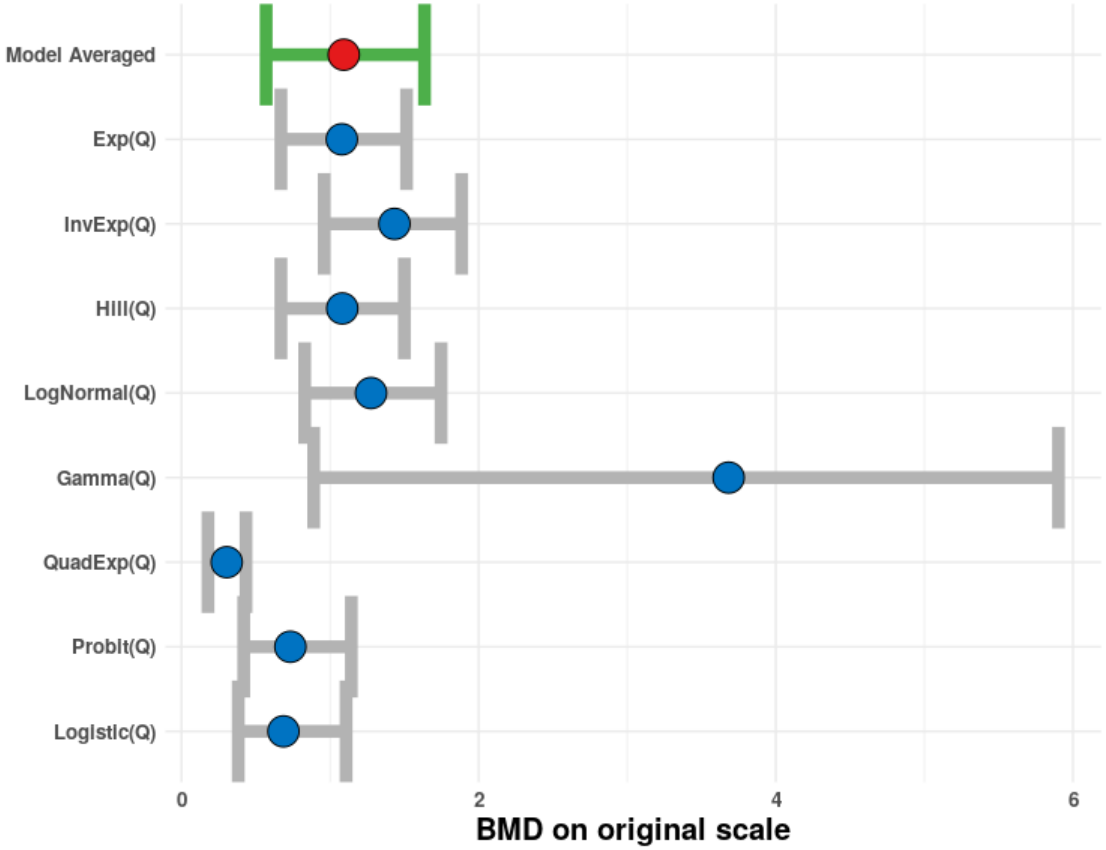
Model Averaged BMD

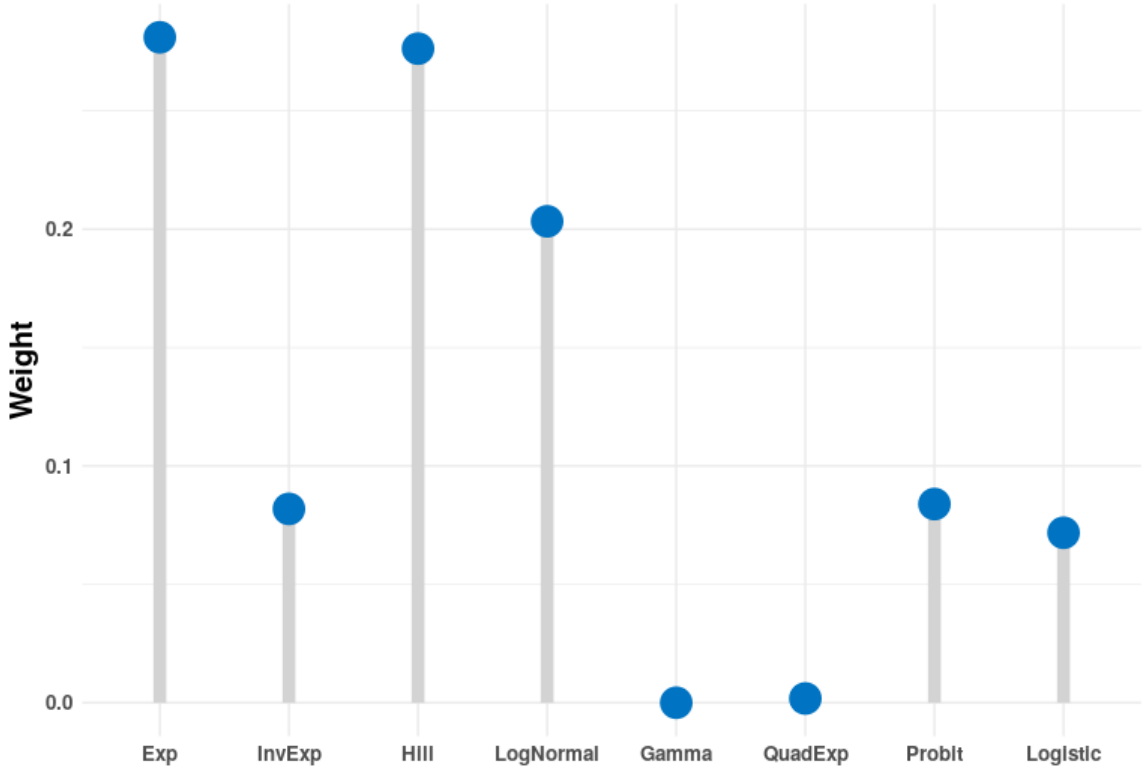
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.57	1.092	1.636

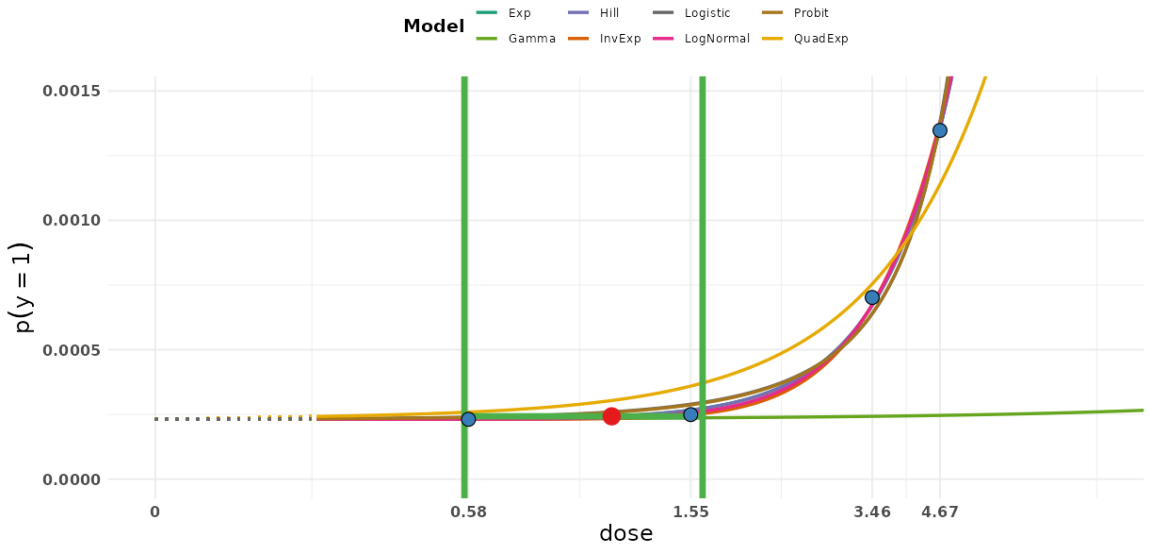
Estimated BMDs per model

Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.669	1.079	1.515	0.281	1
IE4_Q	0.960	1.433	1.886	0.082	1
H4_Q	0.669	1.082	1.500	0.276	1
LN4_Q	0.829	1.276	1.747	0.203	1
G4_Q	0.889	3.682	5.903	0.000	0
QE4_Q	0.178	0.304	0.434	0.002	1
P4_Q	0.419	0.733	1.143	0.084	1
L4_Q	0.382	0.686	1.108	0.072	1

Plots of Fitted Models




Weight
0.2
0.1
0.0
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
0.0015
0.0010
0.0005
0.0000
p(y = 1)
0
0.58
1.55
3.46
4.67
dose


Model Averaged
0.8
0.6
0.4
0.2
0.0
p(y = 1)
400
300
200
100
0
Rescaled Density
0
0.58
1.55
3.46
4.67
dose

Steinmaus et al. (2013) bladder cancer, relative BMR 5%

Exposure: lifetime average, all years, based on arsenic daily intakes
Sensitivity analysis: the highest exposure point estimate doubled

Data Description
The endpoint to be analyzed is: Adj.cases for bladder cancer

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	N
0.58	32	138516
1.55	34	136406
3.46	76	108281
9.06	90	66797

The 'Value for CES' is set to 1.155e-05.

Extended dose range is applied.

Informative background prior: min: 0.00022871; the most likely: 0.00023102; max: 0.00023333. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 2.81e-01).

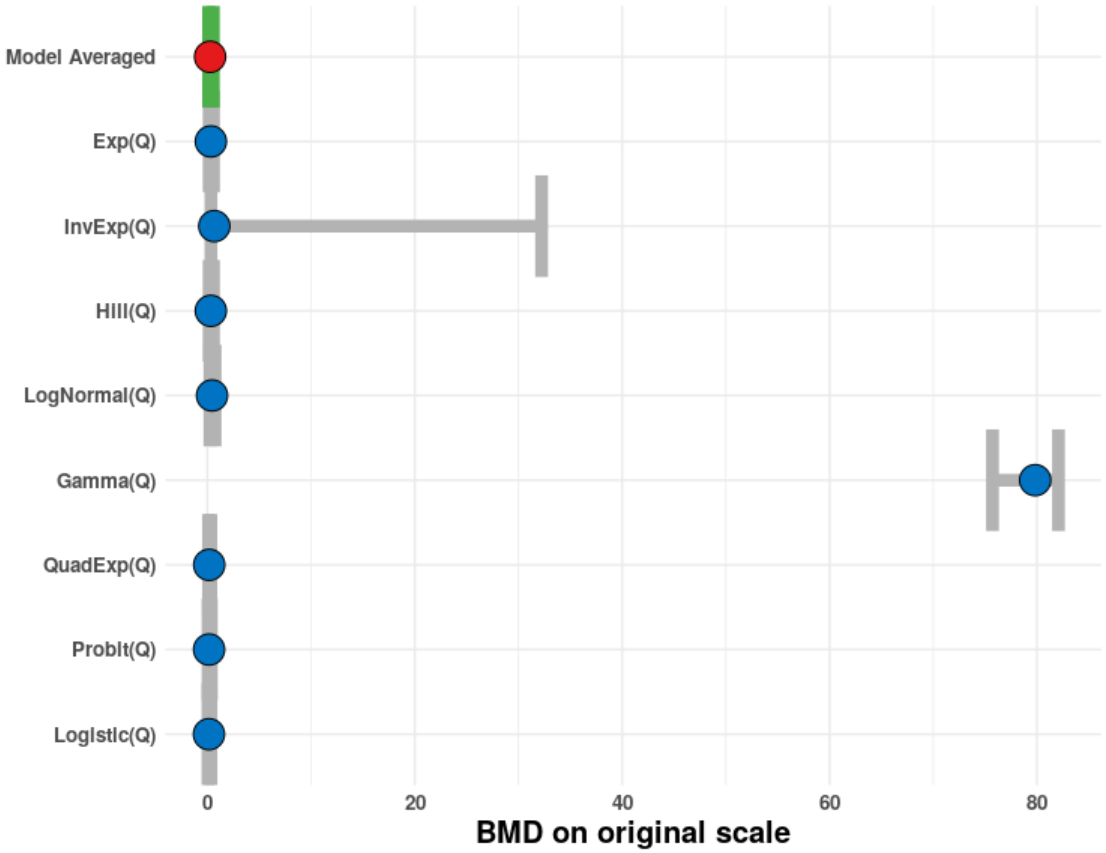
Model Averaged BMD

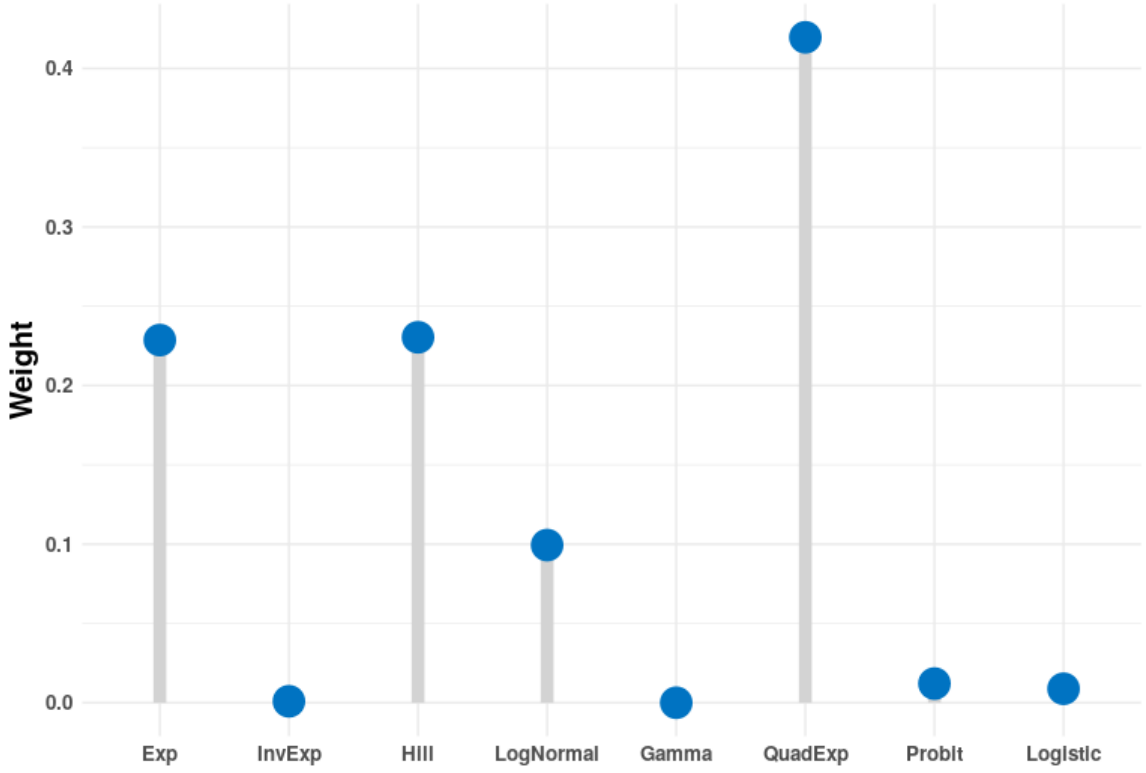
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.117	0.258	0.571

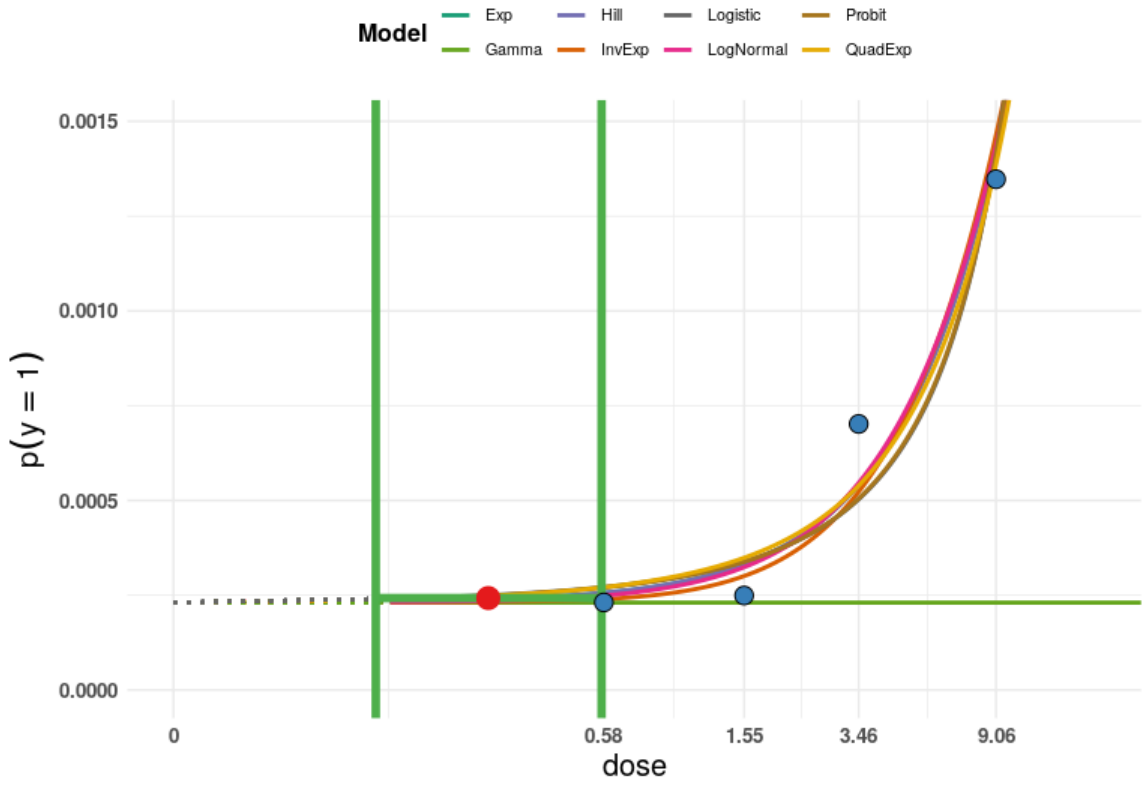
Estimated BMDs per model

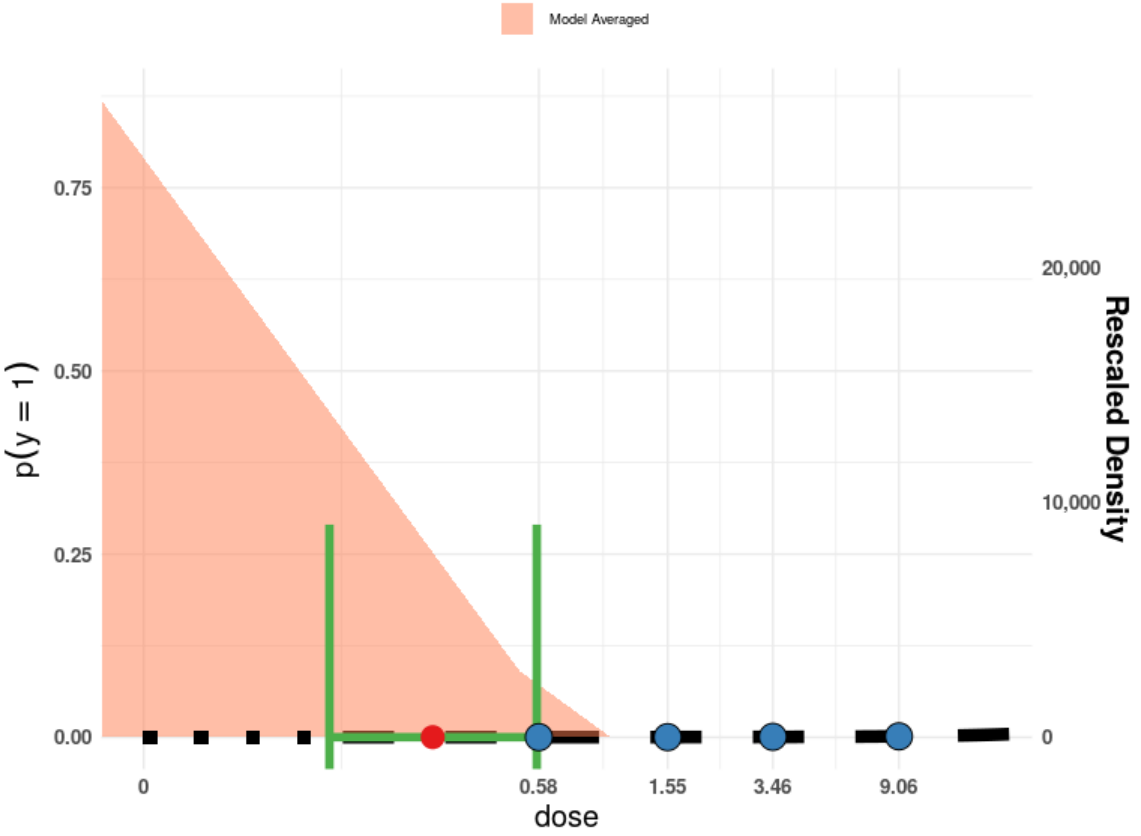
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.168	0.334	0.589	0.229	1
IE4_Q	0.341	0.665	32.231	0.001	0
H4_Q	0.167	0.330	0.587	0.230	1
LN4_Q	0.241	0.447	0.741	0.099	1
G4_Q	75.714	79.830	82.079	0.000	0
QE4_Q	0.109	0.173	0.333	0.420	1
P4_Q	0.064	0.162	0.372	0.012	1
L4_Q	0.057	0.149	0.342	0.009	1

Plots of Fitted Models




Weight
0.4
0.3
0.2
0.1
0.0
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
p(y = 1)
0.0015
0.0010
0.0005
0.0000
0
0.58
1.55
3.46
9.06
dose


Model Averaged
0.75
0.50
0.25
0.00
p(y = 1)
20,000
10,000
0
Rescaled Density
0
0.58
1.55
3.46
9.06
dose

Steinmaus et al. (2013) bladder cancer, relative BMR 5%

Exposure: lifetime average before 1971, based on arsenic water concentrations and water intake of 1.9L (included only in the uncertainty analysis)

Data Description

The endpoint to be analyzed is: Adj.cases for bladder cancer

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	N
0.44	27	140802
1.66	36	135849
6.07	73	97642
9.38	95	75708

The 'Value for CES' is set to 9.59e-06.

Extended dose range is applied.

Informative background prior: min: 0.00018217; the most likely: 0.00019176; max: 0.00020135. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 1.95e-03).

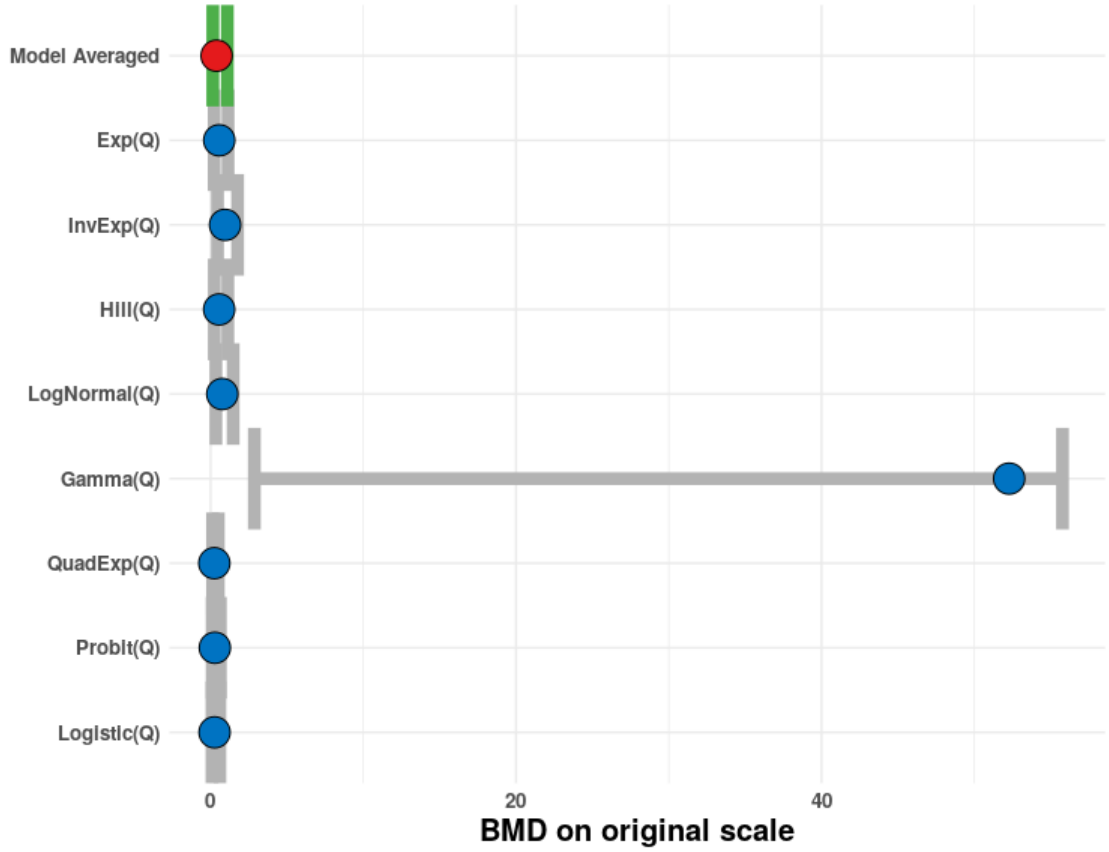
Model Averaged BMD

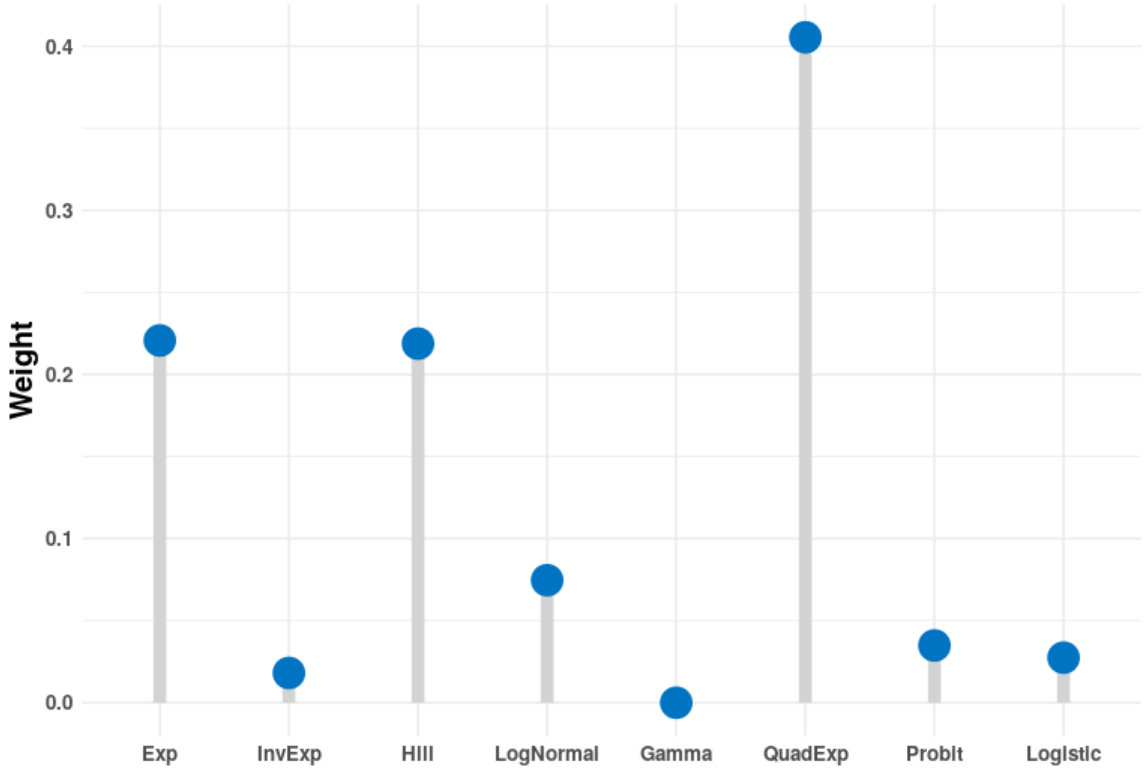
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.143	0.392	1.095

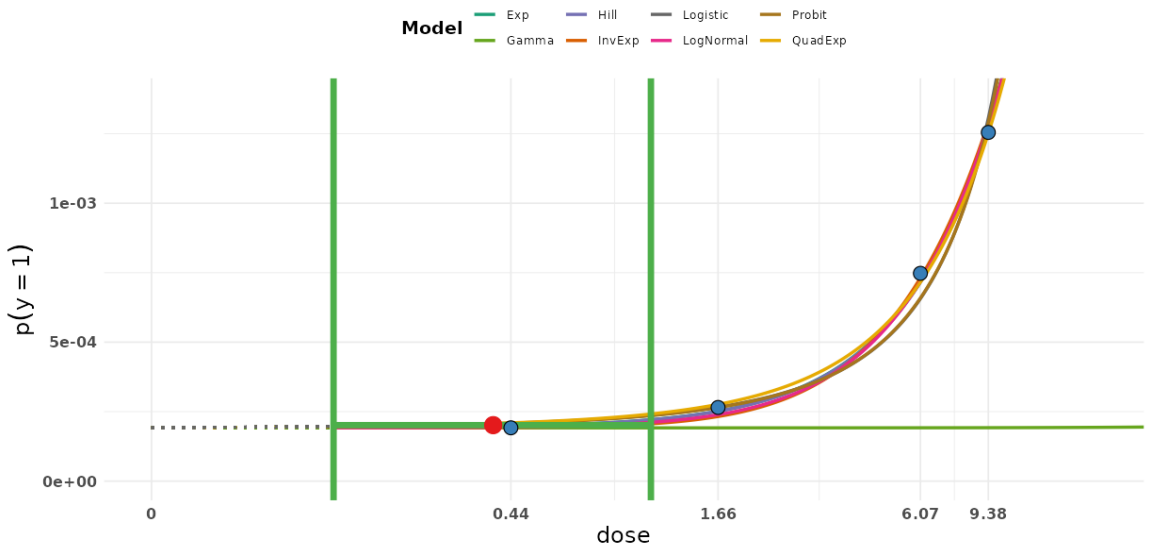
Estimated BMDs per model

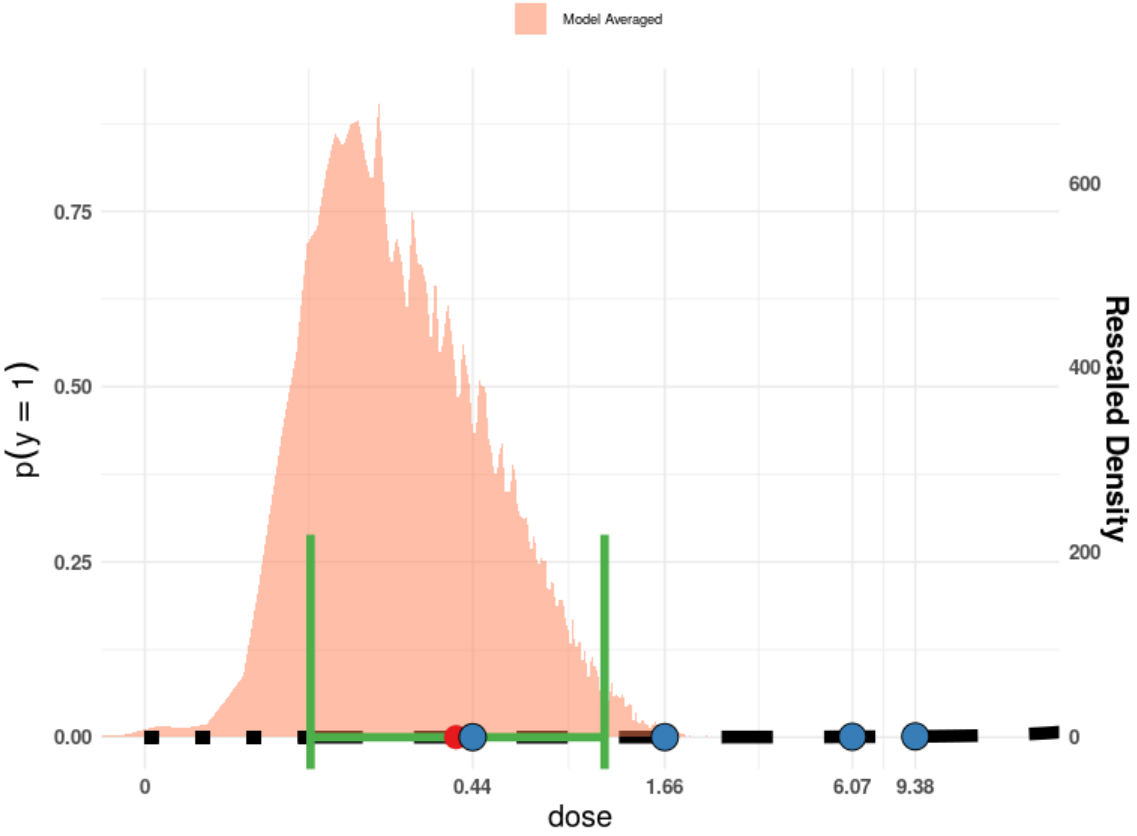
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.236	0.565	1.142	0.221	1
IE4_Q	0.453	0.947	1.767	0.018	1
H4_Q	0.242	0.560	1.129	0.219	1
LN4_Q	0.347	0.763	1.478	0.075	1
G4_Q	2.865	52.283	55.775	0.000	0
QE4_Q	0.127	0.243	0.504	0.405	1
P4_Q	0.104	0.278	0.638	0.035	1
L4_Q	0.091	0.260	0.605	0.027	1

Plots of Fitted Models




Weight
0.4
0.3
0.2
0.1
0.0
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
p(y = 1)
1e-03
5e-04
0e+00
0
0.44
1.66
6.07
9.38
dose


Model Averaged
0.75
0.50
0.25
0.00
p(y = 1)
600
400
200
0
Rescaled Density
0
0.44
1.66
6.07
9.38
dose

Steinmaus et al. (2013) bladder cancer, relative BMR 5%

Exposure: lifetime average before 1971, based on arsenic daily intakes (included only in the uncertainty analysis)

Data Description

The endpoint to be analyzed is: Adj.cases for bladder cancer

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	N
0.44	30	140802
1.57	36	136557
5.18	74	108962
7.79	92	63679

The 'Value for CES' is set to 1.066e-05.

Extended dose range is applied.

Informative background prior: min: 0.00021093; the most likely: 0.00021307; max: 0.00021520. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 1.39e-03).

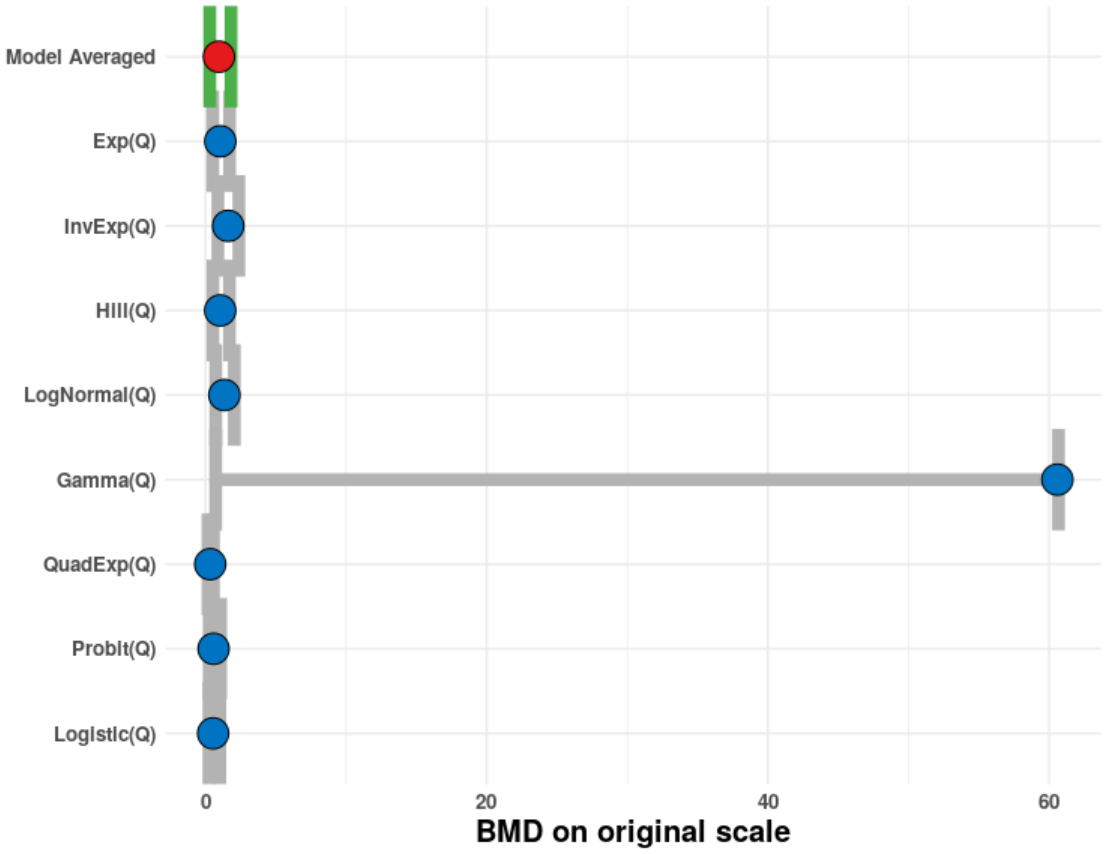
Model Averaged BMD

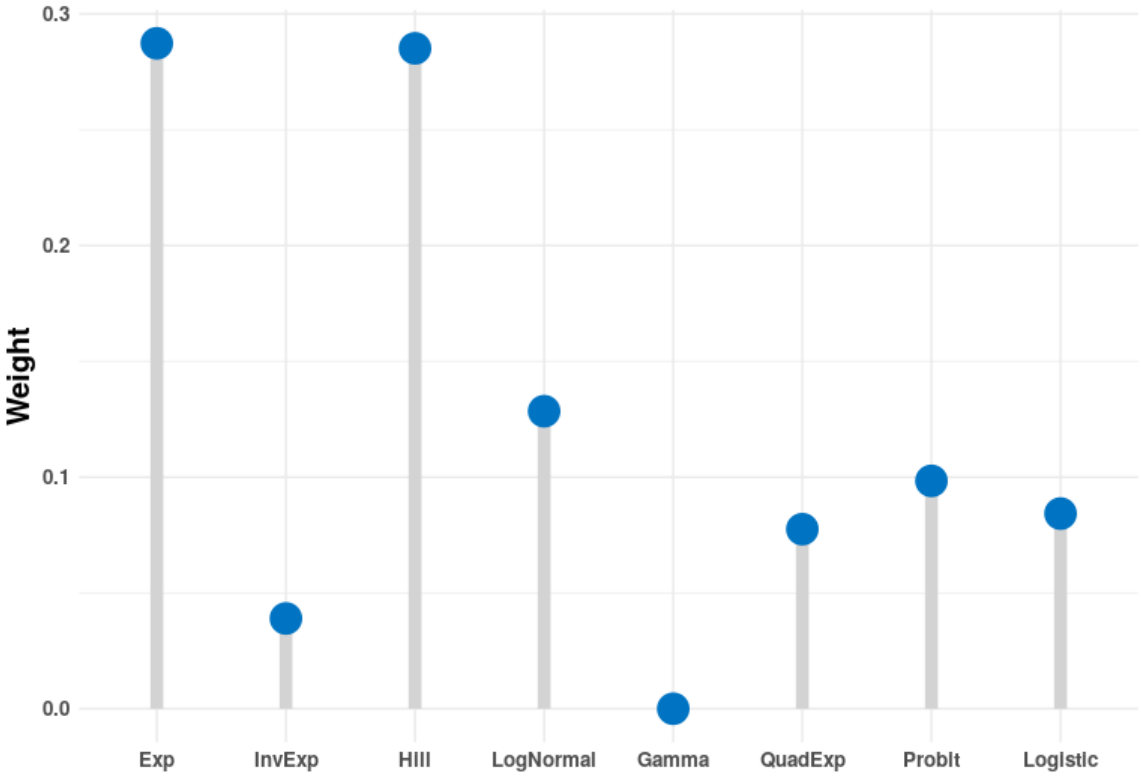
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.302	0.955	1.812

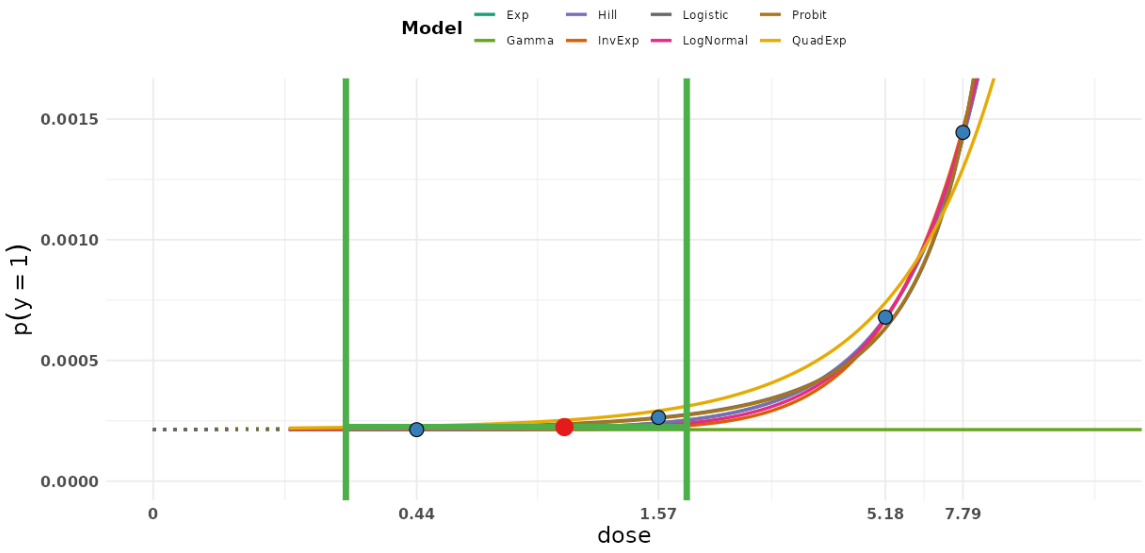
Estimated BMDs per model

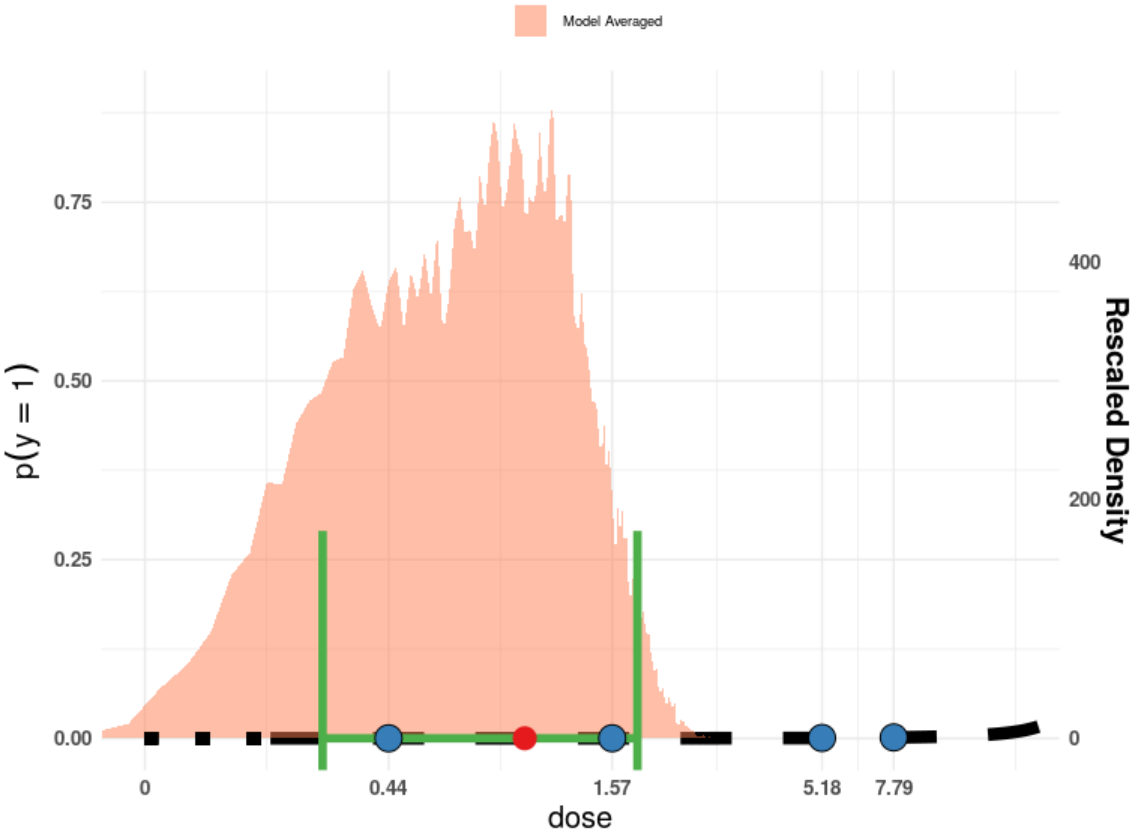
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.515	1.050	1.707	0.287	1
IE4_Q	0.881	1.610	2.371	0.039	1
H4_Q	0.525	1.043	1.701	0.285	1
LN4_Q	0.727	1.338	2.046	0.128	1
G4_Q	0.722	60.595	60.675	0.000	0
QE4_Q	0.175	0.333	0.563	0.078	1
P4_Q	0.262	0.574	1.071	0.098	1
L4_Q	0.242	0.540	1.014	0.084	1

Plots of Fitted Models




Weight
0.3
0.2
0.1
0.0
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
p(y = 1)
0.0015
0.0010
0.0005
0.0000
0
0.44
1.57
5.18
7.79
dose


Model Averaged
0.75
0.50
0.25
0.00
p(y = 1)
400
200
0
Rescaled Density
0
0.44
1.57
5.18
7.79
dose

Steinmaus et al. (2013) lung cancer, relative BMR 5%

Exposure: lifetime average, all years, based on arsenic water concentrations and water intake of 1.9L (included only in the uncertainty analysis)

Data Description

The endpoint to be analyzed is: Adj.cases for lung cancer

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	N
0.64	64	142031
1.71	58	132891
4.05	76	99844
5.63	107	75234

The 'Value for CES' is set to 2.254e-05.

Extended dose range is applied.

Informative background prior: min: 0.00044610; the most likely: 0.00045061; max: 0.00045511. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 1.72e-03).

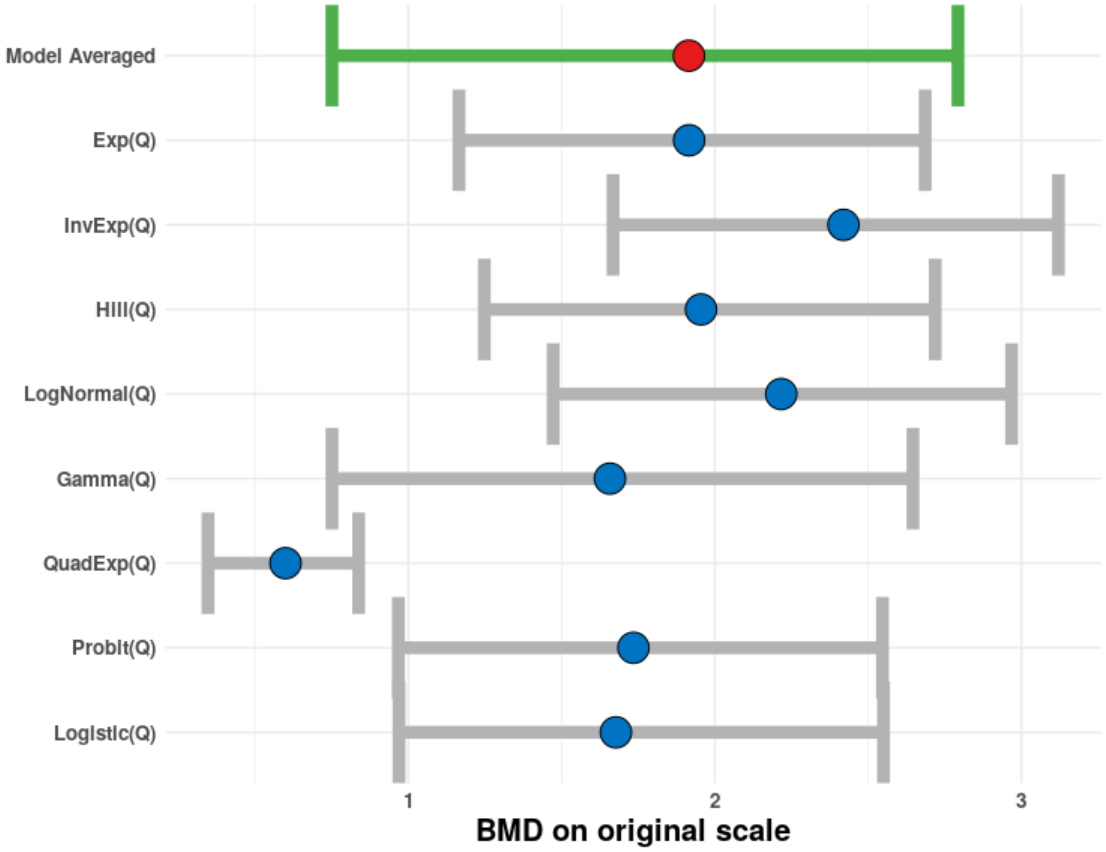
Model Averaged BMD

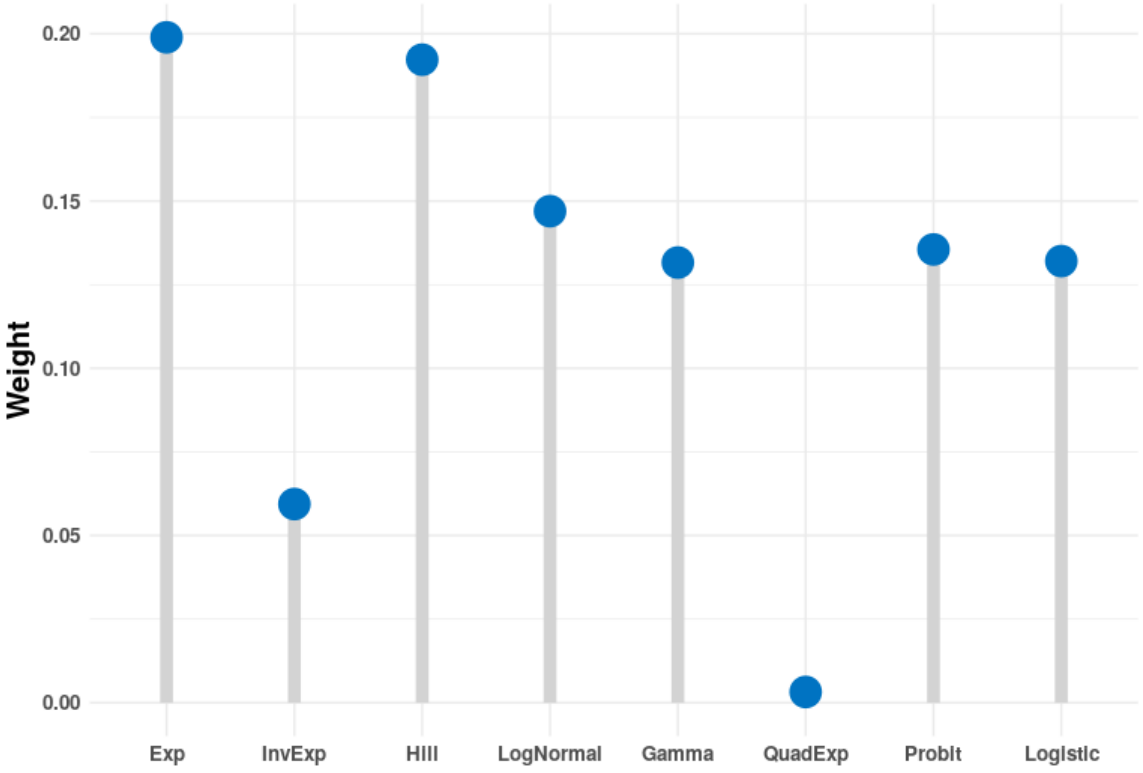
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.751	1.915	2.793

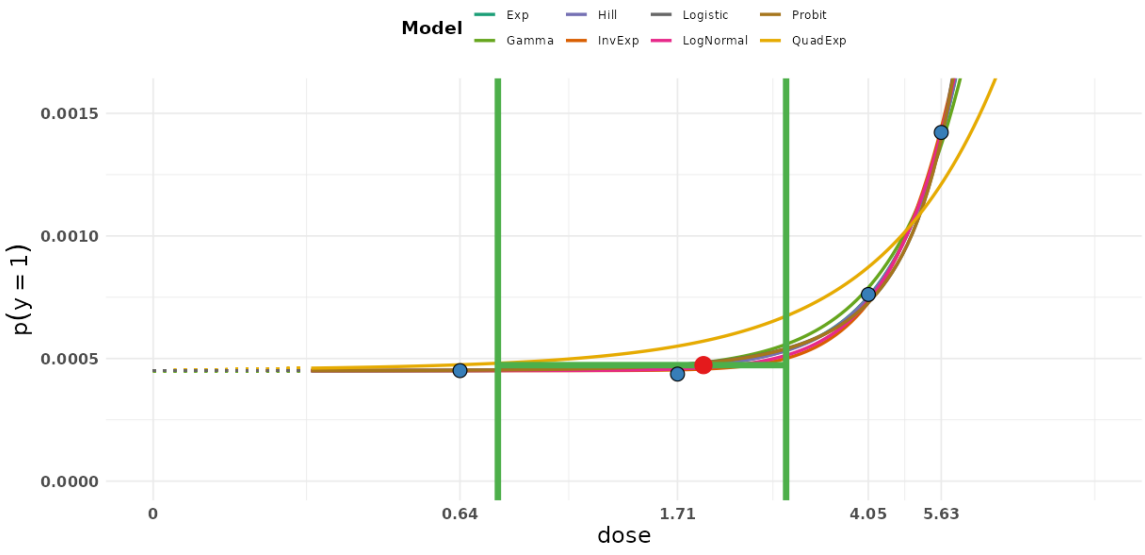
Estimated BMDs per model

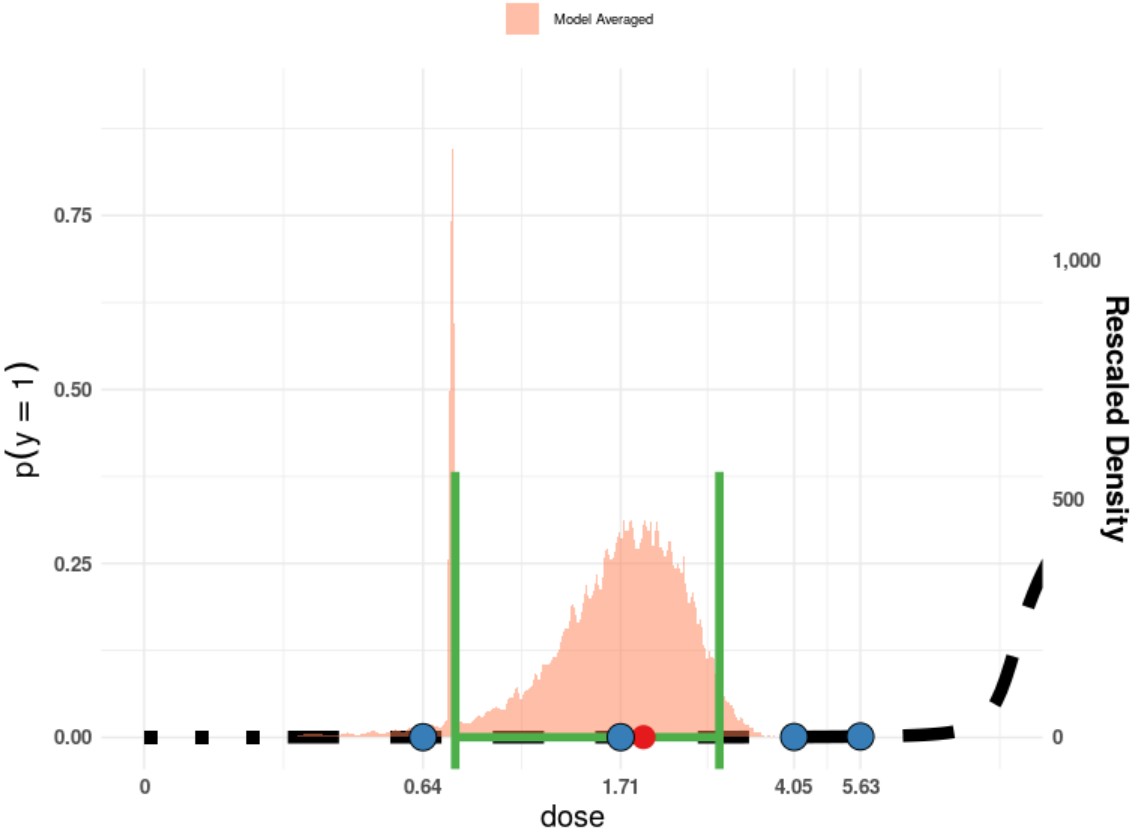
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	1.165	1.916	2.686	0.199	1
IE4_Q	1.668	2.420	3.121	0.059	1
H4_Q	1.248	1.955	2.719	0.192	1
LN4_Q	1.473	2.217	2.968	0.147	1
G4_Q	0.751	1.658	2.646	0.132	0
QE4_Q	0.347	0.600	0.838	0.003	1
P4_Q	0.968	1.735	2.547	0.136	1
L4_Q	0.970	1.677	2.550	0.132	1

Plots of Fitted Models




Weight
0.20
0.15
0.10
0.05
0.00
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
p(y = 1)
0.0015
0.0010
0.0005
0.0000
0
0.64
1.71
4.05
5.63
dose


Model Averaged
0.75
0.50
0.25
0.00
p(y = 1)
1,000
500
0
Rescaled Density
0
0.64
1.71
4.05
5.63
dose

Steinmaus et al. (2013) lung cancer, relative BMR 5%

Exposure: lifetime average, all years, based on arsenic daily intakes (the preferred exposure estimate for the study)

Data Description

The endpoint to be analyzed is: Adj.cases for lung cancer

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	N
0.58	70	138516
1.55	60	136406
3.46	68	108281
4.67	107	66797

The 'Value for CES' is set to 2.528e-05.

Extended dose range is applied.

Informative background prior: min: 0.00048009; the most likely: 0.00050536; max: 0.00053062. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 3.00e-03).

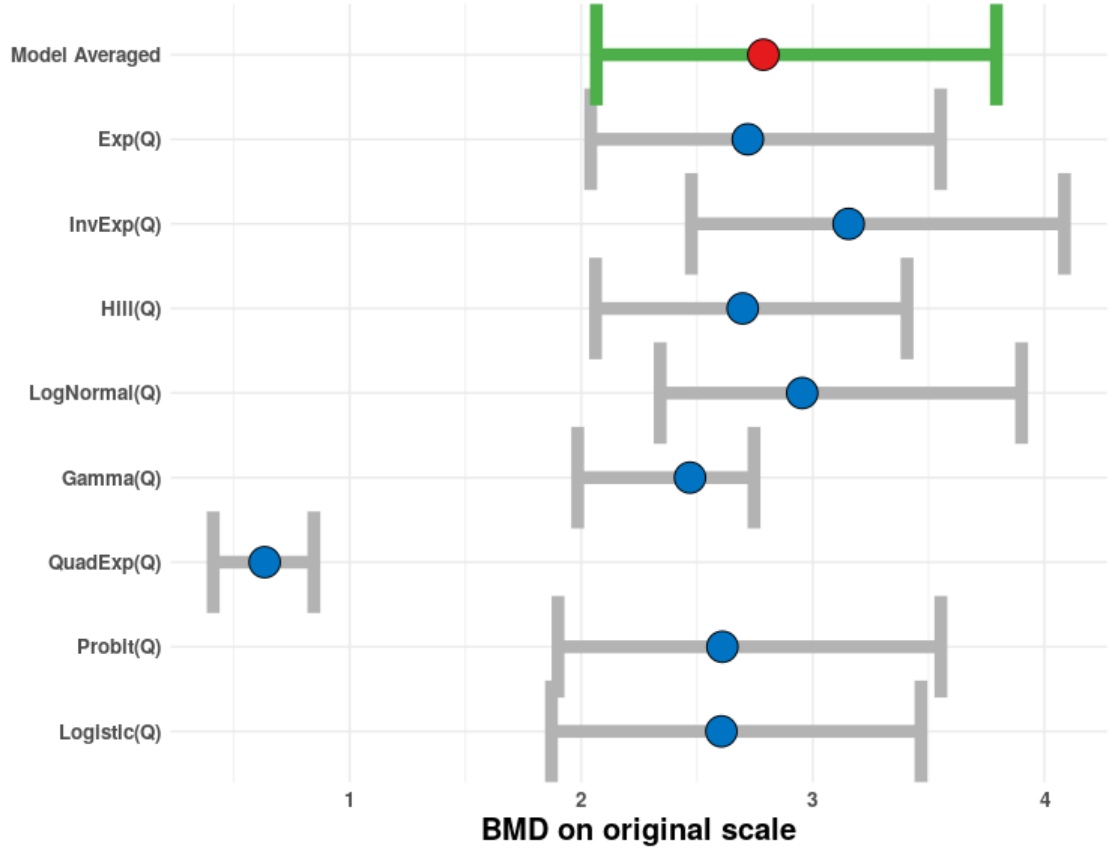
Model Averaged BMD

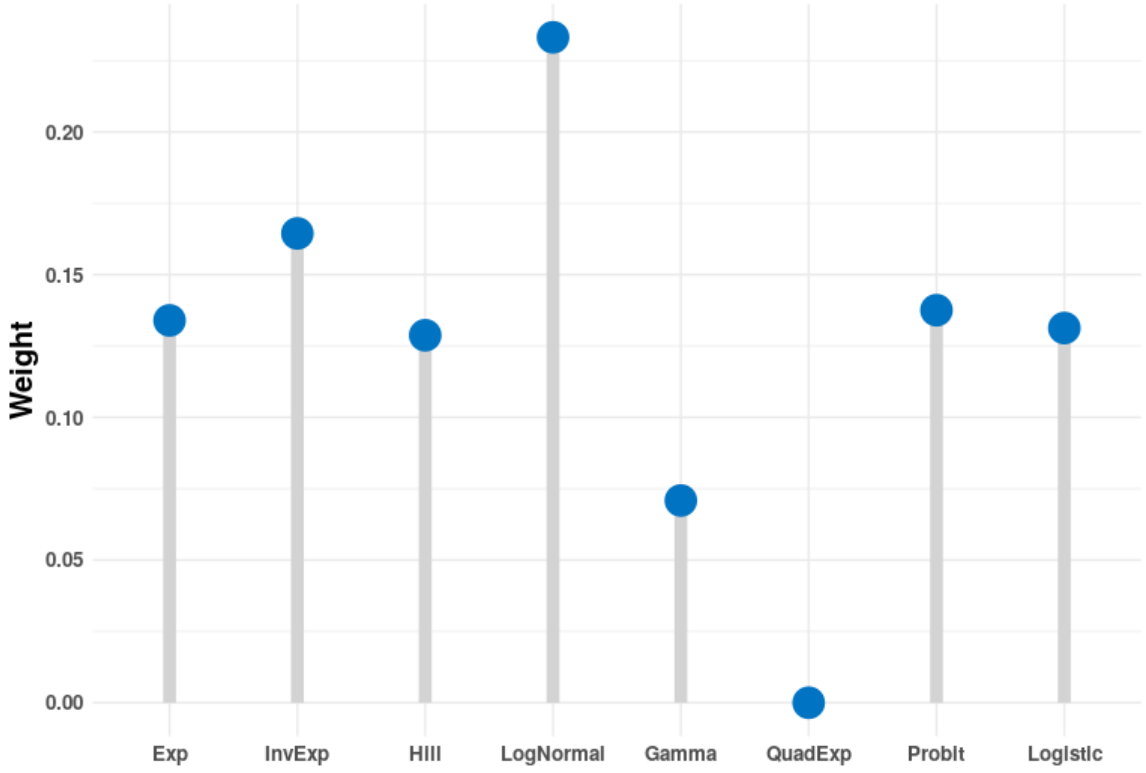
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	2.065	2.787	3.793

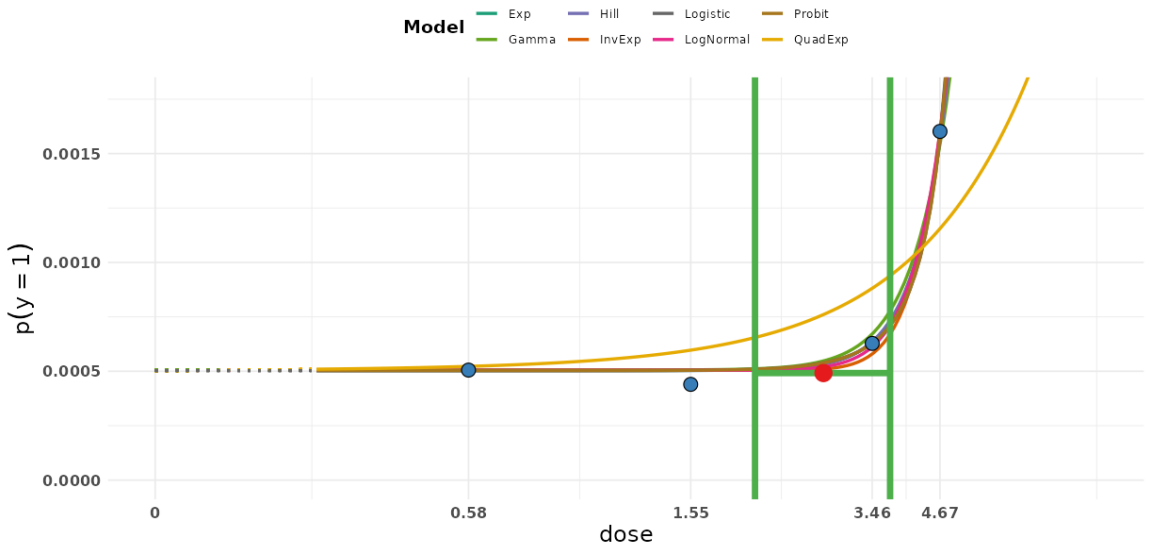
Estimated BMDs per model

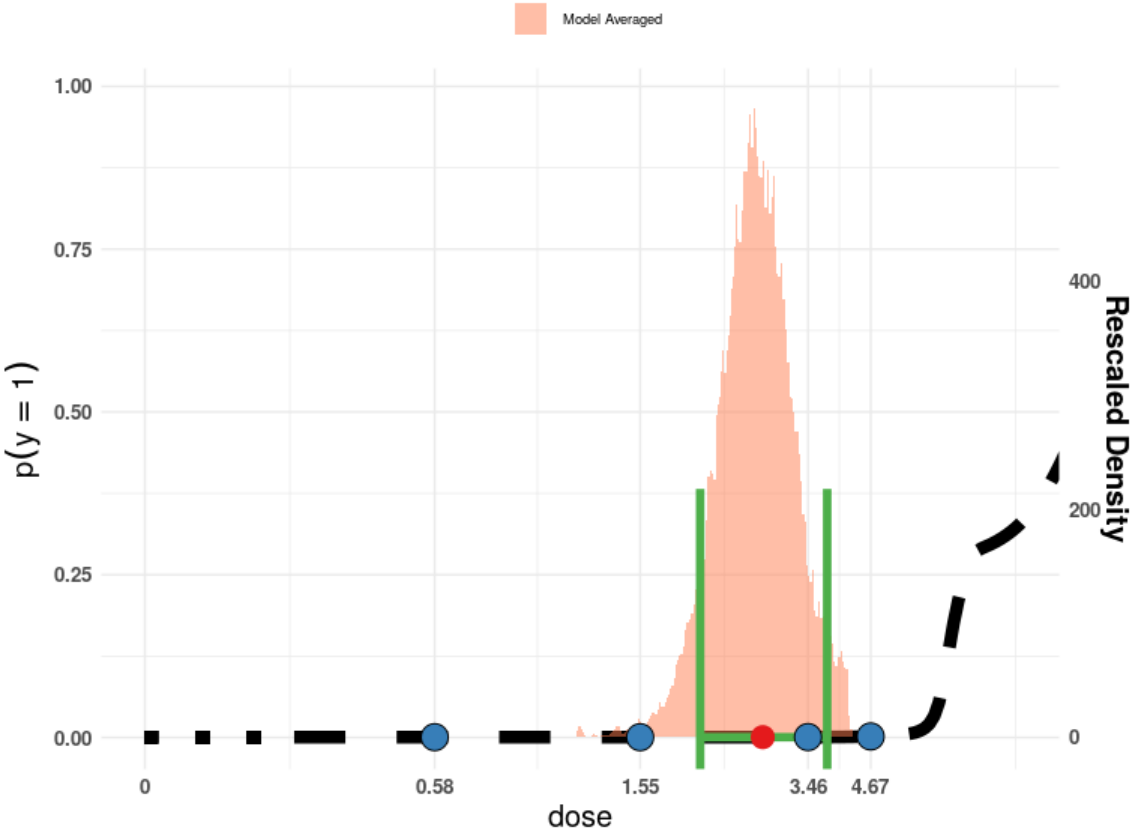
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	2.041	2.719	3.552	0.134	1
IE4_Q	2.475	3.155	4.087	0.164	1
H4_Q	2.062	2.697	3.407	0.129	1
LN4_Q	2.341	2.954	3.902	0.233	1
G4_Q	1.985	2.470	2.746	0.071	1
QE4_Q	0.411	0.633	0.845	0.000	1
P4_Q	1.900	2.610	3.553	0.138	1
L4_Q	1.871	2.605	3.467	0.131	1

Plots of Fitted Models




Weight
0.20
0.15
0.10
0.05
0.00
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
p(y = 1)
0.0015
0.0010
0.0005
0.0000
0
0.58
1.55
3.46
4.67
dose


Model Averaged
1.00
0.75
0.50
0.25
0.00
p(y = 1)
400
200
0
Rescaled Density
0
0.58
1.55
3.46
4.67
dose

Steinmaus et al. (2013) lung cancer, relative BMR 5%

Exposure: lifetime average, all years, based on arsenic daily intakes
Sensitivity analysis: the highest exposure point estimate doubled

Data Description
The endpoint to be analyzed is: Adj.cases for lung cancer

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	N
0.58	70	138516
1.55	60	136406
3.46	68	108281
9.06	107	66797

The 'Value for CES' is set to 2.528e-05.

Extended dose range is applied.

Informative background prior: min: 0.00045482; the most likely: 0.00050536; max: 0.00055589. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 4.37e-03).

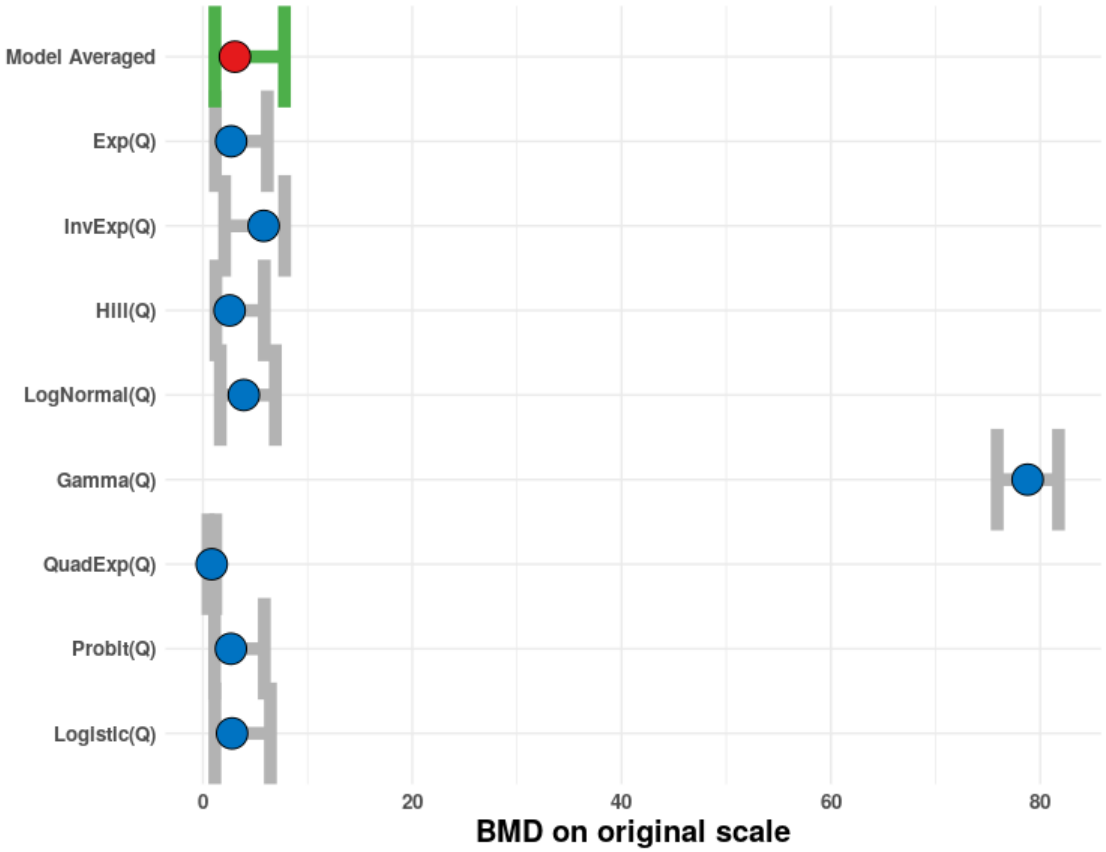
Model Averaged BMD

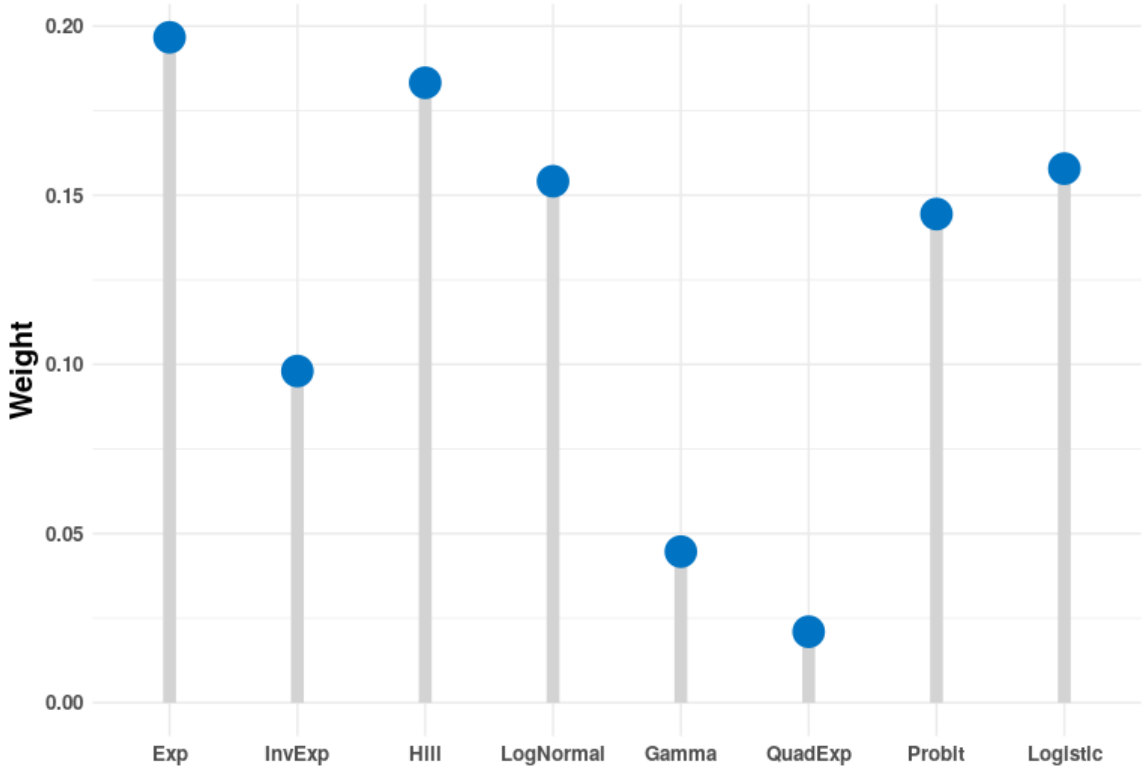
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	1.139	3.055	7.786

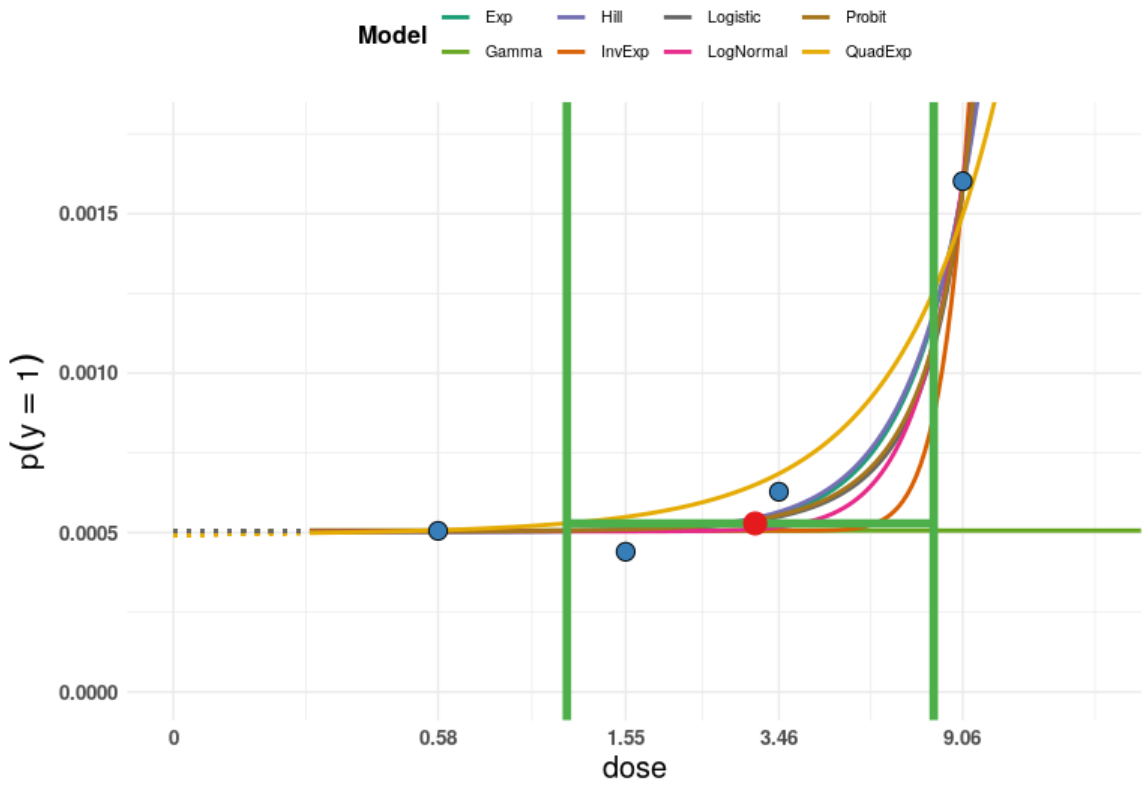
Estimated BMDs per model

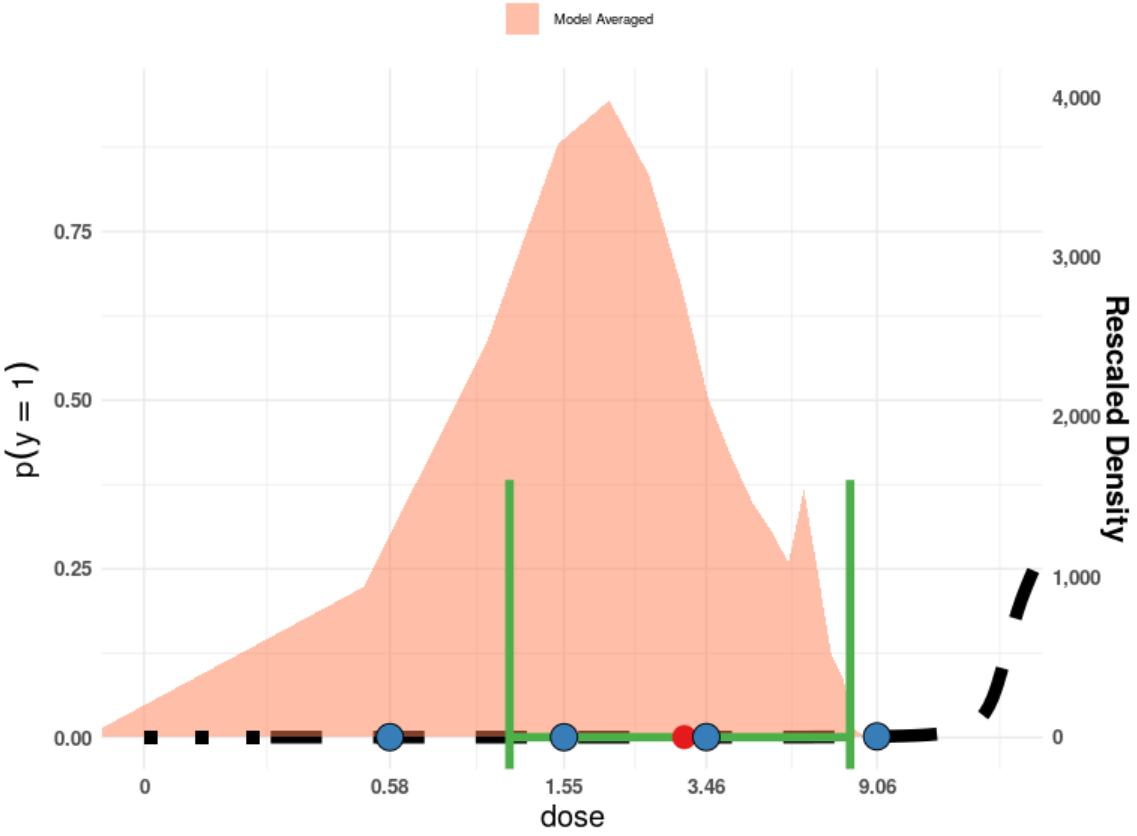
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	1.189	2.693	6.151	0.197	1
IE4_Q	2.073	5.798	7.807	0.098	0
H4_Q	1.234	2.546	5.860	0.183	1
LN4_Q	1.655	3.905	6.918	0.154	1
G4_Q	75.889	78.794	81.744	0.045	1
QE4_Q	0.480	0.838	1.227	0.021	1
P4_Q	1.105	2.669	5.864	0.144	1
L4_Q	1.135	2.783	6.445	0.158	1

Plots of Fitted Models




Weight
0.20
0.15
0.10
0.05
0.00
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
p(y = 1)
0.0015
0.0010
0.0005
0.0000
0
0.58
1.55
3.46
9.06
dose


Model Averaged
p(y = 1)
0.75
0.50
0.25
0.00
4,000
3,000
2,000
1,000
0
Rescaled Density
0
0.58
1.55
3.46
9.06
dose

Steinmaus et al. (2013) lung cancer, relative BMR 5%

Exposure: lifetime average before 1971, based on arsenic water concentrations and water intake of 1.9L (included only in the uncertainty analysis)

Data Description

The endpoint to be analyzed is: Adj.cases for lung cancer

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	N
0.44	51	140802
1.66	62	135849
6.07	71	97642
9.38	118	75708

The 'Value for CES' is set to 1.812e-05.

Extended dose range is applied.

Informative background prior: min: 0.00034410; the most likely: 0.00036221; max: 0.00038032. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 3.29e-03).

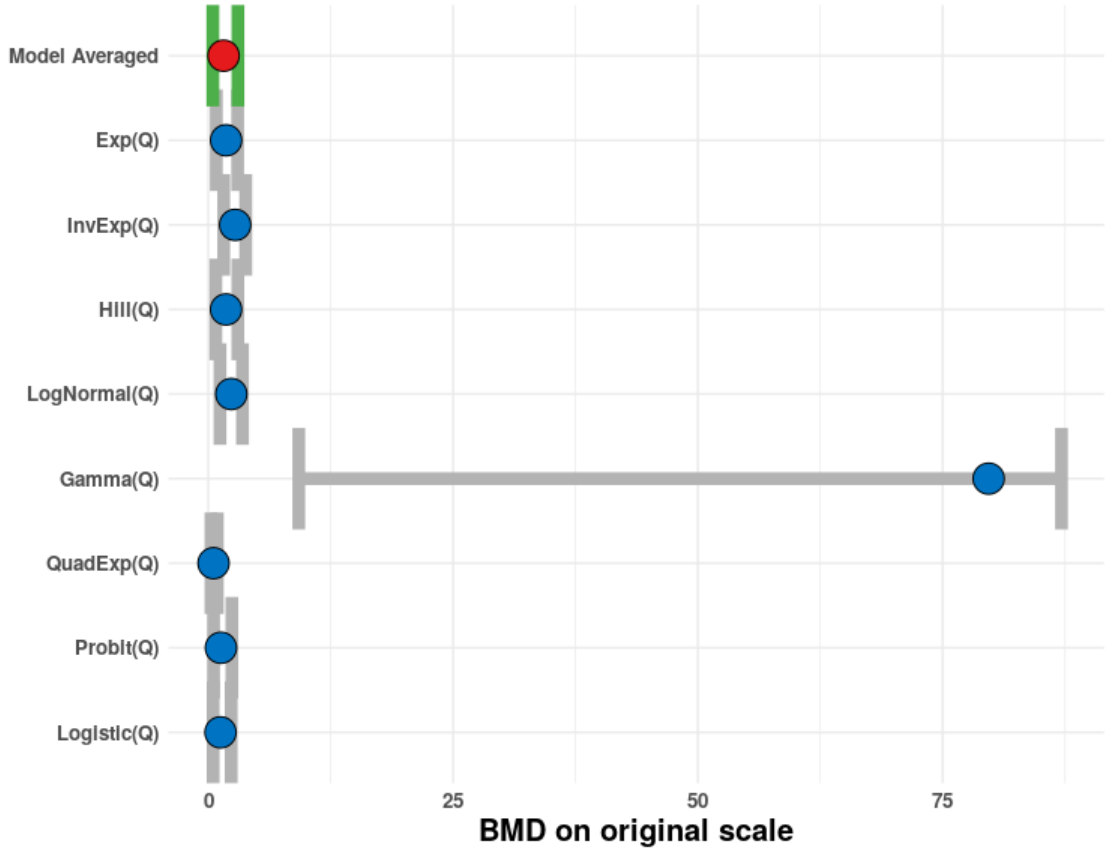
Model Averaged BMD

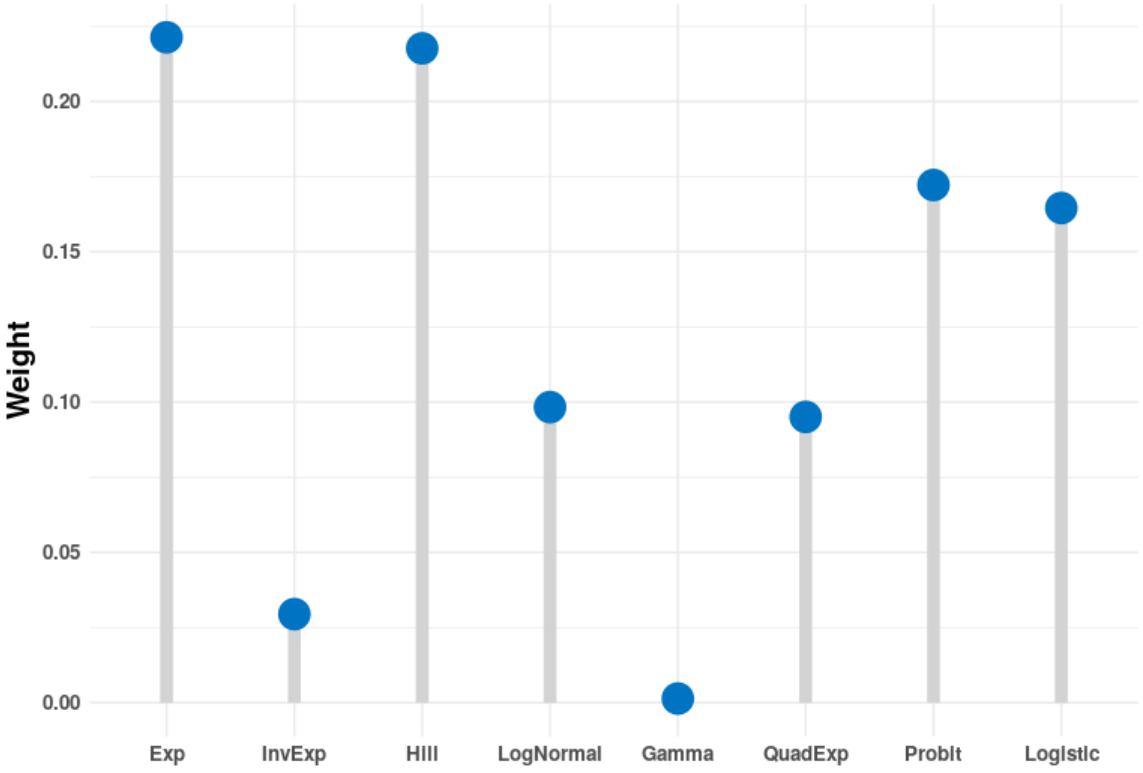
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.458	1.556	3.022

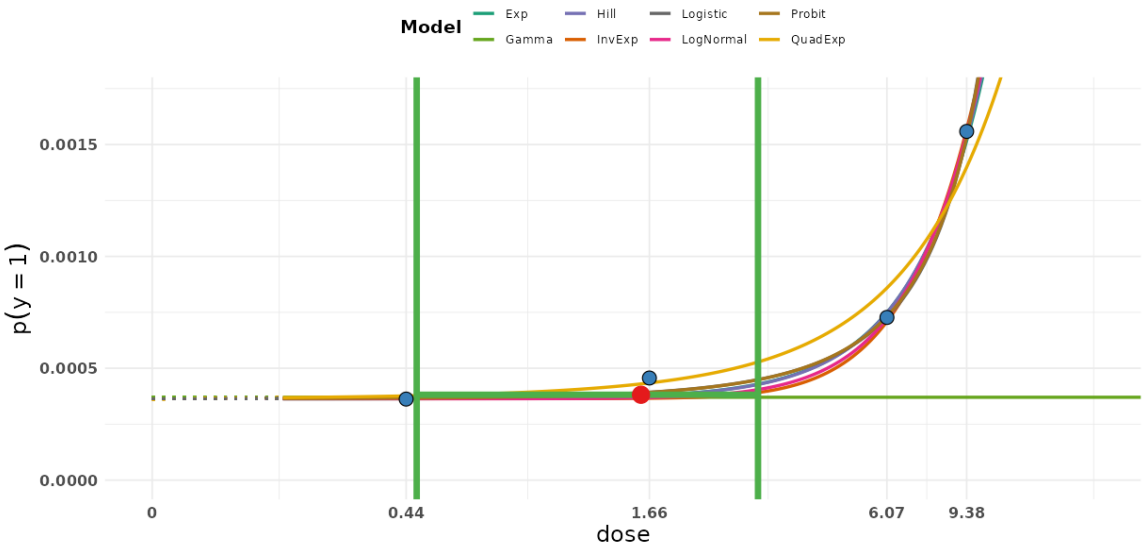
Estimated BMDs per model

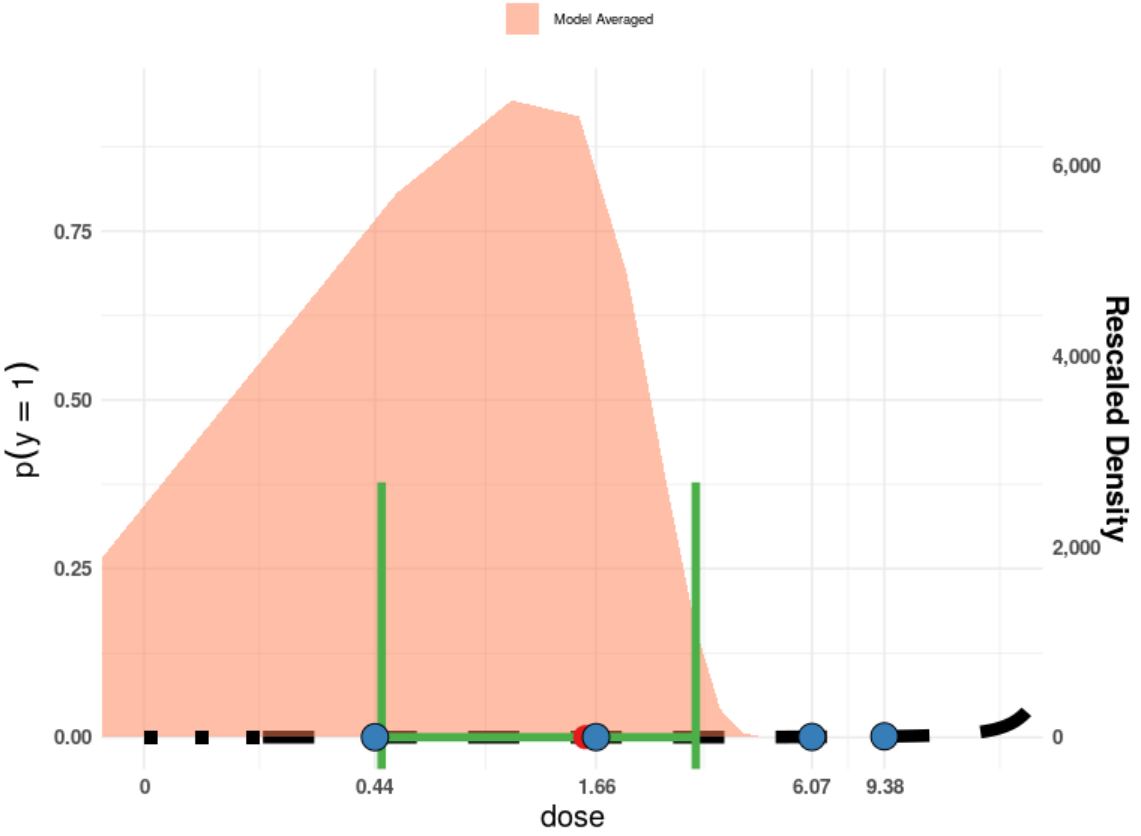
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.816	1.814	2.993	0.221	1
IE4_Q	1.570	2.740	3.819	0.029	1
H4_Q	0.760	1.809	3.014	0.218	1
LN4_Q	1.189	2.343	3.488	0.098	1
G4_Q	9.237	79.696	87.136	0.001	0
QE4_Q	0.269	0.530	0.914	0.095	1
P4_Q	0.534	1.285	2.405	0.172	1
L4_Q	0.487	1.242	2.332	0.165	1

Plots of Fitted Models




Weight
0.20
0.15
0.10
0.05
0.00
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
p(y = 1)
0.0015
0.0010
0.0005
0.0000
0
0.44
1.66
6.07
9.38
dose


Model Averaged
p(y = 1)
0.75
0.50
0.25
0.00
6,000
4,000
2,000
0
Rescaled Density
0
0.44
1.66
6.07
9.38
dose

Steinmaus et al. (2013) lung cancer, relative BMR 5%

Exposure: lifetime average before 1971, based on arsenic daily intakes (included only in the uncertainty analysis)

Data Description

The endpoint to be analyzed is: Adj.cases for lung cancer

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	N
0.44	54	140802
1.57	62	136557
5.18	68	108962
7.79	119	63679

The 'Value for CES' is set to 0.00001918.

Extended dose range is applied.

Informative background prior: min: 0.00037968; the most likely: 0.00038352; max: 0.00038735. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 2.50e-03).

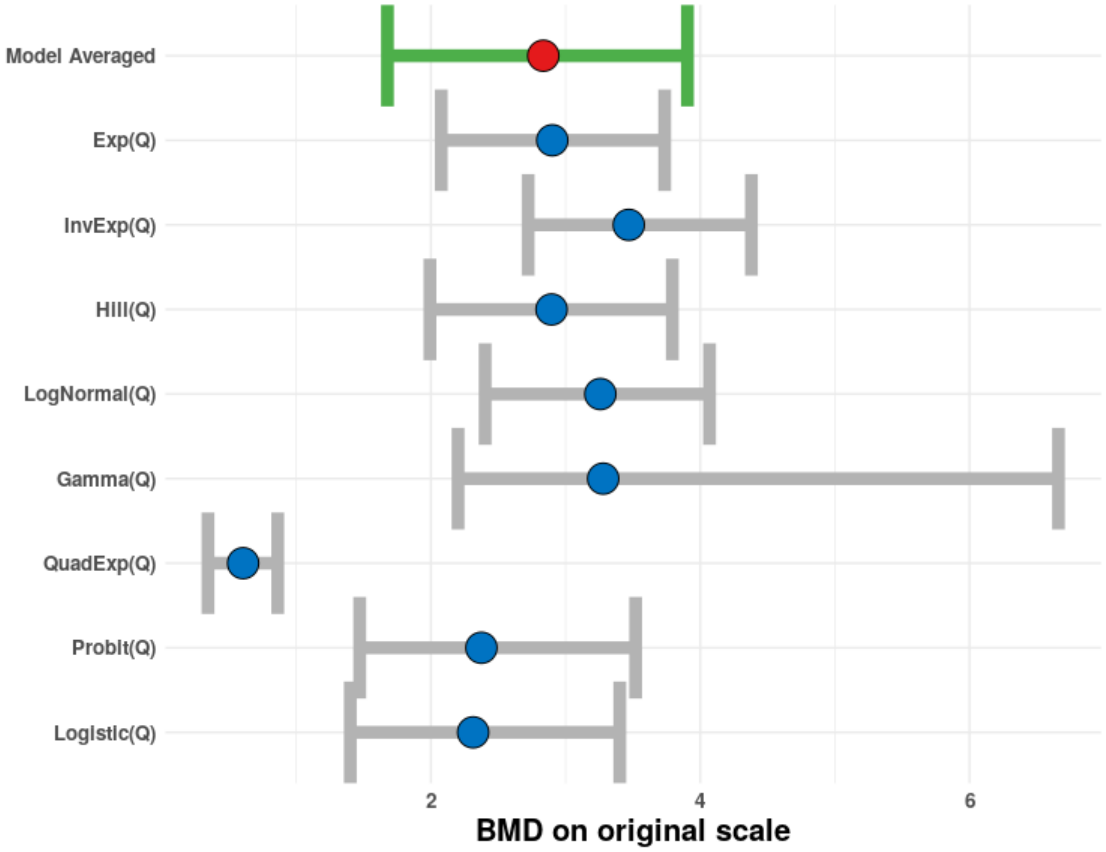
Model Averaged BMD

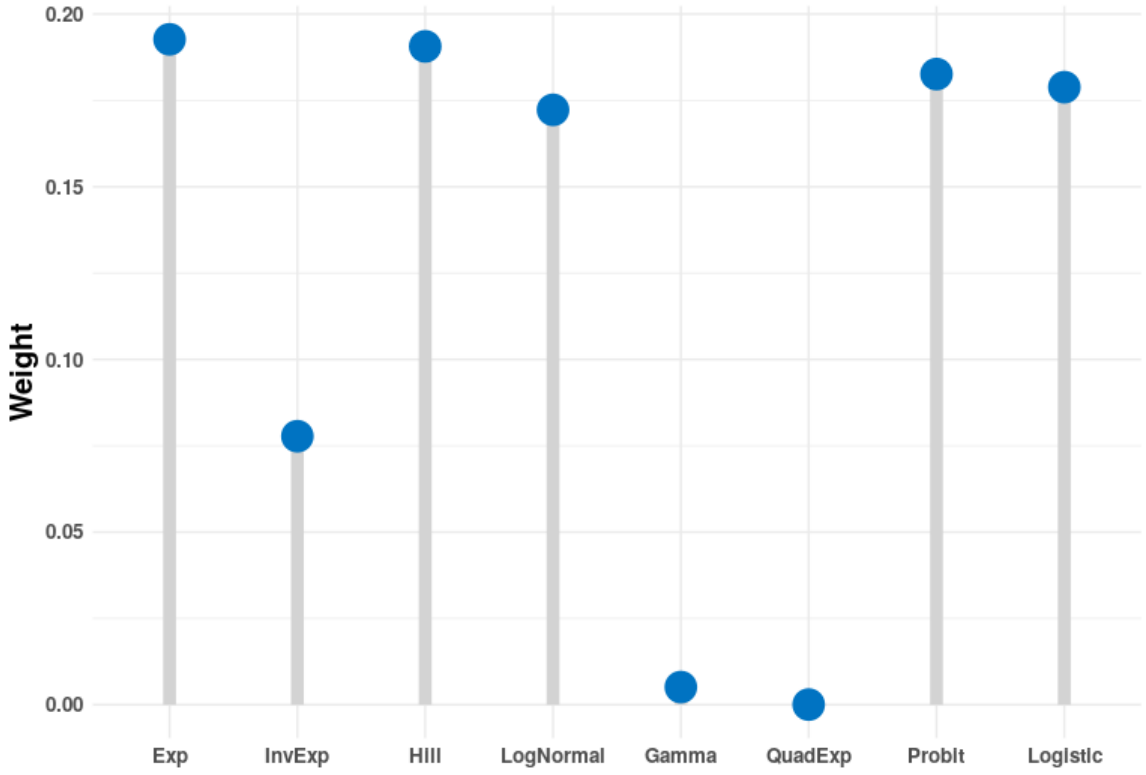
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	1.677	2.834	3.905

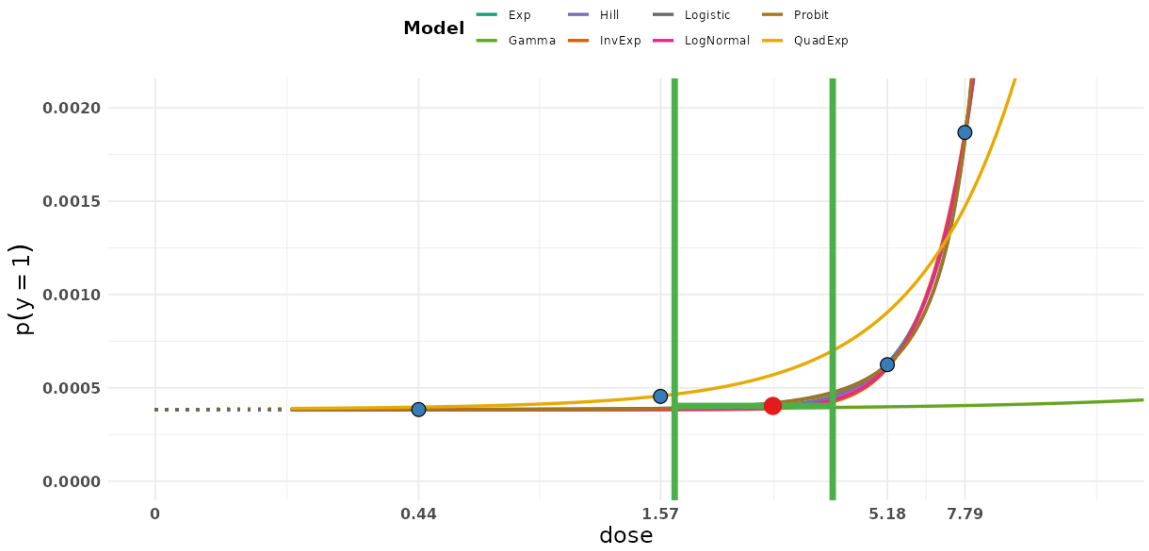
Estimated BMDs per model

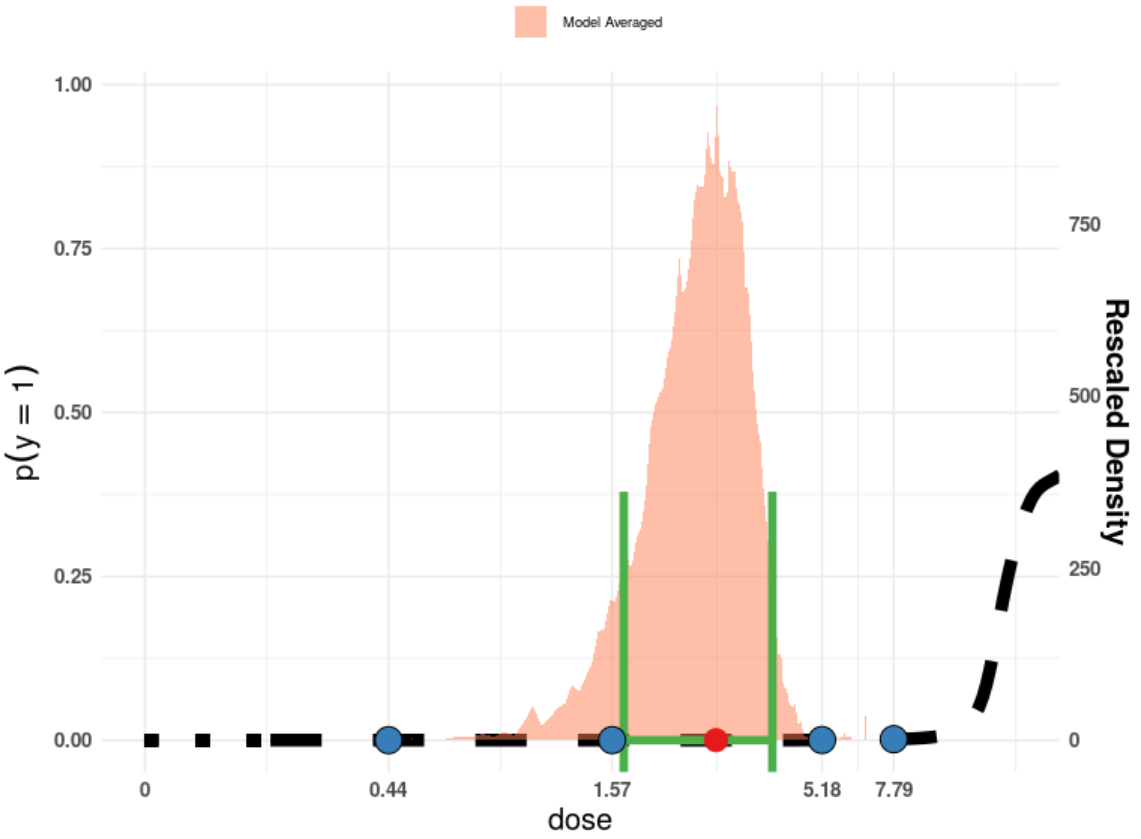
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	2.077	2.901	3.736	0.193	1
IE4_Q	2.722	3.469	4.380	0.078	1
H4_Q	1.993	2.896	3.793	0.191	1
LN4_Q	2.403	3.258	4.069	0.172	1
G4_Q	2.202	3.279	6.661	0.005	0
QE4_Q	0.344	0.605	0.862	0.000	1
P4_Q	1.471	2.375	3.520	0.183	1
L4_Q	1.401	2.313	3.402	0.179	1

Plots of Fitted Models




Weight
0.20
0.15
0.10
0.05
0.00
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
p(y = 1)
0.0020
0.0015
0.0010
0.0005
0.0000
0
0.44
1.57
5.18
7.79
dose


Model Averaged
1.00
0.75
0.50
0.25
0.00
p(y = 1)
750
500
250
0
Rescaled Density
0
0.44
1.57
5.18
7.79
dose

Steinmaus et al. (2014a) lung cancer, relative BMR 5%

Exposure: lifetime average, based on arsenic daily intakes (only included in the uncertainty analysis)

Data Description

The endpoint to be analyzed is: Adj.cases for lung cancer

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	N
0.32	27	80469
0.53	28	74219
1.58	37	70313

The 'Value for CES' is set to 1.678e-05.

Extended dose range is not applied.

Informative background prior: min: 0.00033218; the most likely: 0.00033553; max: 0.00033889. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 1.74e+00).

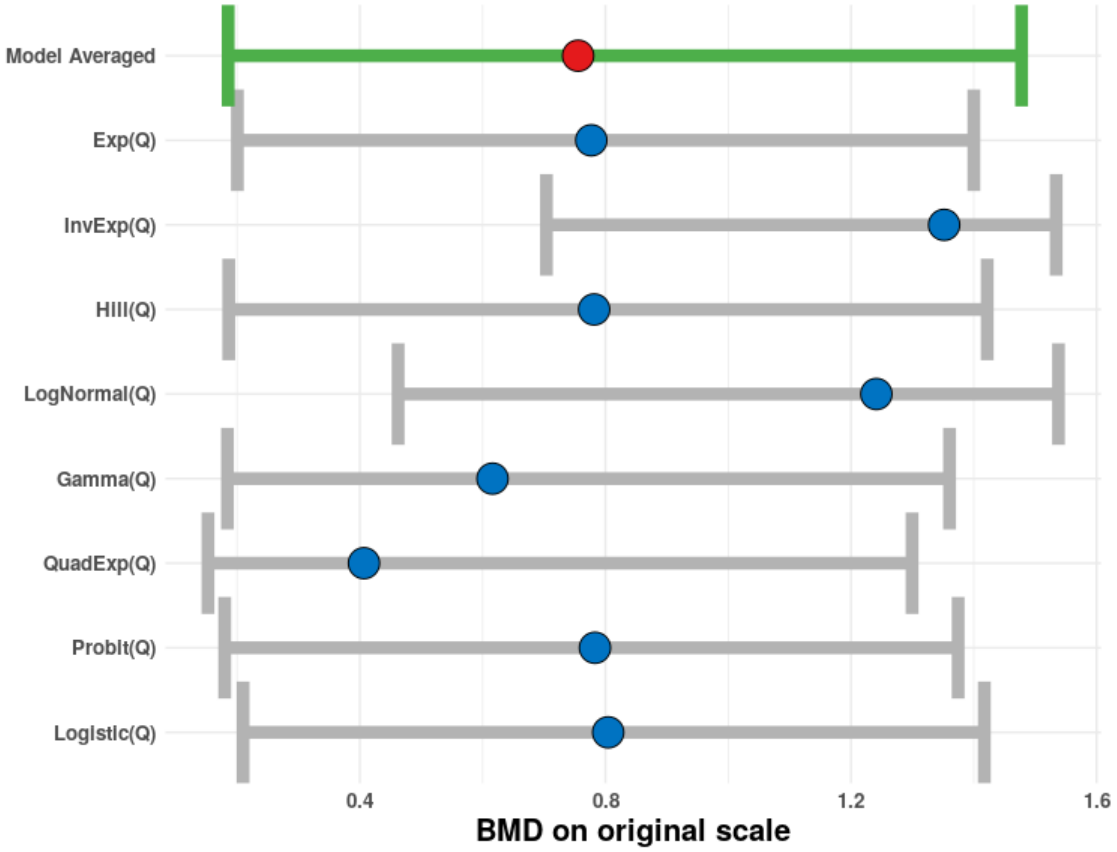
Model Averaged BMD

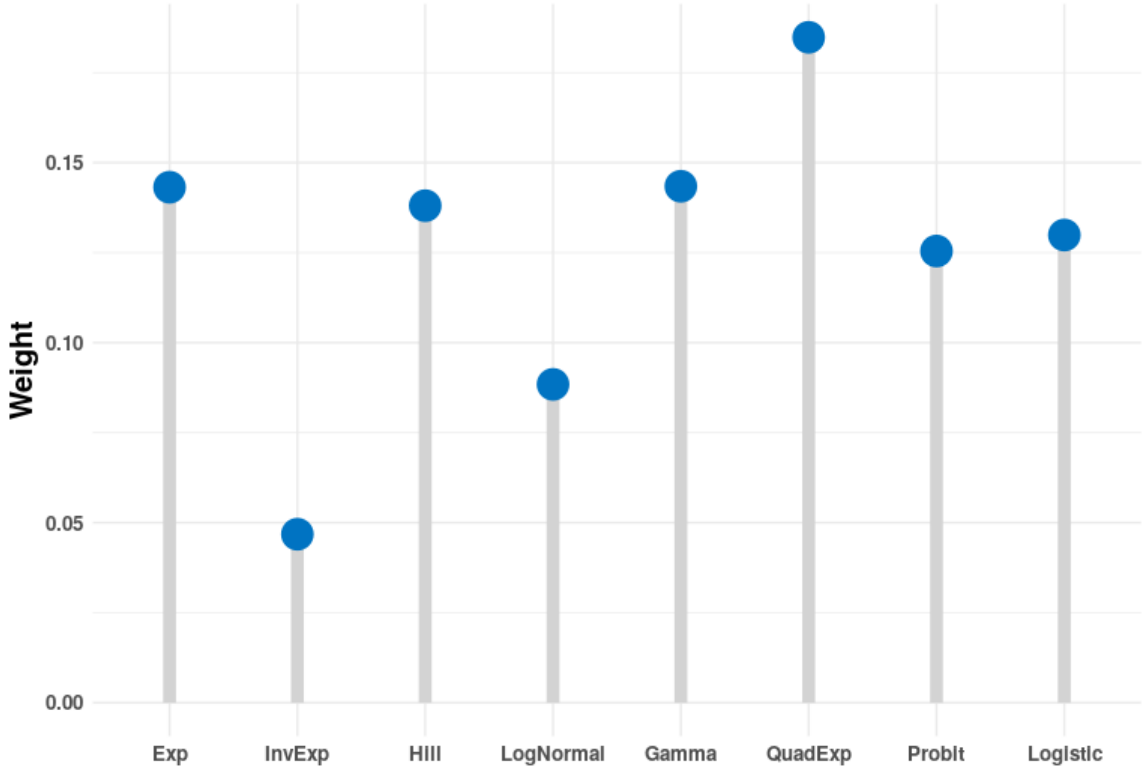
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.186	0.756	1.478

Estimated BMDs per model

Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.201	0.777	1.400	0.143	1
IE4_Q	0.704	1.352	1.534	0.047	0
H4_Q	0.186	0.782	1.422	0.138	1
LN4_Q	0.462	1.241	1.538	0.088	0
G4_Q	0.184	0.616	1.361	0.143	0
QE4_Q	0.153	0.407	1.300	0.185	1
P4_Q	0.180	0.783	1.375	0.125	1
L4_Q	0.210	0.804	1.417	0.130	1

Plots of Fitted Models




Weight
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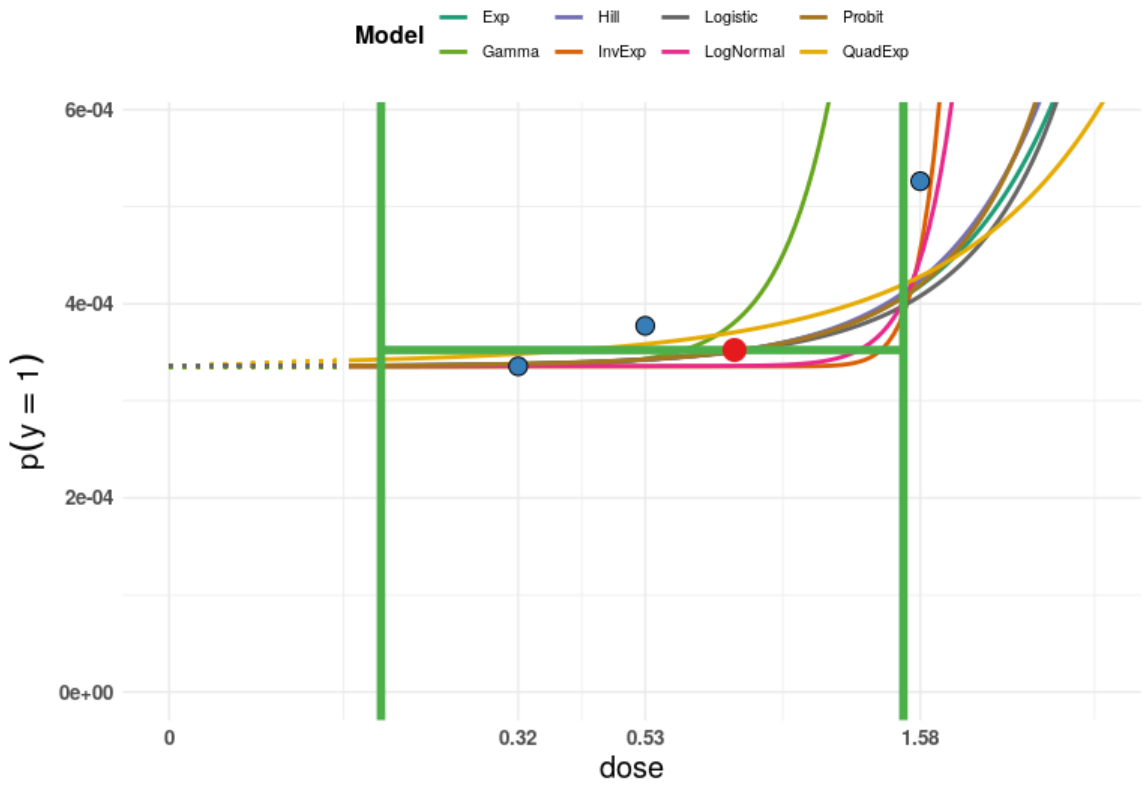
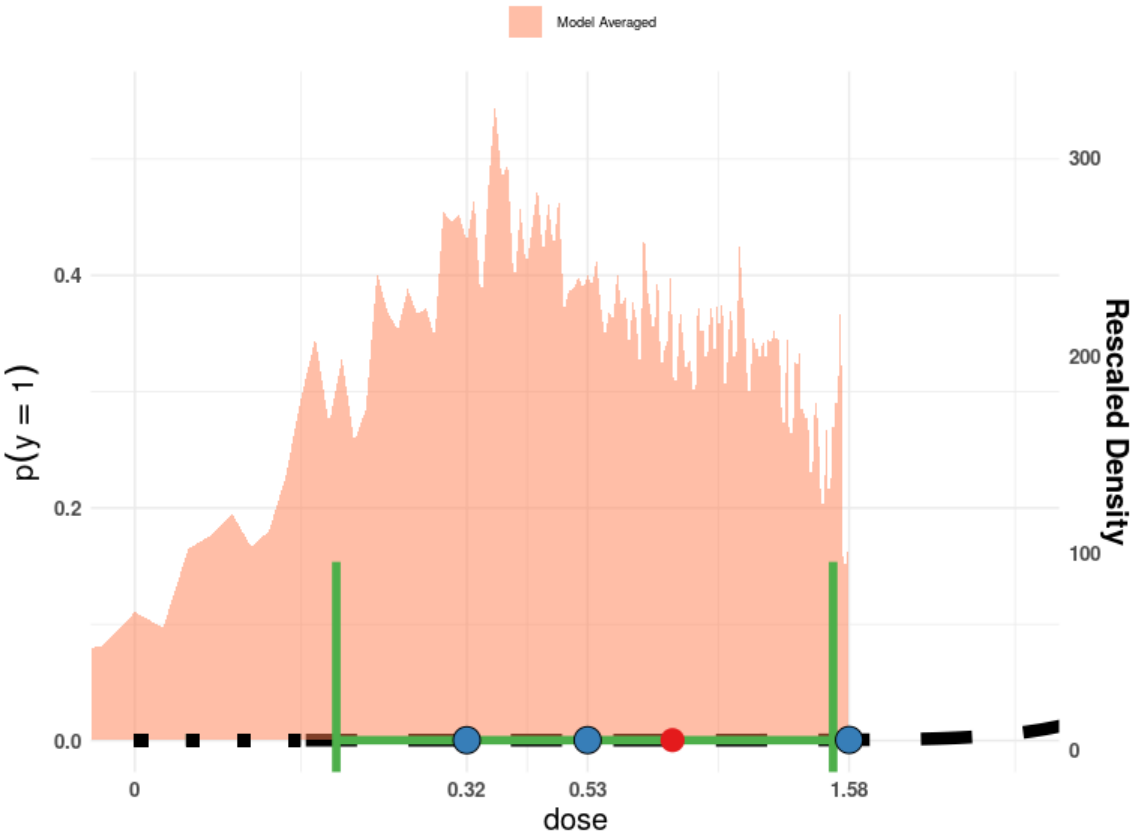
0.10
0.05
0.00
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
p(y = 1)
6e-04
4e-04
2e-04
0e+00
0
0.32
0.53
1.58
dose


Model Averaged
p(y = 1)
0.0
0.2
0.4
Rescaled Density
0
100
200
300
0
0.32
0.53
1.58
dose

Steinmaus et al. (2014a) lung cancer, relative BMR 5%

Exposure: lifetime average, based on arsenic daily intakes, source population decreased by 10% (only included in the uncertainty analysis)

Data Description

The endpoint to be analyzed is: Adj.cases for lung cancer

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	N
0.32	27	72422
0.53	28	66797
1.58	37	63281

The 'Value for CES' is set to 1.865e-05.

Extended dose range is not applied.

Informative background prior: min: 0.00036909; the most likely: 0.00037281; max: 0.00037654. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 1.84e+00).

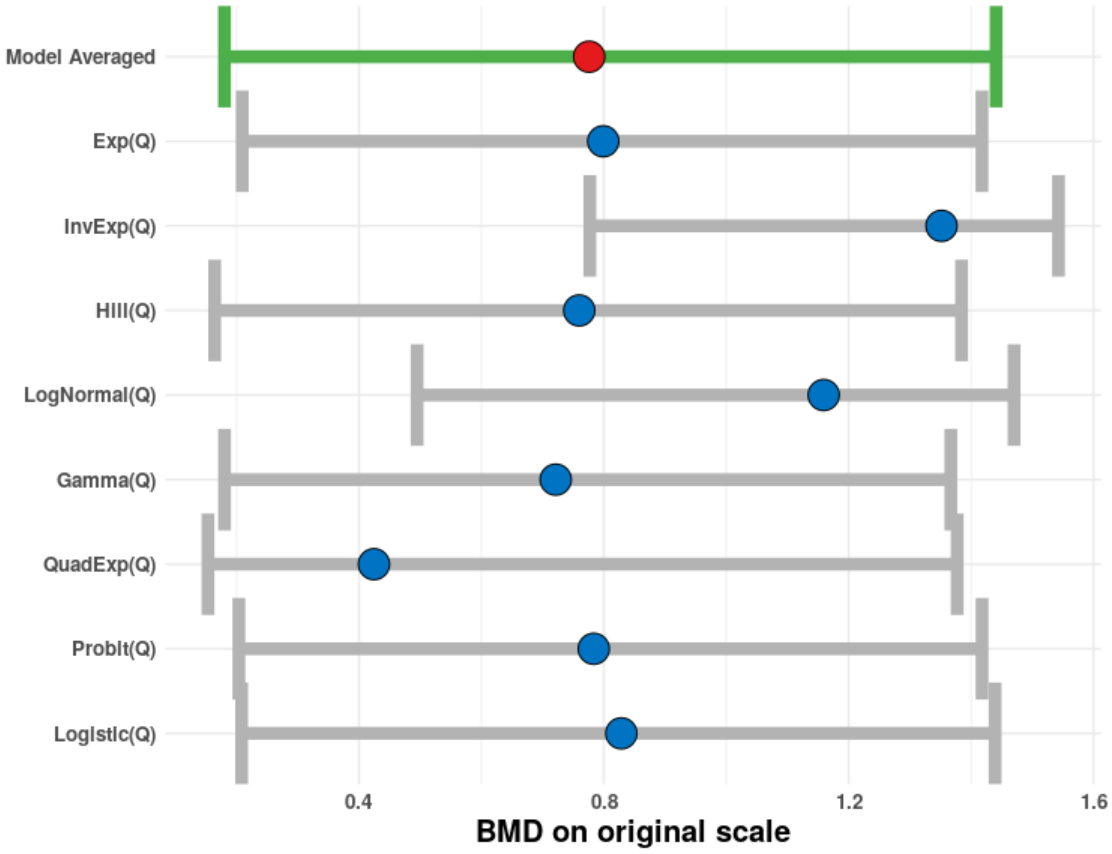
Model Averaged BMD

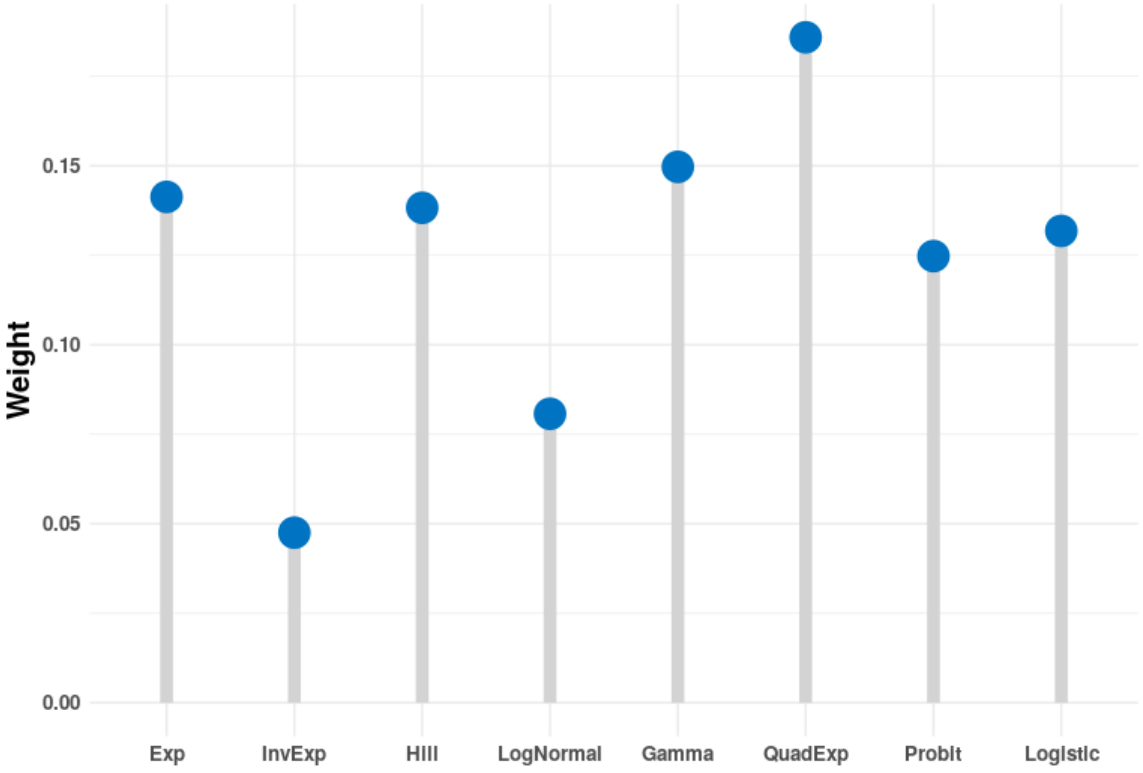
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.18	0.776	1.441

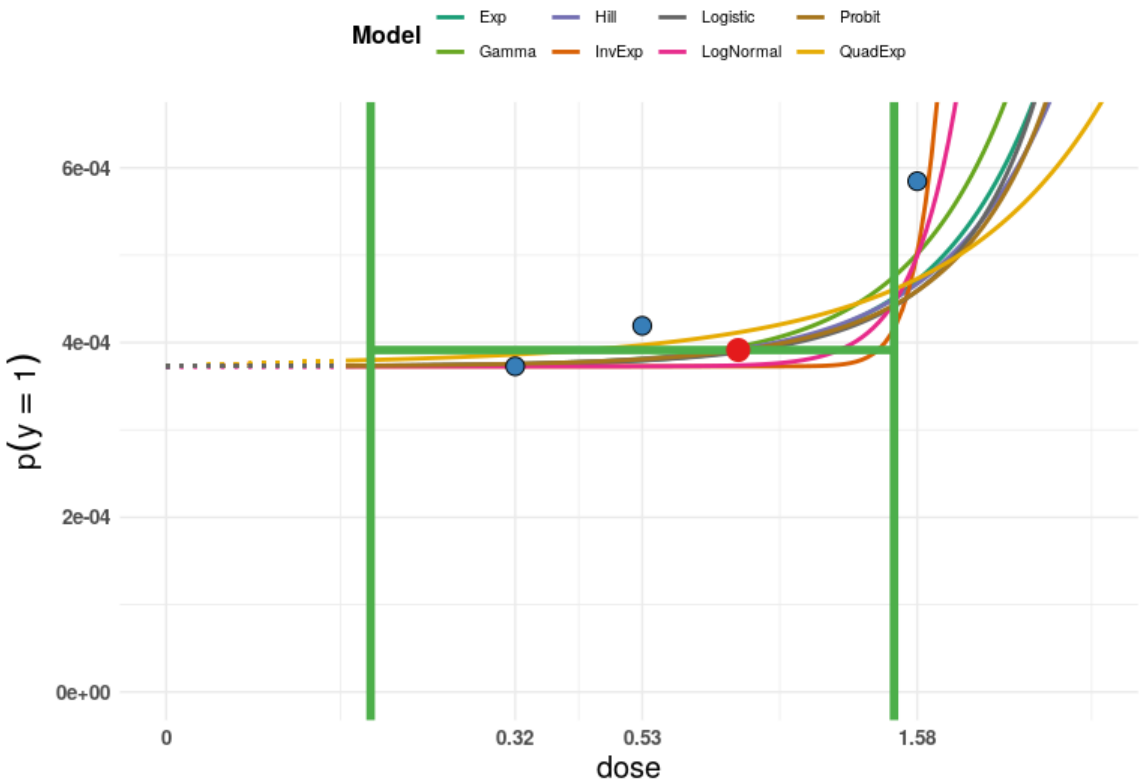
Estimated BMDs per model

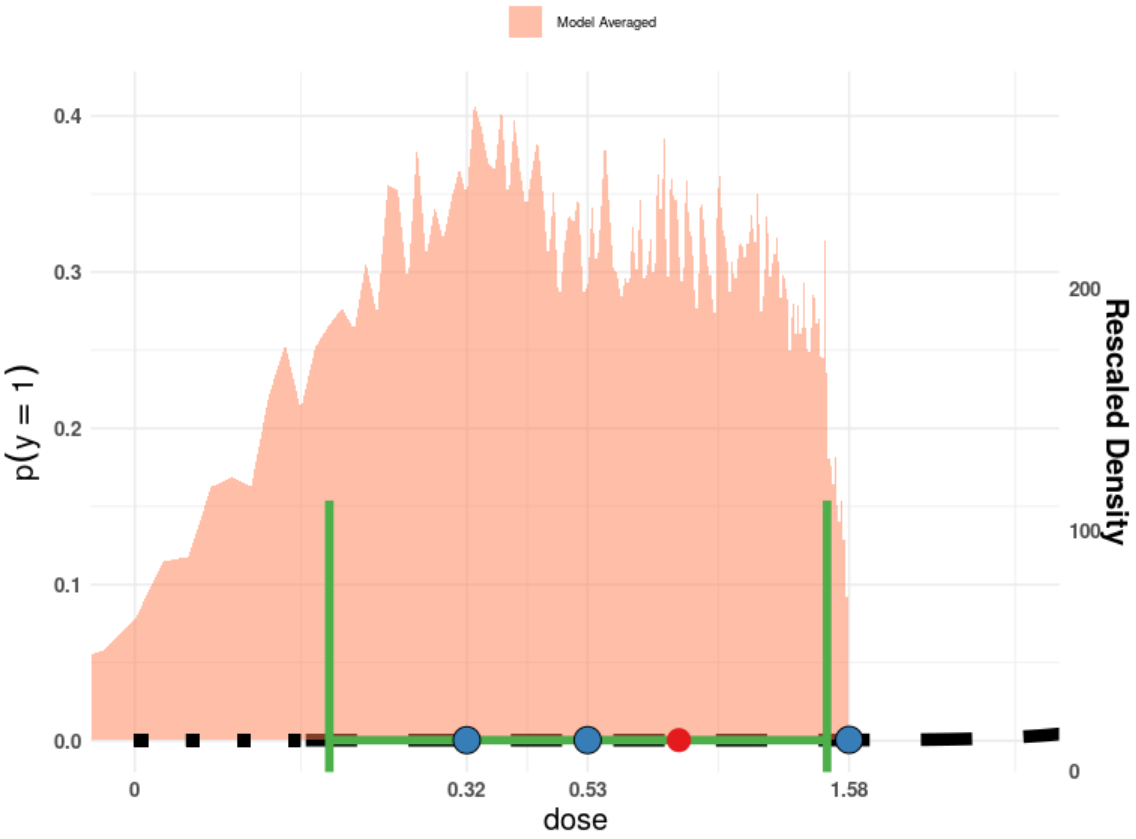
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.209	0.799	1.418	0.141	1
IE4_Q	0.777	1.352	1.543	0.048	1
H4_Q	0.164	0.760	1.385	0.138	1
LN4_Q	0.495	1.159	1.470	0.081	1
G4_Q	0.180	0.721	1.367	0.150	1
QE4_Q	0.153	0.424	1.377	0.186	1
P4_Q	0.204	0.784	1.418	0.125	1
L4_Q	0.208	0.829	1.439	0.132	1

Plots of Fitted Models




Weight
0.15
0.10
0.05
0.00
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
p(y = 1)
6e-04
4e-04
2e-04
0e+00
0
0.32
0.53
1.58
dose


Model Averaged
0.4
0.3
0.2
0.1
0.0
p(y = 1)
200
100
0
Rescaled Density
0
0.32
0.53
1.58
dose

Steinmaus et al. (2014a) lung cancer, relative BMR 5%

Exposure: lifetime average, based on arsenic daily intakes, source population decreased by 20% (only included in the uncertainty analysis)

Data Description

The endpoint to be analyzed is: Adj.cases for lung cancer

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	N
0.32	27	64375
0.53	28	59375
1.58	37	56250

The 'Value for CES' is set to 2.098e-05.

Extended dose range is not applied.

Informative background prior: min: 0.00041522; the most likely: 0.00041942; max: 0.00042361. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 1.92e+00).

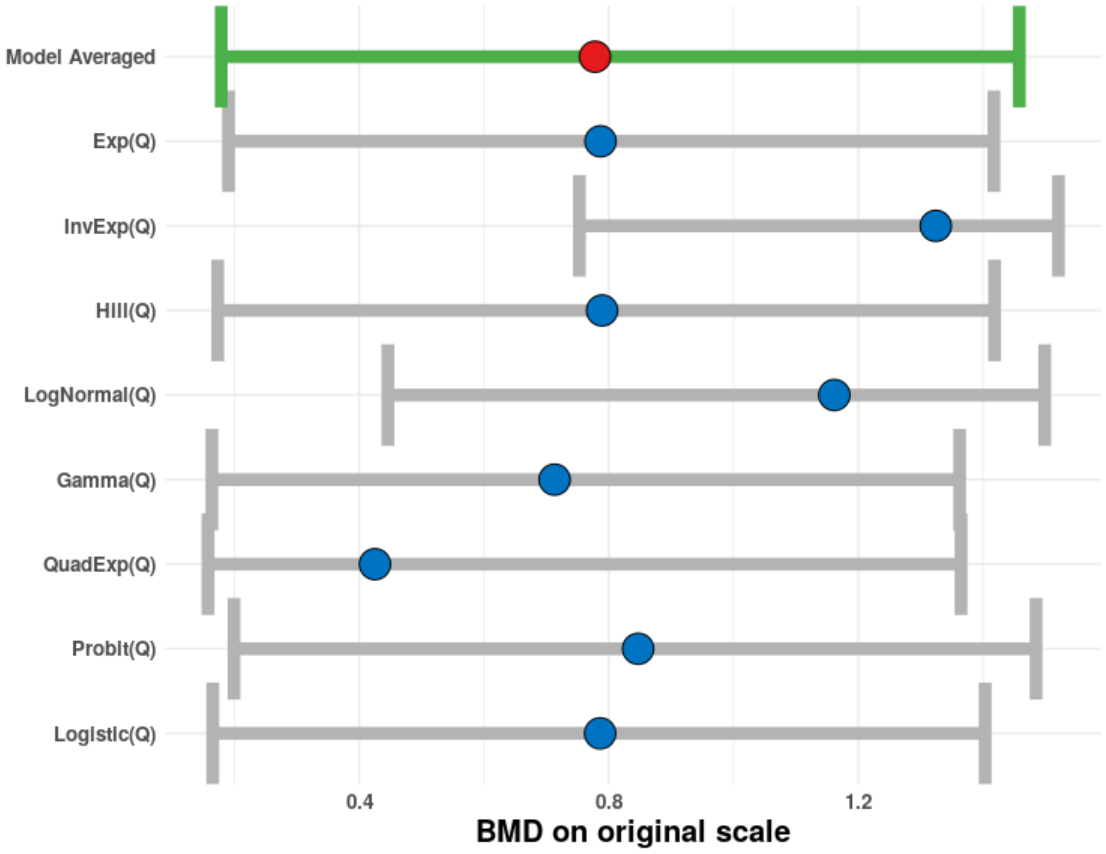
Model Averaged BMD

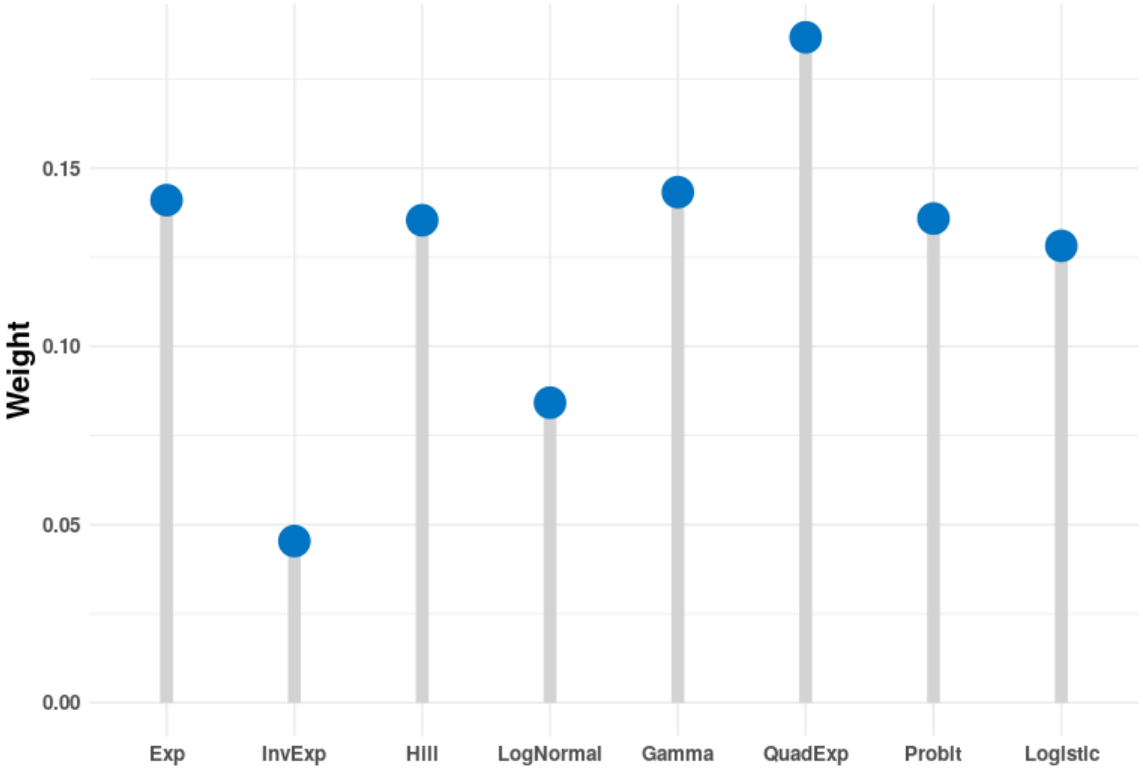
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.179	0.778	1.458

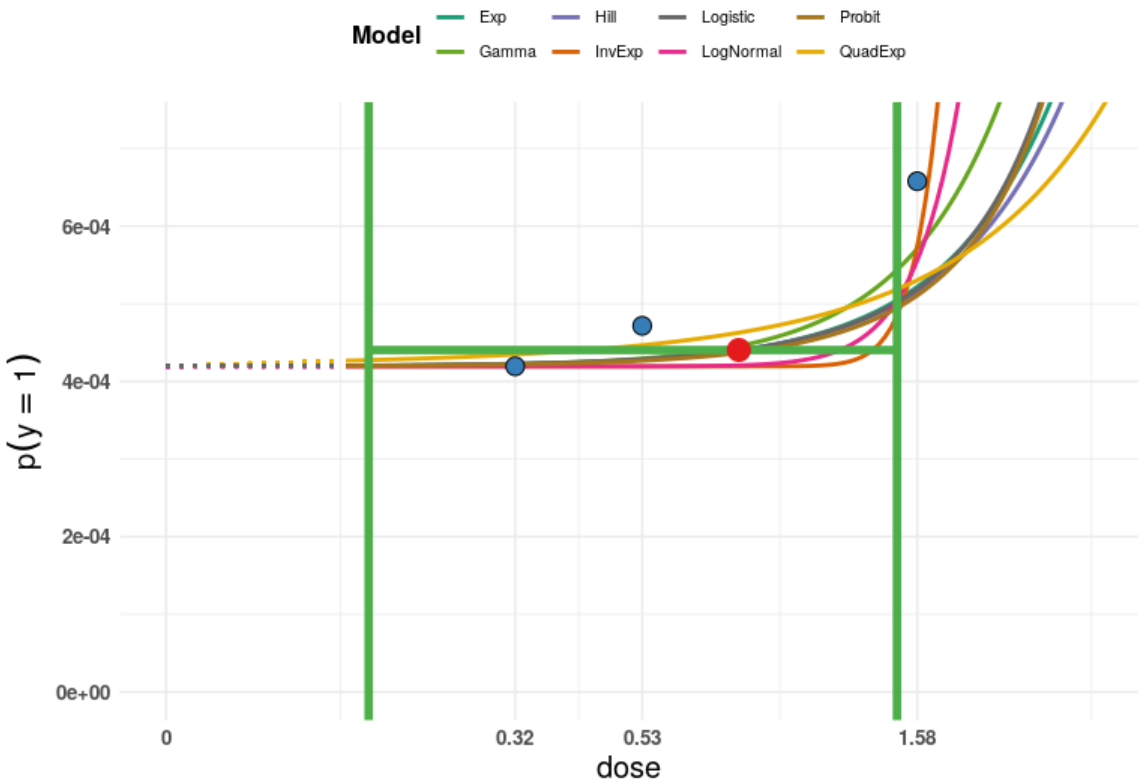
Estimated BMDs per model

Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.191	0.787	1.417	0.141	1
IE4_Q	0.753	1.324	1.521	0.045	1
H4_Q	0.173	0.789	1.418	0.135	1
LN4_Q	0.446	1.162	1.499	0.084	1
G4_Q	0.164	0.713	1.362	0.143	1
QE4_Q	0.158	0.425	1.365	0.187	1
P4_Q	0.199	0.847	1.485	0.136	1
L4_Q	0.165	0.786	1.403	0.128	1

Plots of Fitted Models




Weight
0.15
0.10
0.05
0.00
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
p(y = 1)
6e-04
4e-04
2e-04
0e+00
0
0.32
0.53
1.58
dose


Model Averaged
p(y = 1)
0.4
0.3
0.2
0.1
0.0
300
200
100
0
Rescaled Density
0
0.32
0.53
1.58
dose

Steinmaus et al. (2014a) lung cancer, relative BMR 5%

Exposure: lifetime average, based on arsenic daily intakes, source population increased by 10% (only included in the uncertainty analysis)

Data Description

The endpoint to be analyzed is: Adj.cases for lung cancer

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	N
0.32	27	88516
0.53	28	81641
1.58	37	77344

The 'Value for CES' is set to 1.526e-05.

Extended dose range is not applied.

Informative background prior: min: 0.00030198; the most likely: 0.00030503; max: 0.00030808. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 1.73e+00).

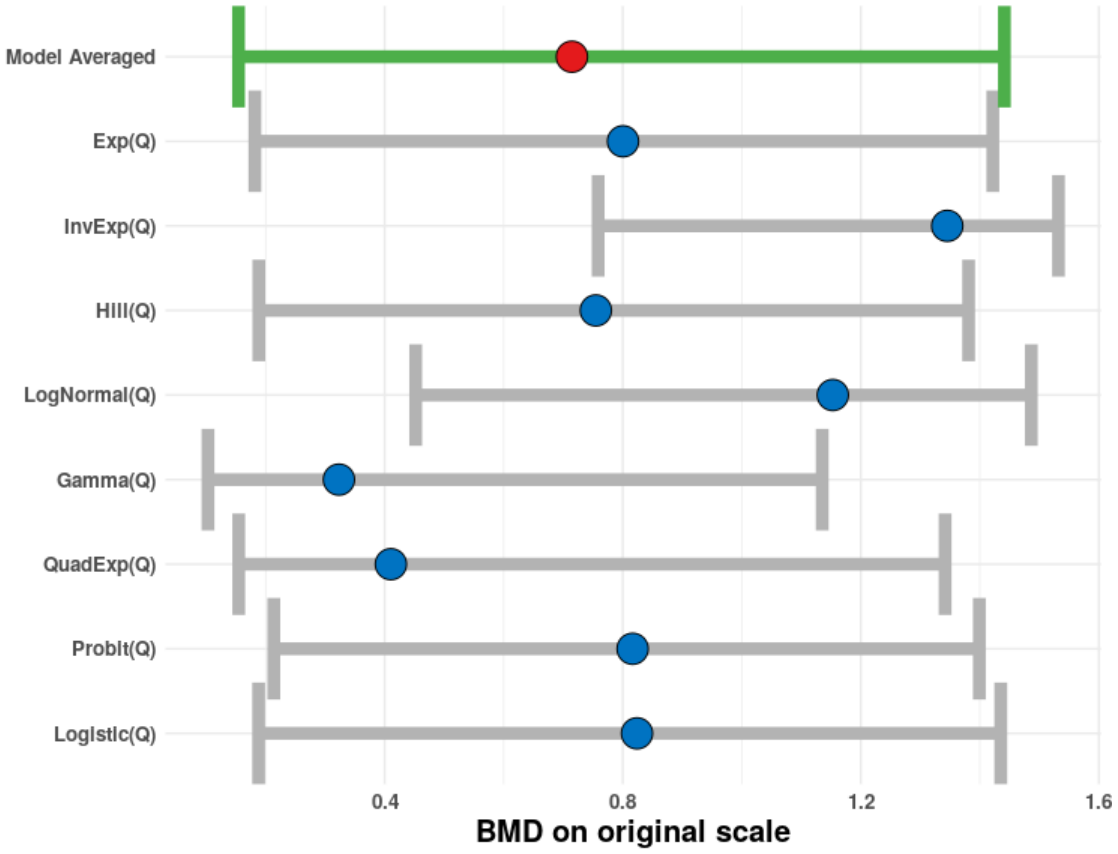
Model Averaged BMD

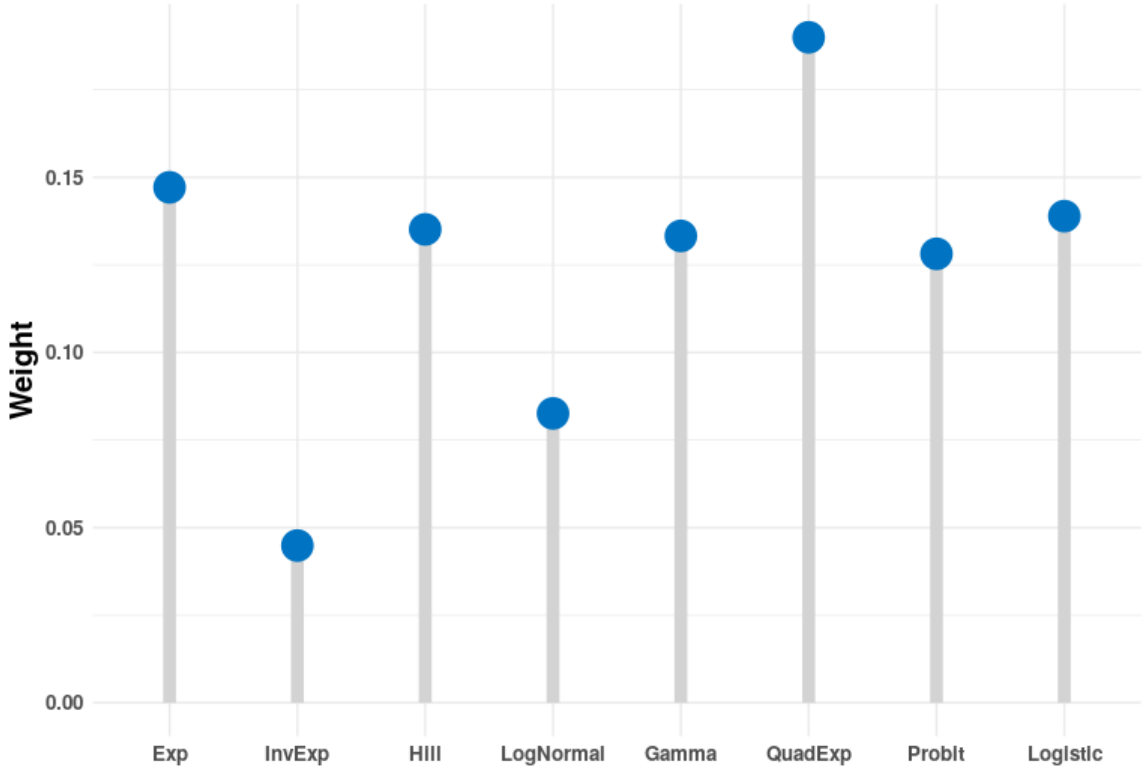
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.154	0.715	1.441

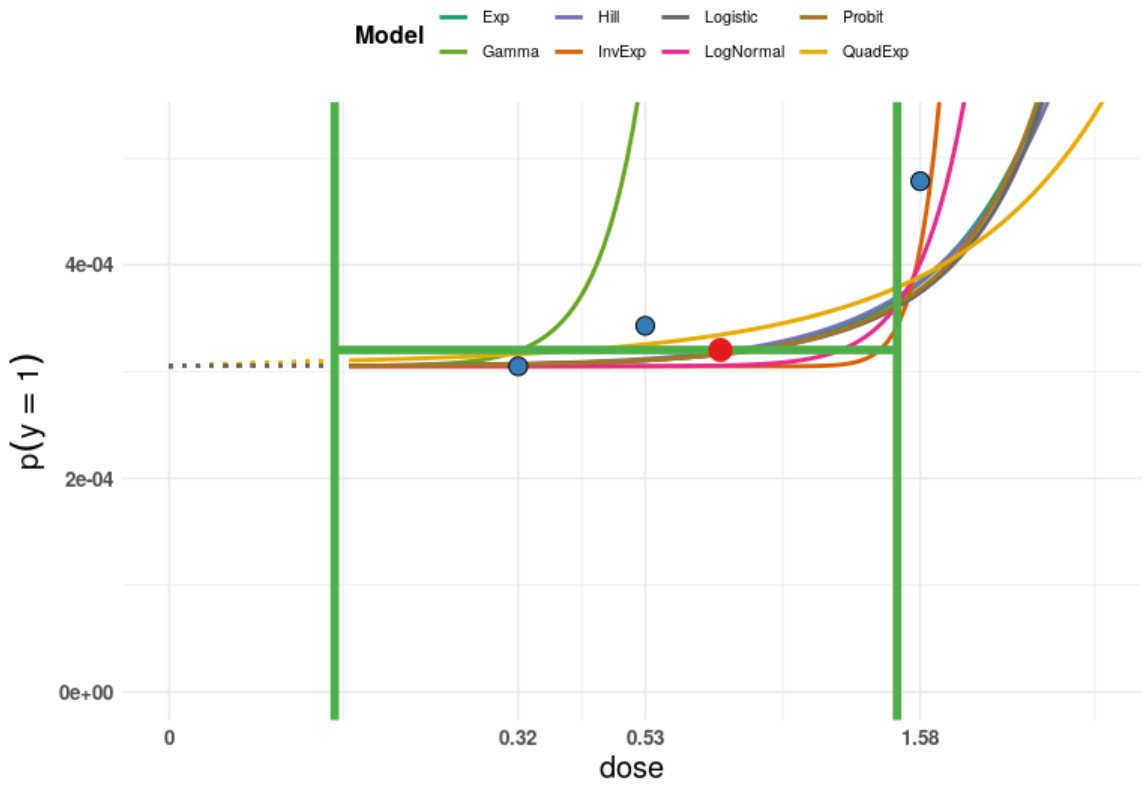
Estimated BMDs per model

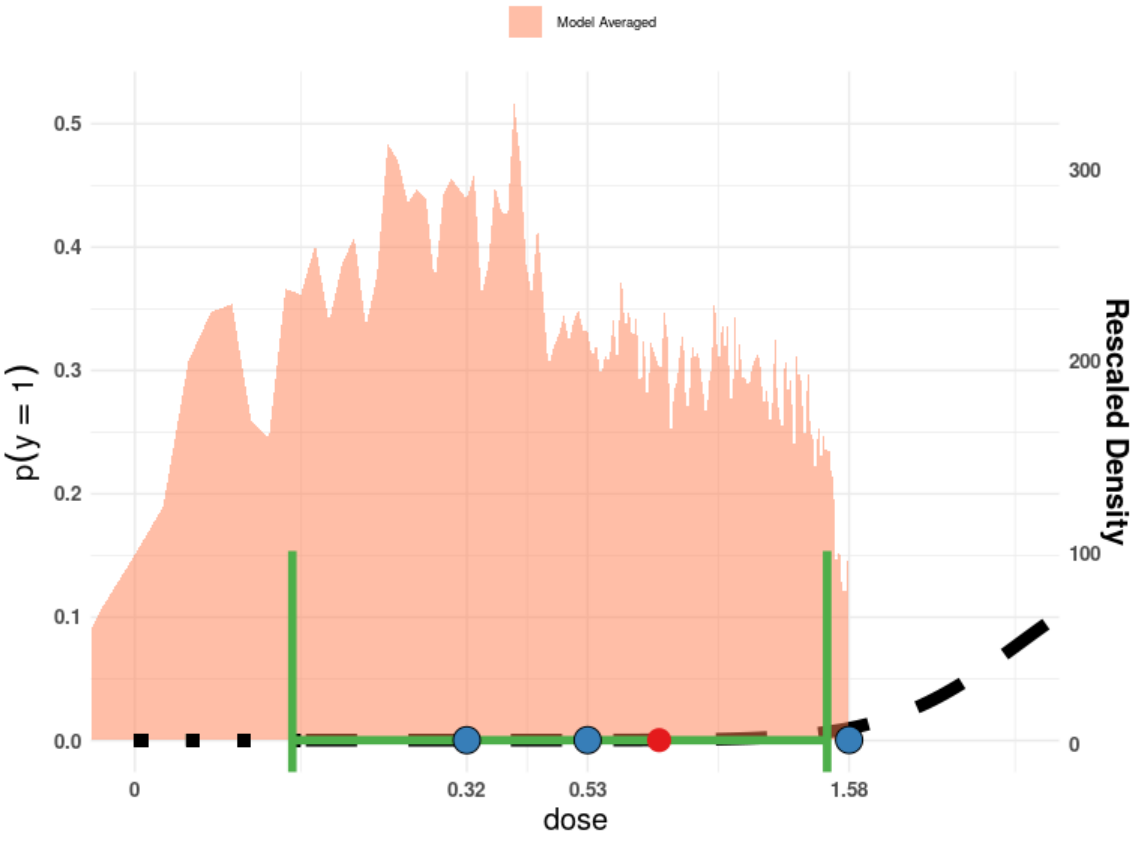
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.182	0.800	1.422	0.147	1
IE4_Q	0.759	1.345	1.532	0.045	1
H4_Q	0.189	0.755	1.381	0.135	1
LN4_Q	0.452	1.153	1.486	0.083	1
G4_Q	0.103	0.323	1.135	0.133	0
QE4_Q	0.155	0.410	1.342	0.190	1
P4_Q	0.214	0.817	1.399	0.128	1
L4_Q	0.188	0.824	1.435	0.139	1

Plots of Fitted Models




Weight
0.15
0.10
0.05
0.00
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
p(y = 1)
4e-04
2e-04
0e+00
0
0.32
0.53
1.58
dose


Model Averaged
0.5
0.4
0.3
0.2
0.1
0.0
p(y = 1)
300
200
100
0
Rescaled Density
0
0.32
0.53
1.58
dose

Steinmaus et al. (2014a) lung cancer, relative BMR 5%

Exposure: lifetime average, based on arsenic daily intakes, source population increased by 20% (only included in the uncertainty analysis)

Data Description

The endpoint to be analyzed is: Adj.cases for lung cancer

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	N
0.32	27	96563
0.53	28	89063
1.58	37	84375

The 'Value for CES' is set to 1.398e-05.

Extended dose range is not applied.

Informative background prior: min: 0.00027681; the most likely: 0.00027961; max: 0.00028241. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 1.69e+00).

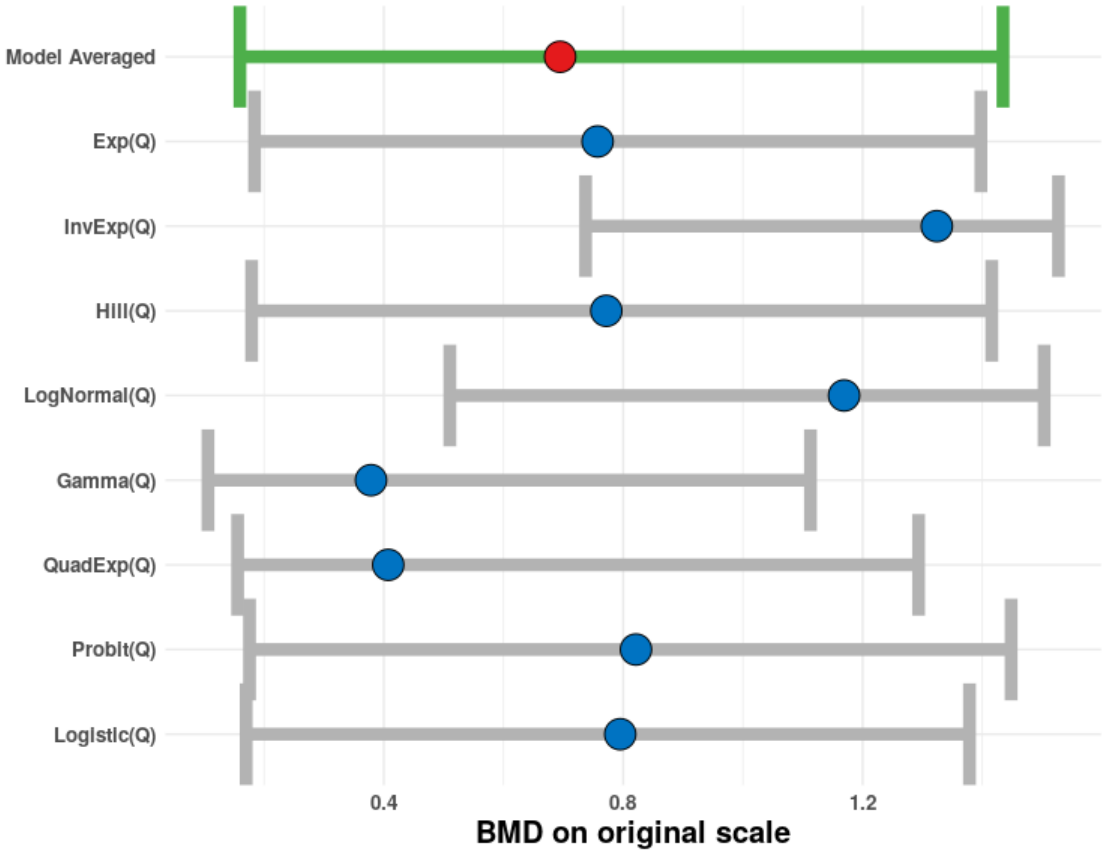
Model Averaged BMD

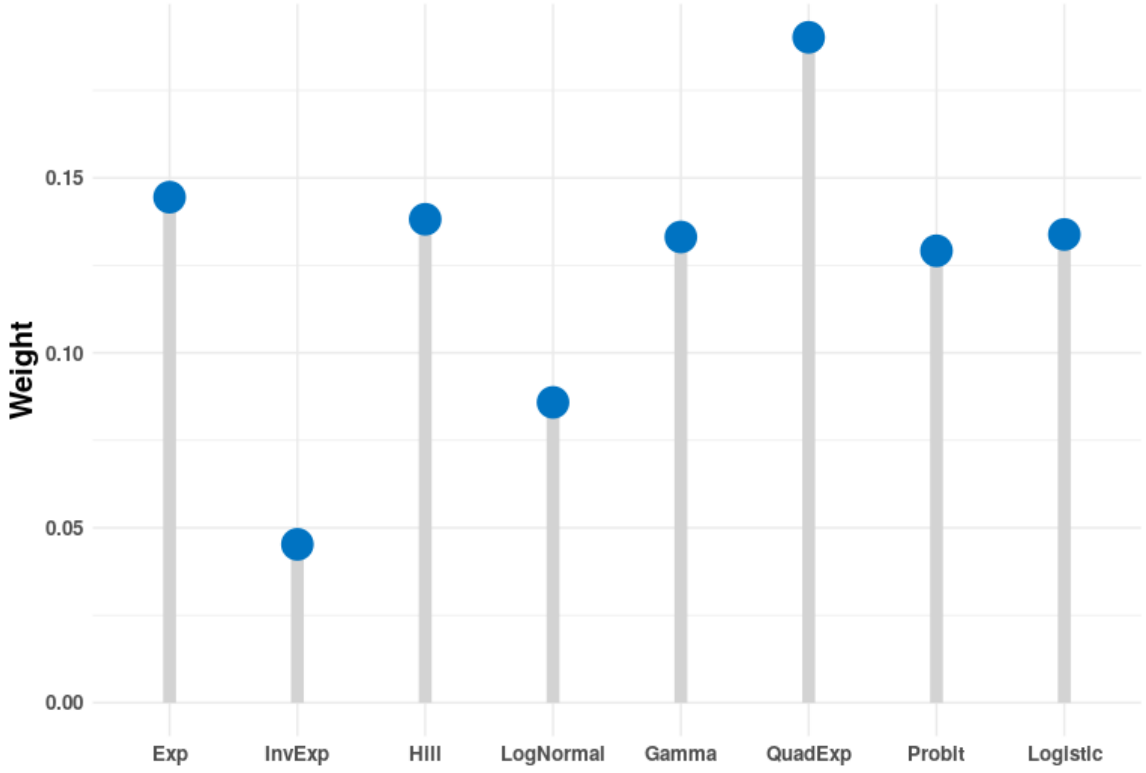
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.16	0.695	1.435

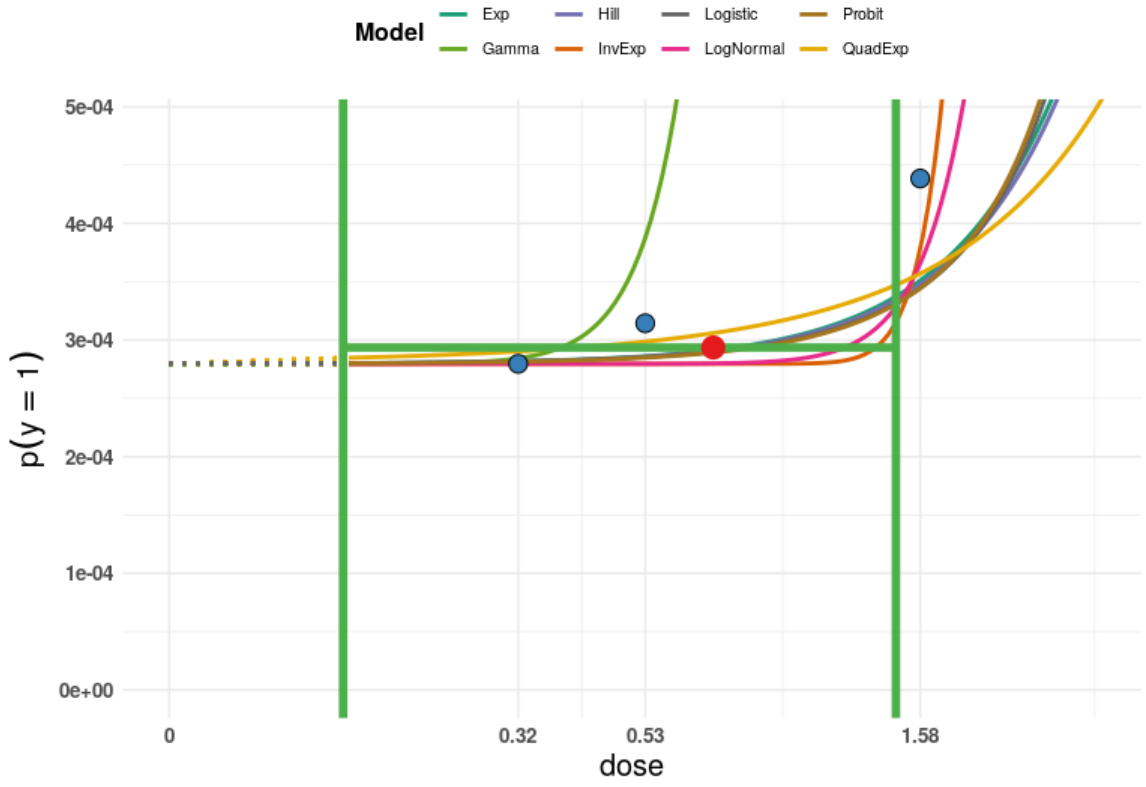
Estimated BMDs per model

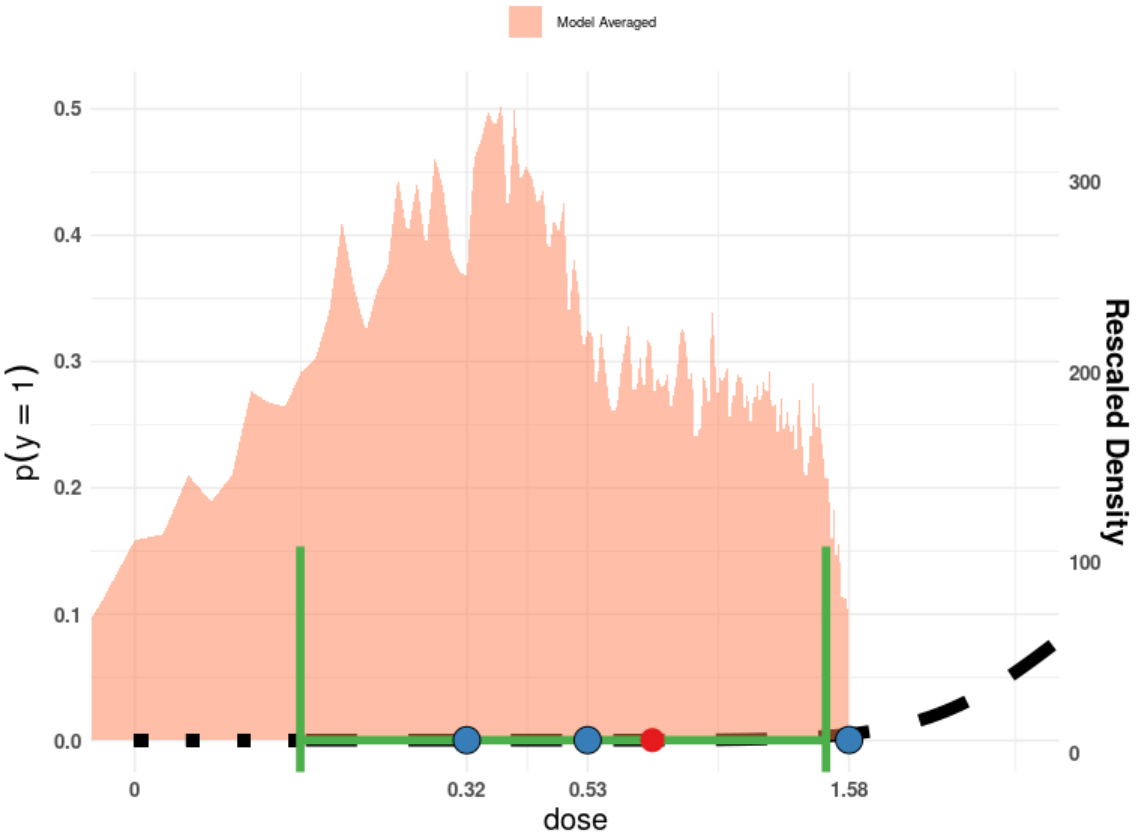
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.184	0.757	1.398	0.144	1
IE4_Q	0.737	1.324	1.527	0.045	1
H4_Q	0.179	0.772	1.416	0.138	1
LN4_Q	0.510	1.169	1.503	0.086	1
G4_Q	0.106	0.379	1.113	0.133	0
QE4_Q	0.156	0.407	1.294	0.190	1
P4_Q	0.176	0.821	1.448	0.129	1
L4_Q	0.170	0.795	1.379	0.134	1

Plots of Fitted Models




Weight
0.15
0.10
0.05
0.00
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
p(y = 1)
5e-04
4e-04
3e-04
2e-04
1e-04
0e+00
0
0.32
0.53
1.58
dose


Model Averaged
0.5
0.4
0.3
0.2
0.1
0.0
p(y = 1)
300
200
100
0
Rescaled Density
0
0.32
0.53
1.58
dose

Steinmaus et al. (2014a) lung cancer, relative BMR 5%

Exposure: the highest 5-year average, based on arsenic daily intakes (the preferred exposure estimate for the study)

Data Description

The endpoint to be analyzed is: Adj.cases for lung cancer

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	N
0.36	25	79688
0.70	30	77344
2.00	37	67969

The 'Value for CES' is set to 1.569e-05.

Extended dose range is not applied.

Informative background prior: min: 0.00031059; the most likely: 0.00031372; max: 0.00031686. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 1.50e+00).

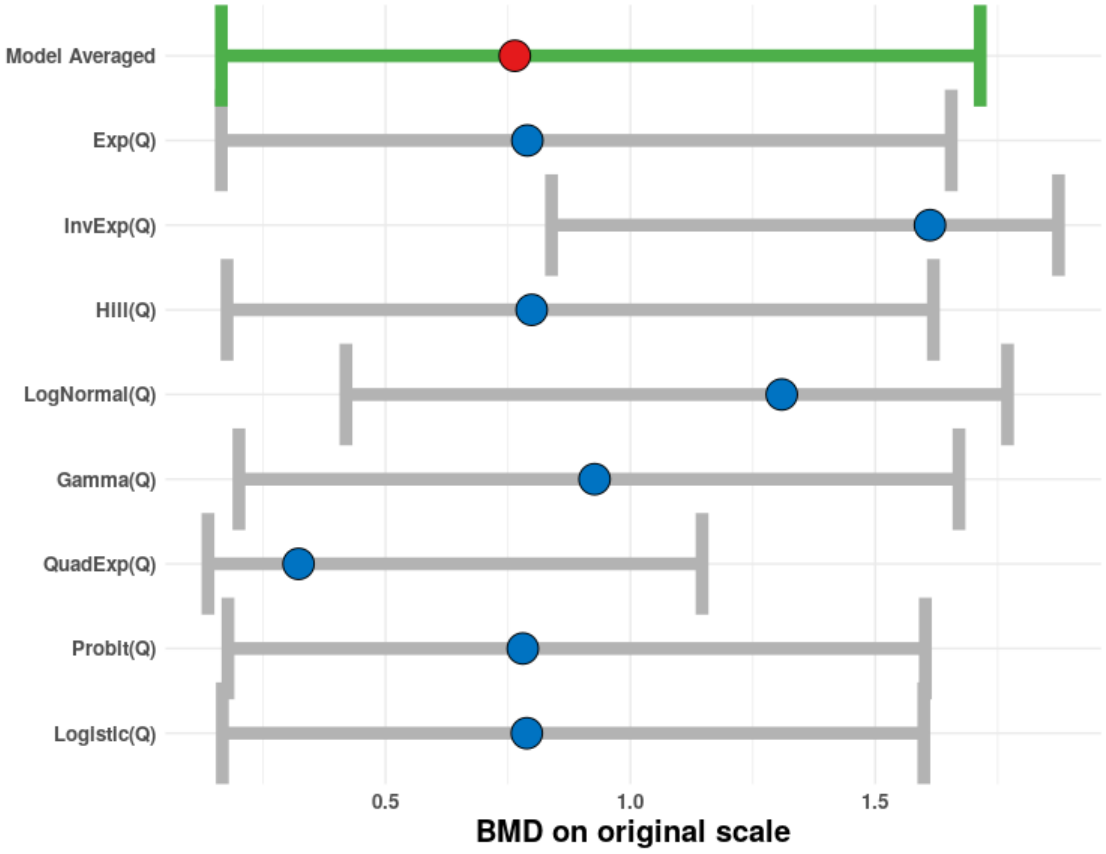
Model Averaged BMD

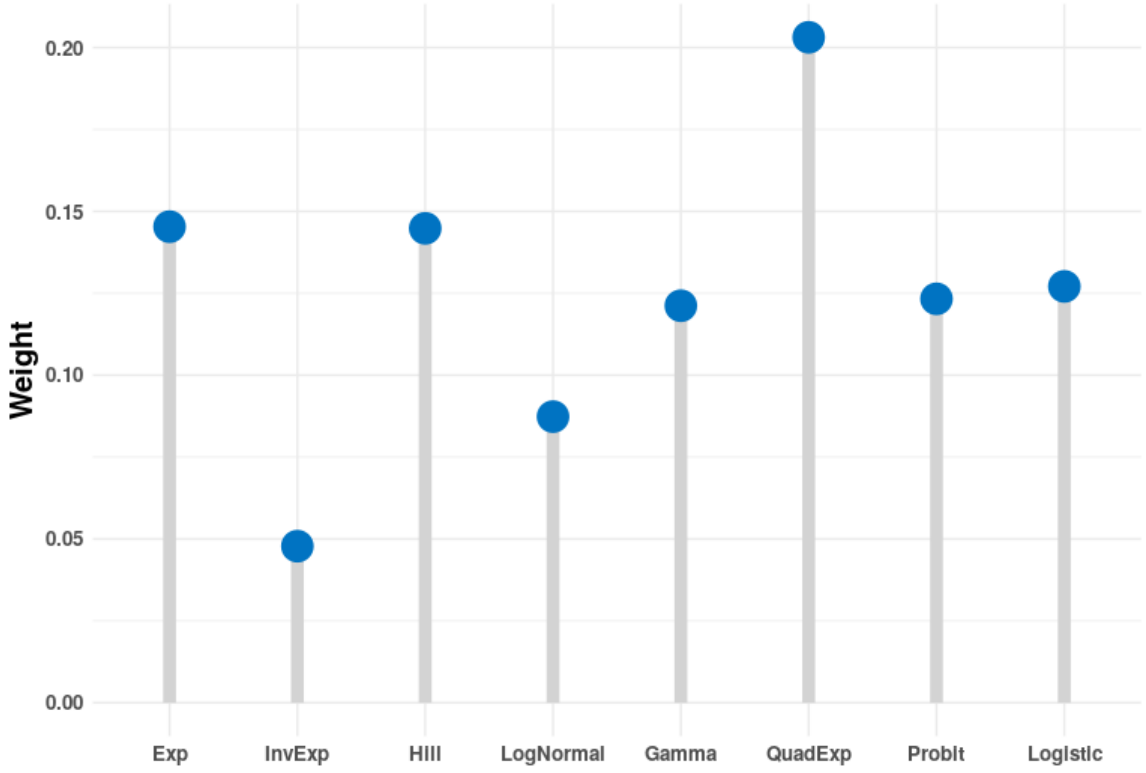
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.165	0.764	1.714

Estimated BMDs per model

Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.165	0.789	1.655	0.145	1
IE4_Q	0.839	1.612	1.874	0.048	1
H4_Q	0.176	0.798	1.619	0.145	1
LN4_Q	0.419	1.309	1.770	0.087	1
G4_Q	0.201	0.927	1.671	0.121	0
QE4_Q	0.137	0.322	1.146	0.203	1
P4_Q	0.178	0.780	1.602	0.123	1
L4_Q	0.167	0.788	1.599	0.127	1

Plots of Fitted Models




Weight
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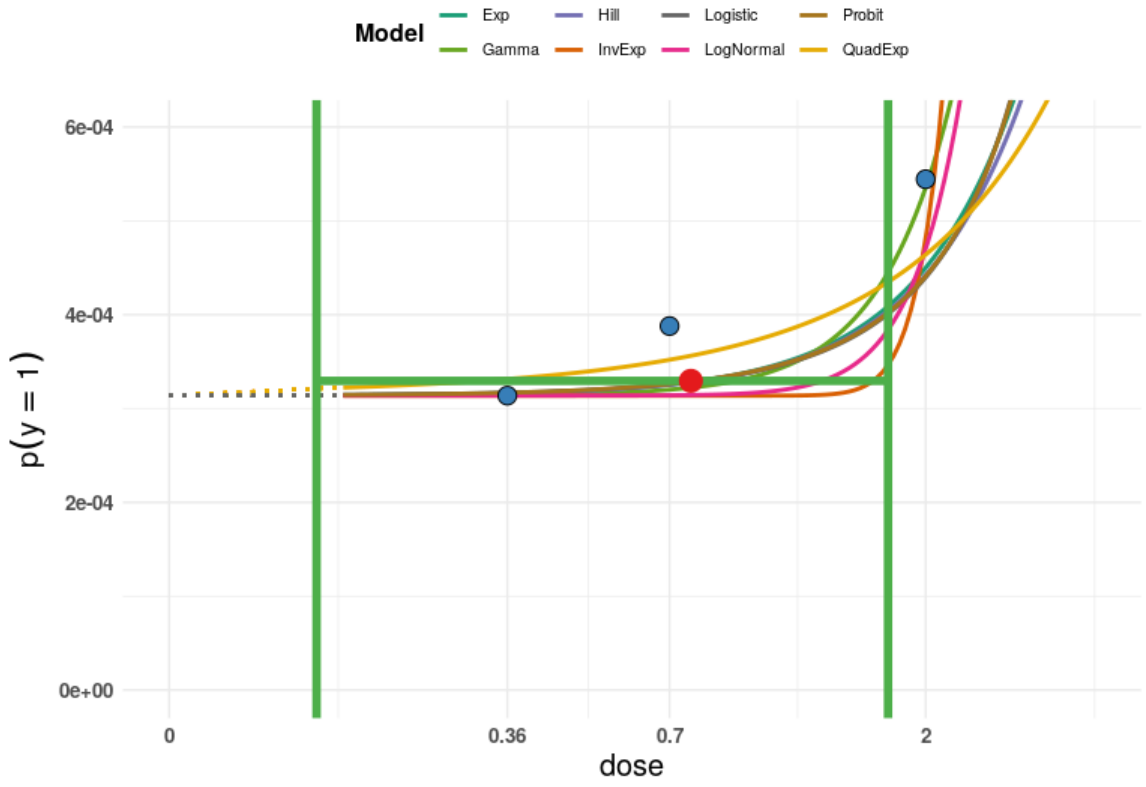
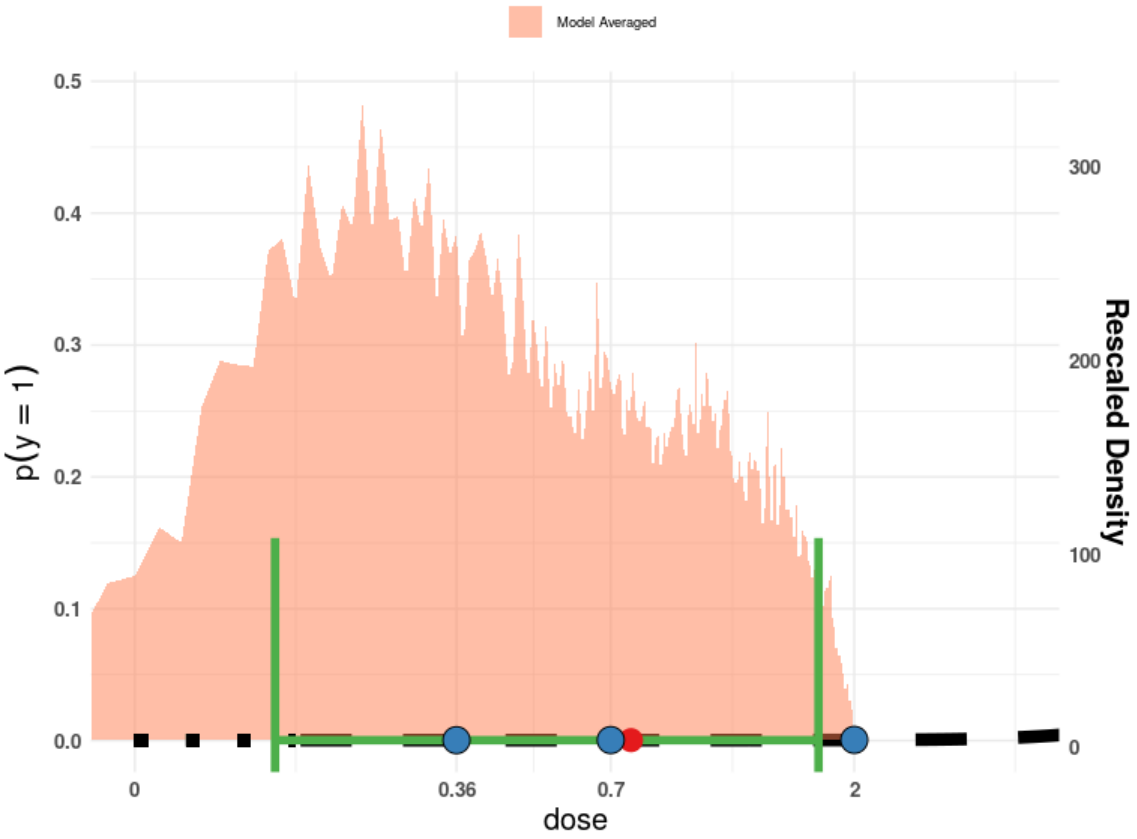
0.15
0.10
0.05
0.00
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
p(y = 1)
6e-04
4e-04
2e-04
0e+00
0
0.36
0.7
2
dose


Model Averaged
0.5
0.4
0.3
0.2
0.1
0.0
p(y = 1)
300
200
100
0
Rescaled Density
0
0.36
0.7
2
dose

Steinmaus et al. (2014a) lung cancer, relative BMR 5%

Exposure: the highest single year, based on arsenic daily intakes (only included in the uncertainty analysis)

Data Description

The endpoint to be analyzed is: Adj.cases for lung cancer

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	N
0.39	23	80469
0.84	31	76563
1.19	38	67969

The 'Value for CES' is set to 1.43e-05.

Extended dose range is not applied.

Informative background prior: min: 0.00028297; the most likely: 0.00028582; max: 0.00028868. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 1.10e+00).

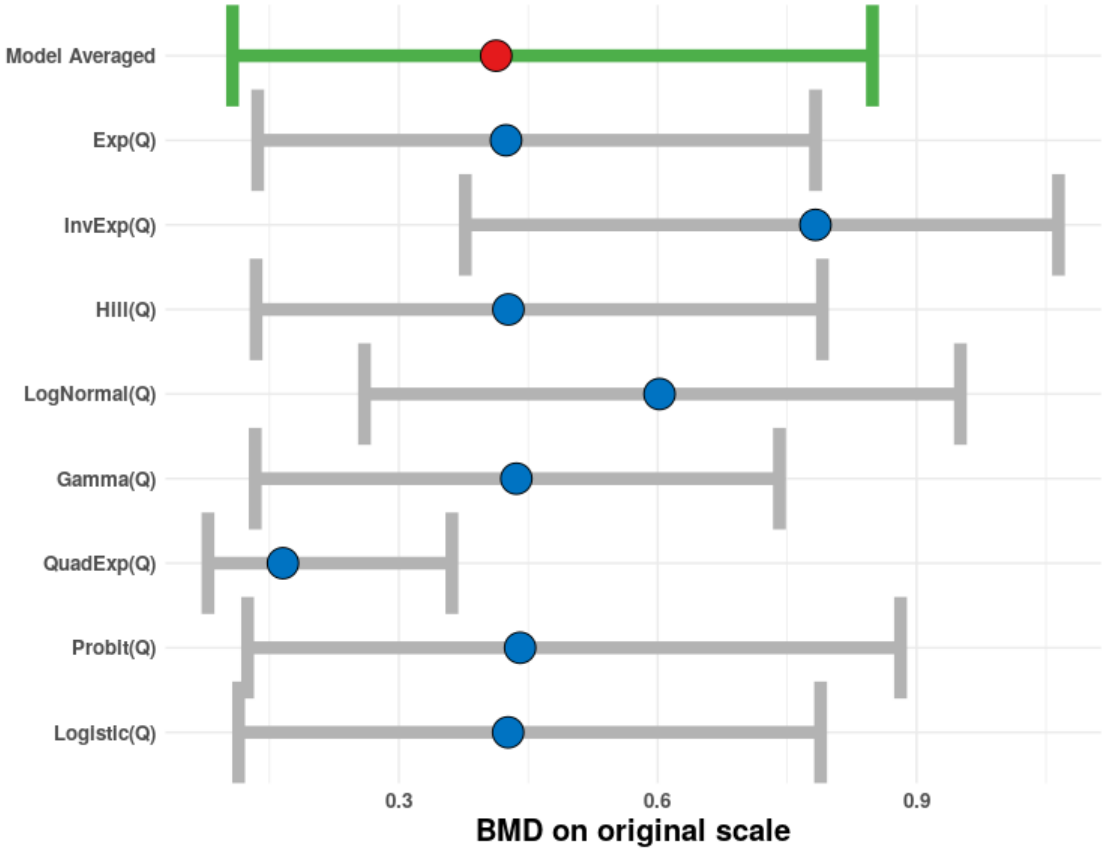
Model Averaged BMD

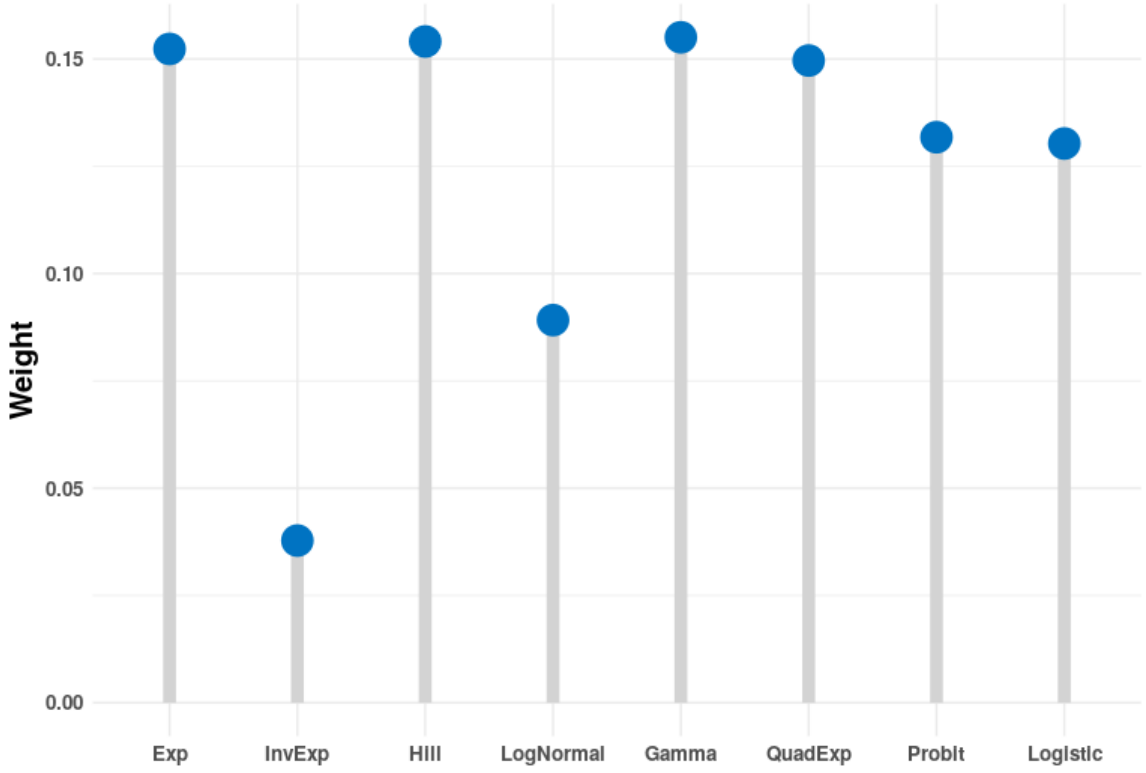
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.107	0.413	0.849

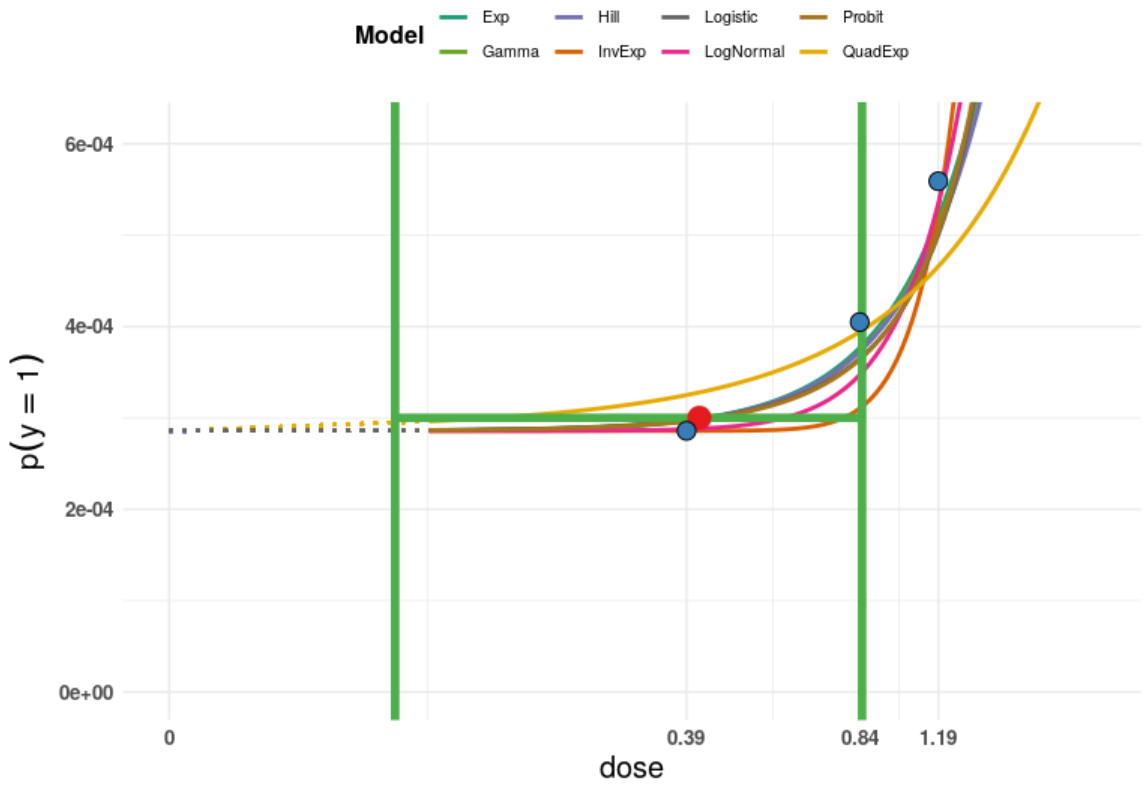
Estimated BMDs per model

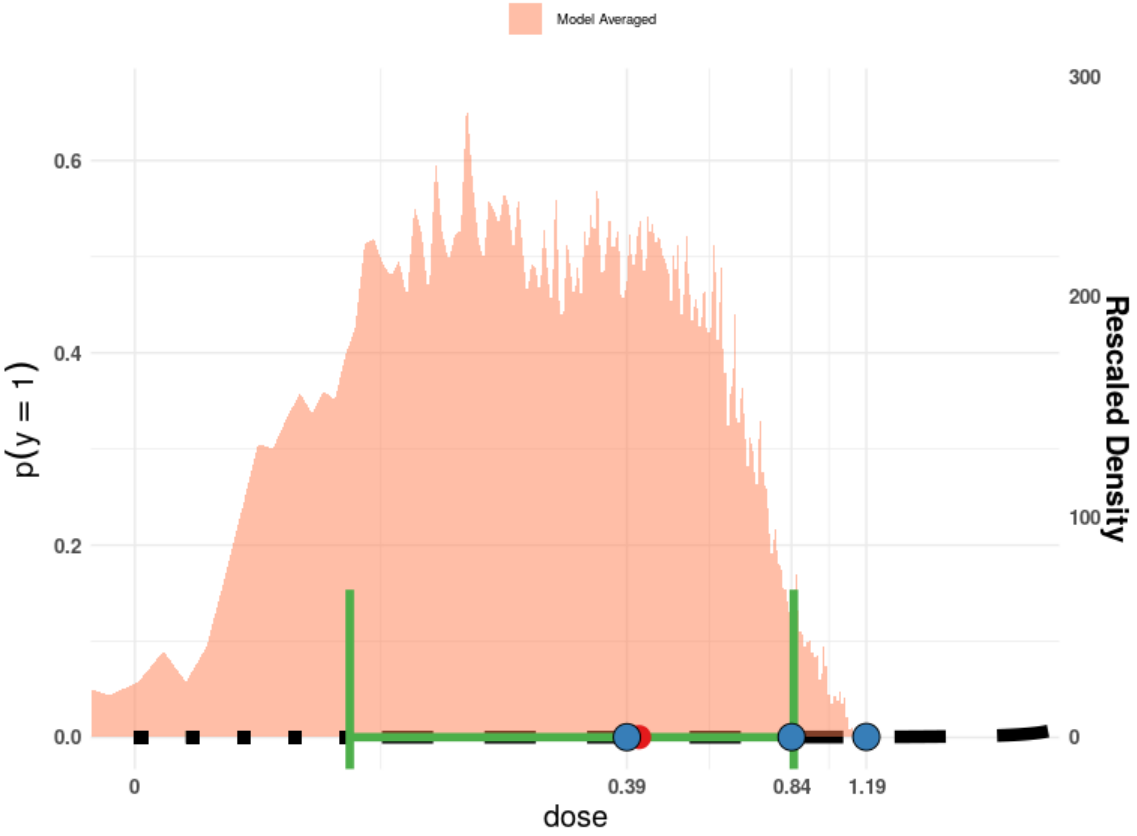
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.136	0.424	0.783	0.152	1
IE4_Q	0.377	0.783	1.064	0.038	1
H4_Q	0.135	0.427	0.791	0.154	1
LN4_Q	0.260	0.602	0.951	0.089	1
G4_Q	0.134	0.436	0.741	0.155	1
QE4_Q	0.079	0.166	0.361	0.150	1
P4_Q	0.125	0.441	0.881	0.132	1
L4_Q	0.114	0.427	0.789	0.130	1

Plots of Fitted Models




0.15
0.10
0.05
0.00
Weight
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
6e-04
4e-04
2e-04
0e+00
p(y = 1)
0
0.39
0.84
1.19
dose


Model Averaged
p(y = 1)
0.0
0.2
0.4
0.6
Rescaled Density
0
100
200
300
0
0.39
0.84
1.19
dose

Vahter et al. (2020) full developmental score, mothers u-tiAs at GW 8, BMR 5%

Data Description

The endpoint to be analyzed is: Full.development.score

Data used for analysis:

Exposure	Full.development.score	SD	N
1.53	141	34	294
1.89	135	33	293
2.47	126	34	294
4.62	127	31	293
7.02	132	31	293

The 'Value for CES' is set to 0.05.

Extended dose range is applied.

Informative background prior: min: 127; the most likely: 141; max: 155. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

Check for constant variance coefficient of variation

Distributional assumption of constant variance is met, Bartlett test p-value is 0.2801

Distributional assumption of constant variance (on log-scale) is met, Bartlett test p-value is 0.1741

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 1.55e+00).

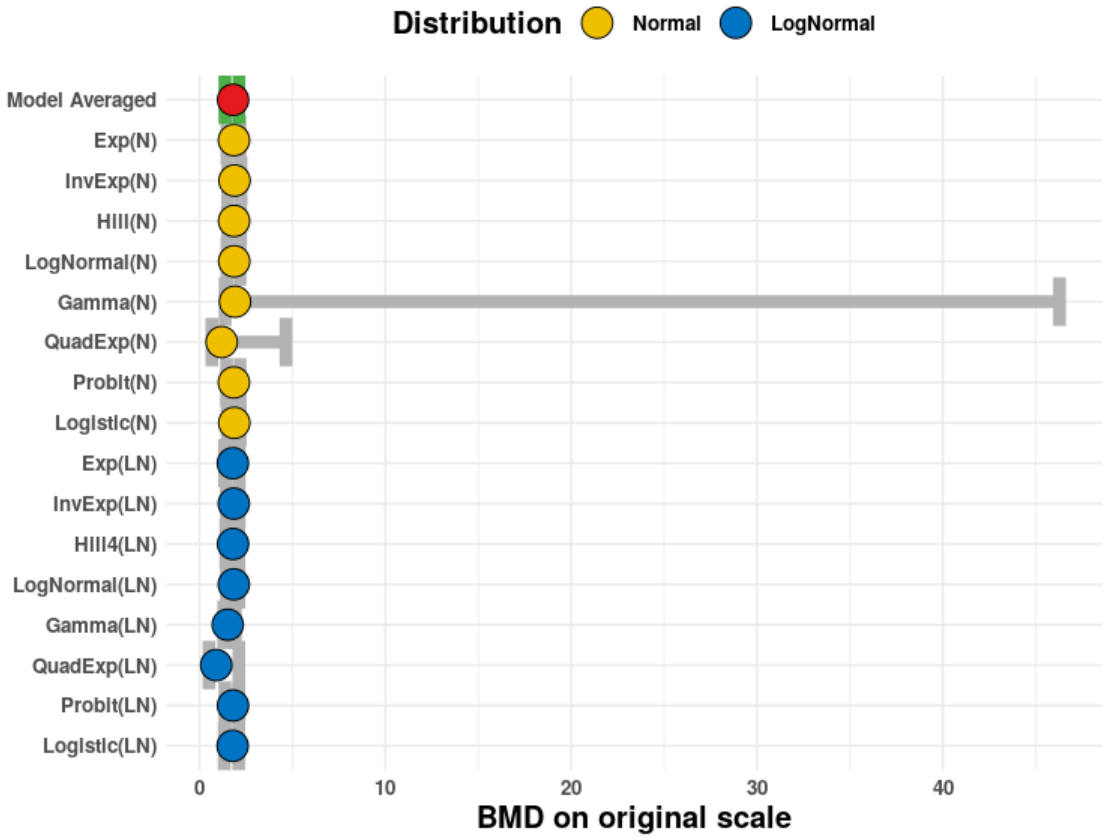
Model Averaged BMD

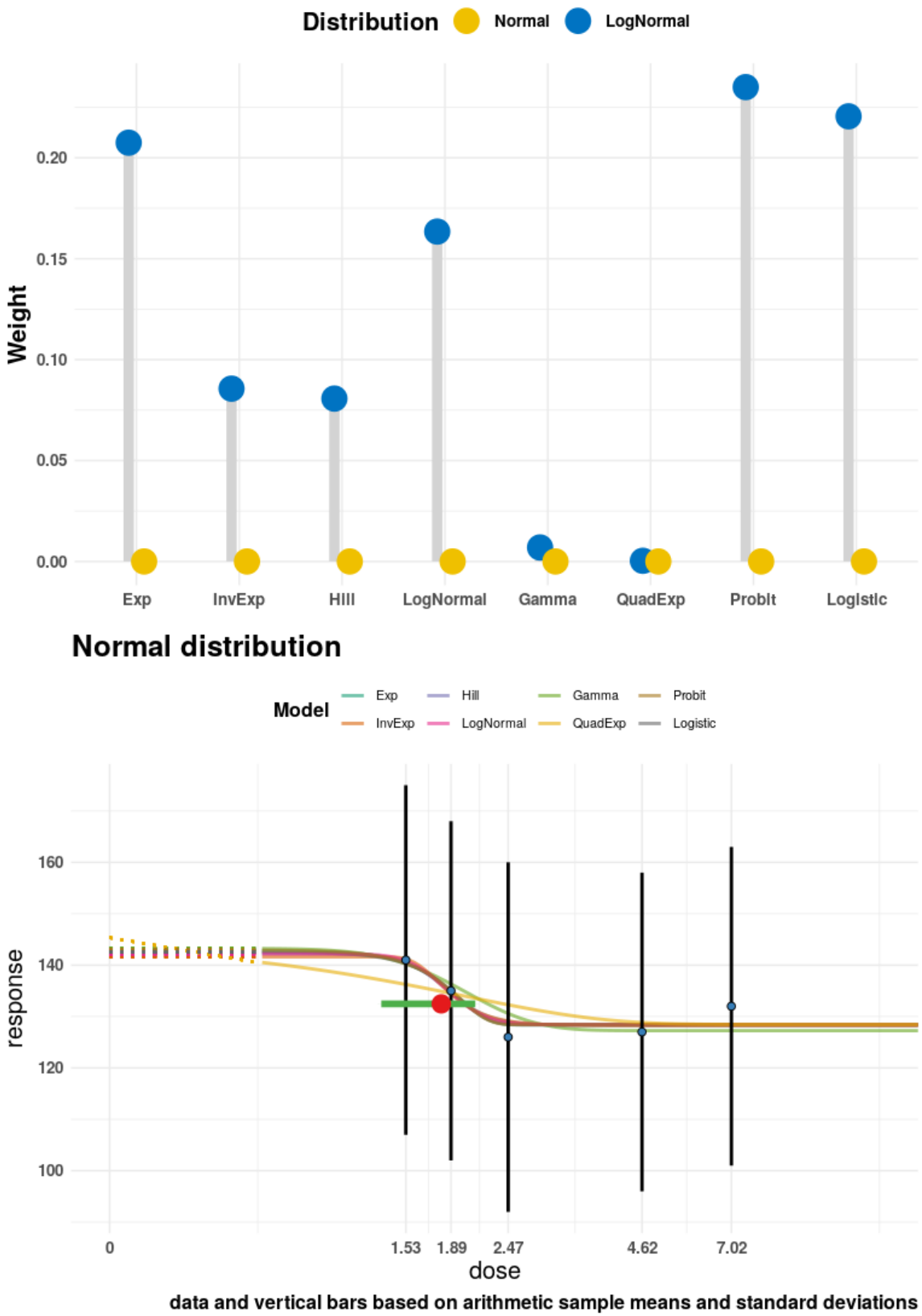
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	1.364	1.806	2.118

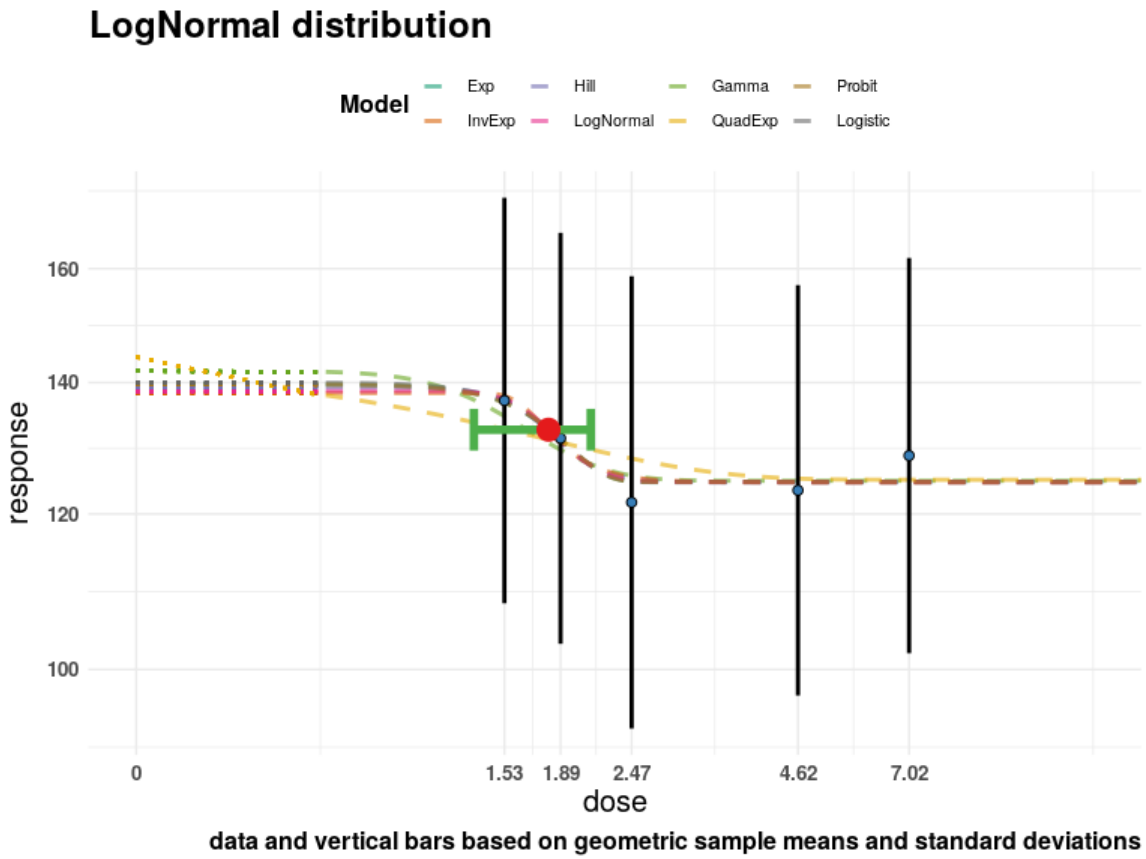
Estimated BMDs per model

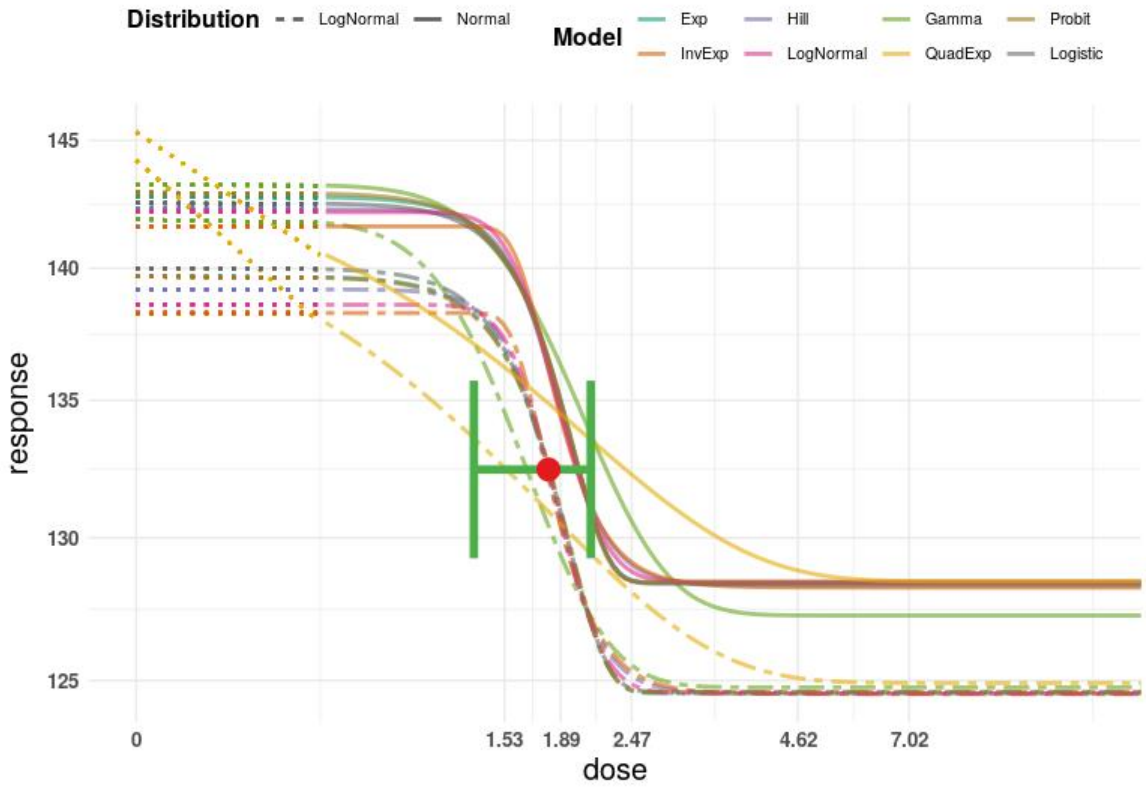
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_N	1.474	1.853	2.174	0.000	1
IE4_N	1.515	1.882	2.228	0.000	1
H4_N	1.503	1.859	2.212	0.000	1
LN4_N	1.475	1.866	2.177	0.000	1
G4_N	1.372	1.910	46.277	0.000	0
QE4_N	0.659	1.193	4.652	0.000	1
P4_N	1.454	1.849	2.181	0.000	1
L4_N	1.483	1.869	2.191	0.000	1
E4_LN	1.337	1.794	2.133	0.207	1
IE4_LN	1.446	1.844	2.126	0.086	1
H4_LN	1.412	1.804	2.120	0.081	1
LN4_LN	1.448	1.844	2.120	0.163	1
G4_LN	1.301	1.517	1.924	0.007	0
QE4_LN	0.508	0.897	2.116	0.000	1
P4_LN	1.365	1.801	2.114	0.235	1
L4_LN	1.329	1.782	2.105	0.221	1

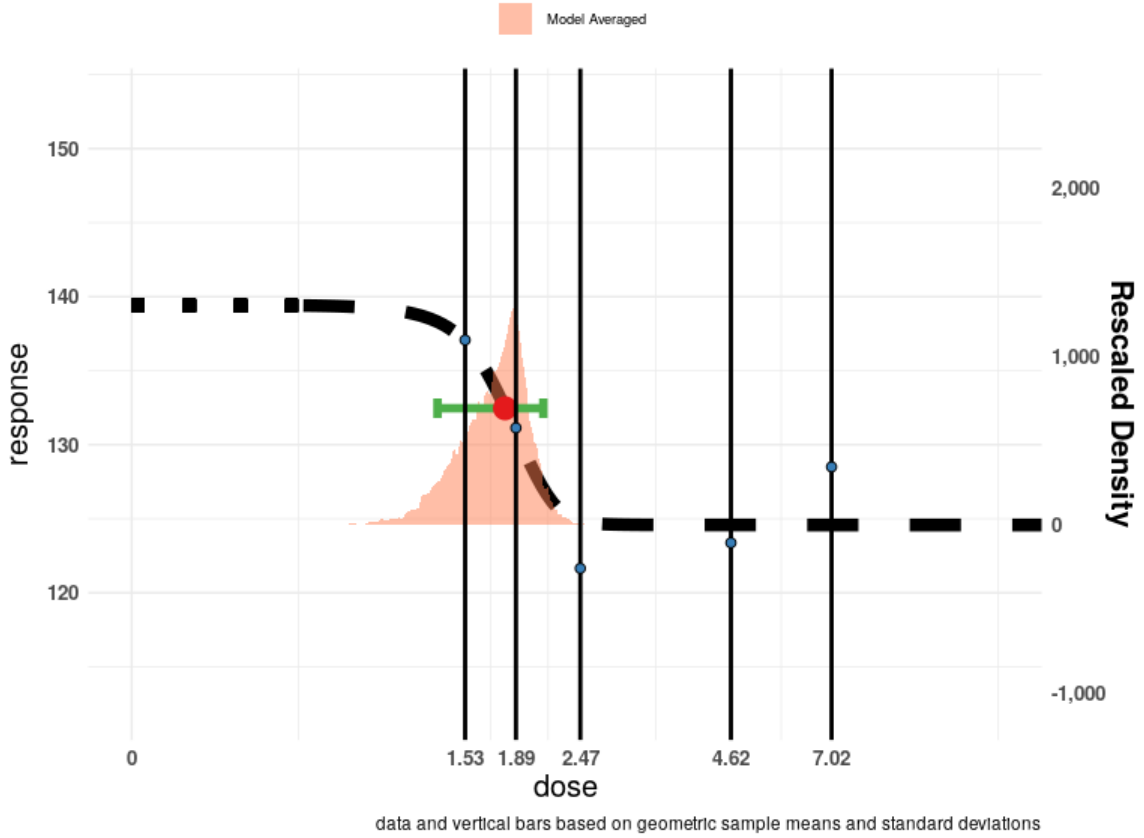
Plots of Fitted Models




Distribution
Normal
LogNormal
Weight
0.20
0.15
0.10
0.05
0.00
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic
Normal distribution
Model
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic
response
160
140
120
100
0
1.53
1.89
2.47
4.62
7.02
dose
data and vertical bars based on arithmetic sample means and standard deviations


LogNormal distribution
Model
Exp
Hill
Gamma
Probit
InvExp
LogNormal
QuadExp
Logistic
response
160
140
120
100
0
1.53
1.89
2.47
4.62
7.02
dose
data and vertical bars based on geometric sample means and standard deviations


Distribution
LogNormal
Normal
Model
Exp
Hill
Gamma
Probit
InvExp
LogNormal
QuadExp
Logistic
response
145
140
135
130
125
0
1.53
1.89
2.47
4.62
7.02
dose


Model Averaged
150
140
130
120
response
2,000
1,000
0
-1,000
Rescaled Density
0
1.53
1.89
2.47
4.62
7.02
dose
data and vertical bars based on geometric sample means and standard deviations

Vahter et al. (2020), full developmental score, children u-tiAs 10 years, BMR 5%

Data Description

The endpoint to be analyzed is: Full.development.score

Data used for analysis:

Exposure	Full.development.score	SD	N
0.98	141	34	305
1.57	135	33	305
2.49	126	34	304
4.52	127	31	305
11.52	132	31	304

The 'Value for CES' is set to 0.05.

Extended dose range is applied.

Informative background prior: min: 127; the most likely; 141; max: 155. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

Check for constant variance coefficient of variation

Distributional assumption of constant variance is met, Bartlett test p-value is 0.2613

Distributional assumption of constant variance (on log-scale) is met, Bartlett test p-value is 0.1598

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 1.85e+00).

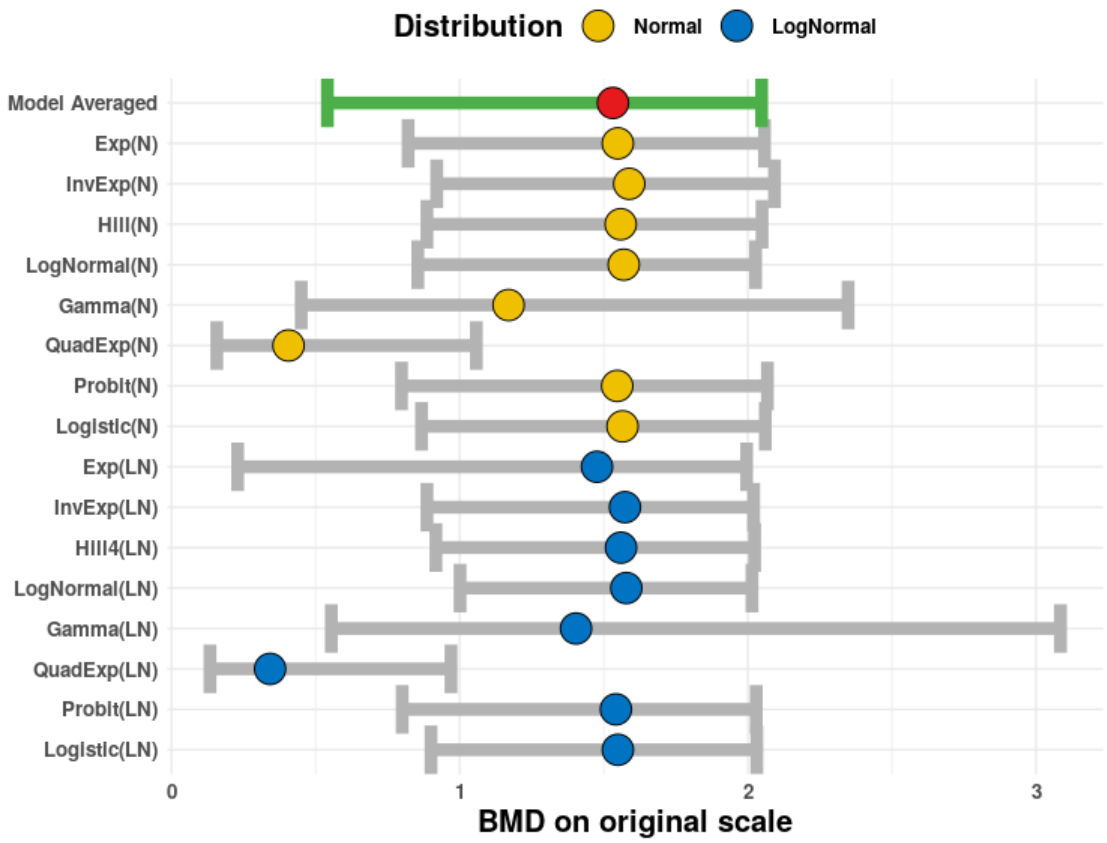
Model Averaged BMD

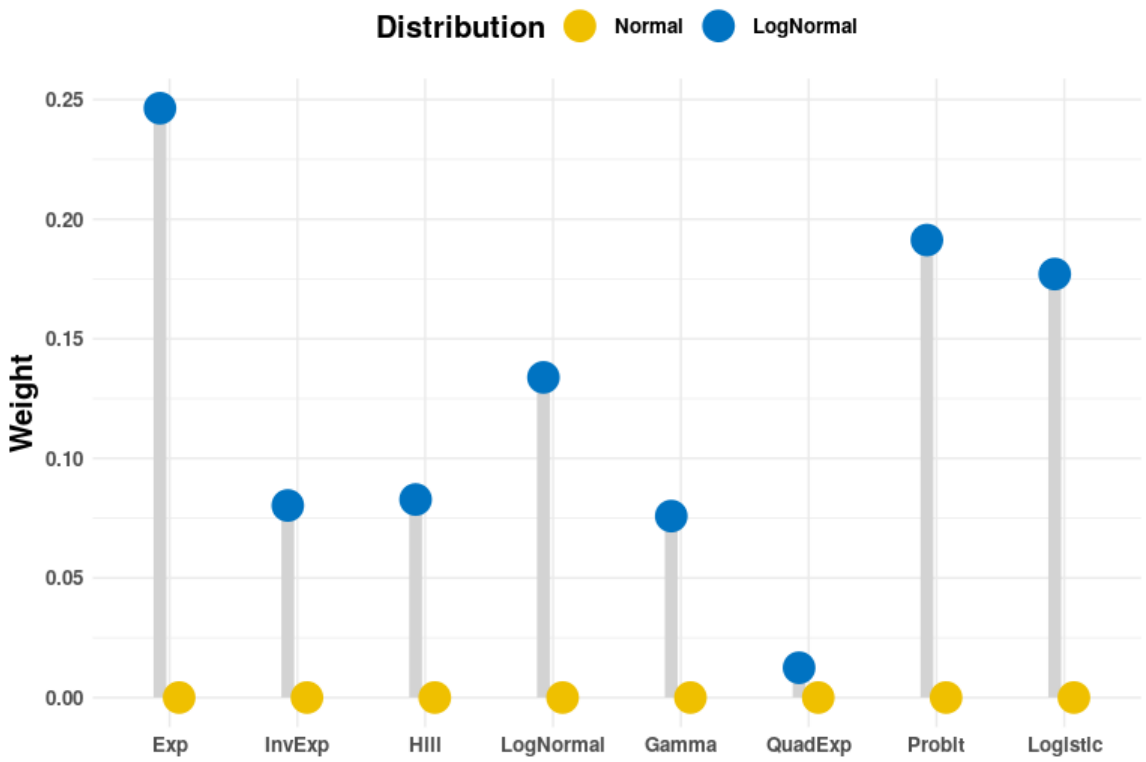
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.541	1.532	2.048

Estimated BMDs per model

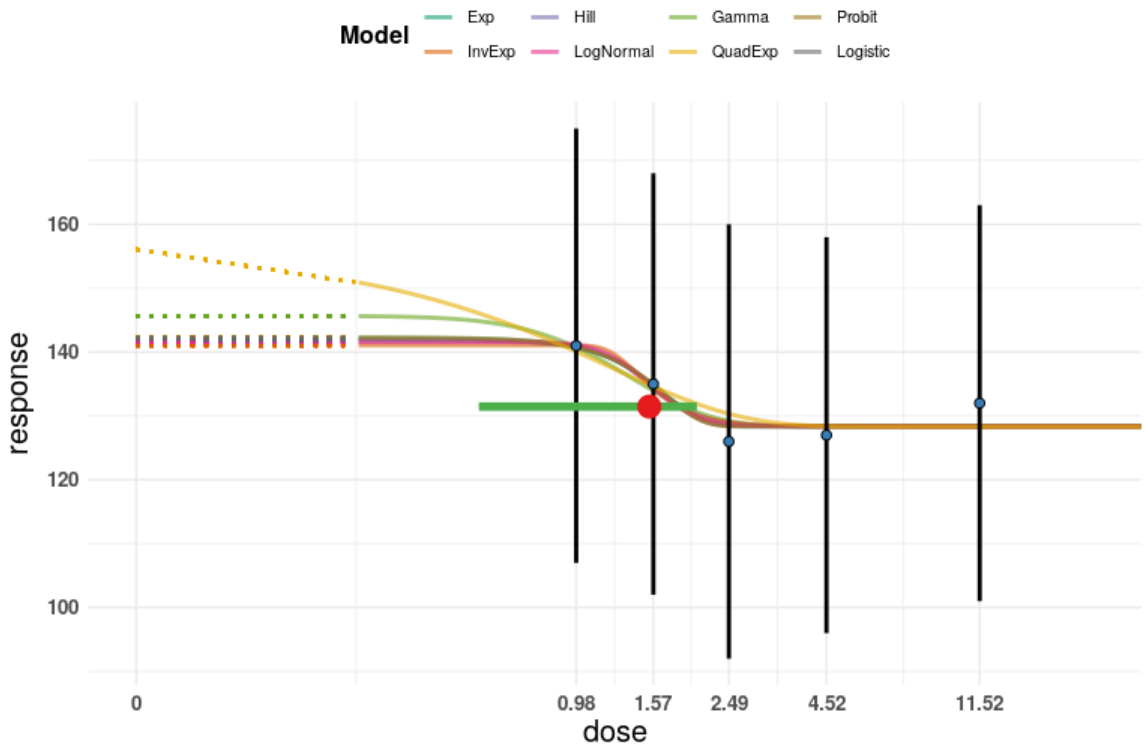
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_N	0.821	1.549	2.058	0.000	1
IE4_N	0.920	1.588	2.093	0.000	1
H4_N	0.886	1.559	2.049	0.000	1
LN4_N	0.855	1.569	2.027	0.000	1
G4_N	0.450	1.170	2.348	0.000	0
QE4_N	0.157	0.406	1.058	0.000	1
P4_N	0.798	1.547	2.068	0.000	1
L4_N	0.868	1.565	2.061	0.000	1
E4_LN	0.229	1.476	1.996	0.246	0
IE4_LN	0.887	1.574	2.020	0.080	1
H4_LN	0.918	1.560	2.024	0.083	1
LN4_LN	1.001	1.578	2.014	0.134	1
G4_LN	0.555	1.404	3.085	0.076	0
QE4_LN	0.133	0.342	0.970	0.012	1
P4_LN	0.801	1.542	2.029	0.191	1
L4_LN	0.900	1.549	2.031	0.177	1

Plots of Fitted Models

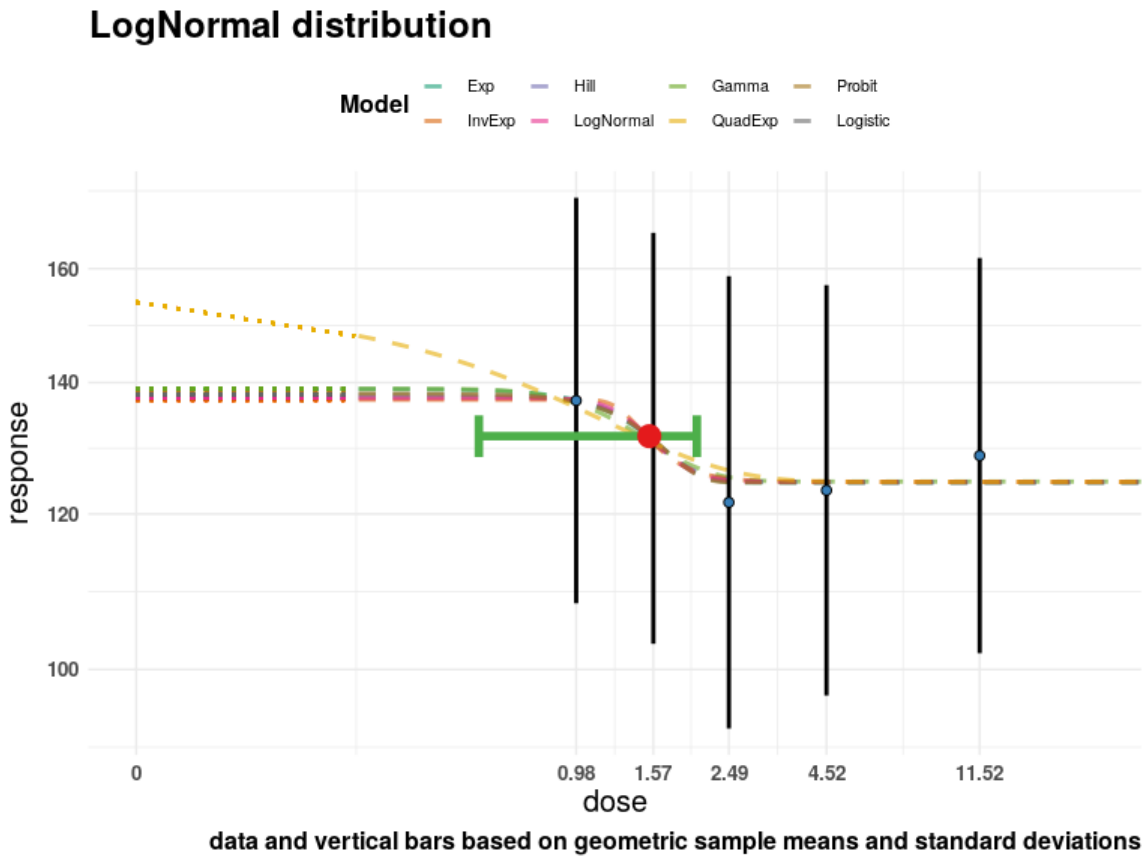


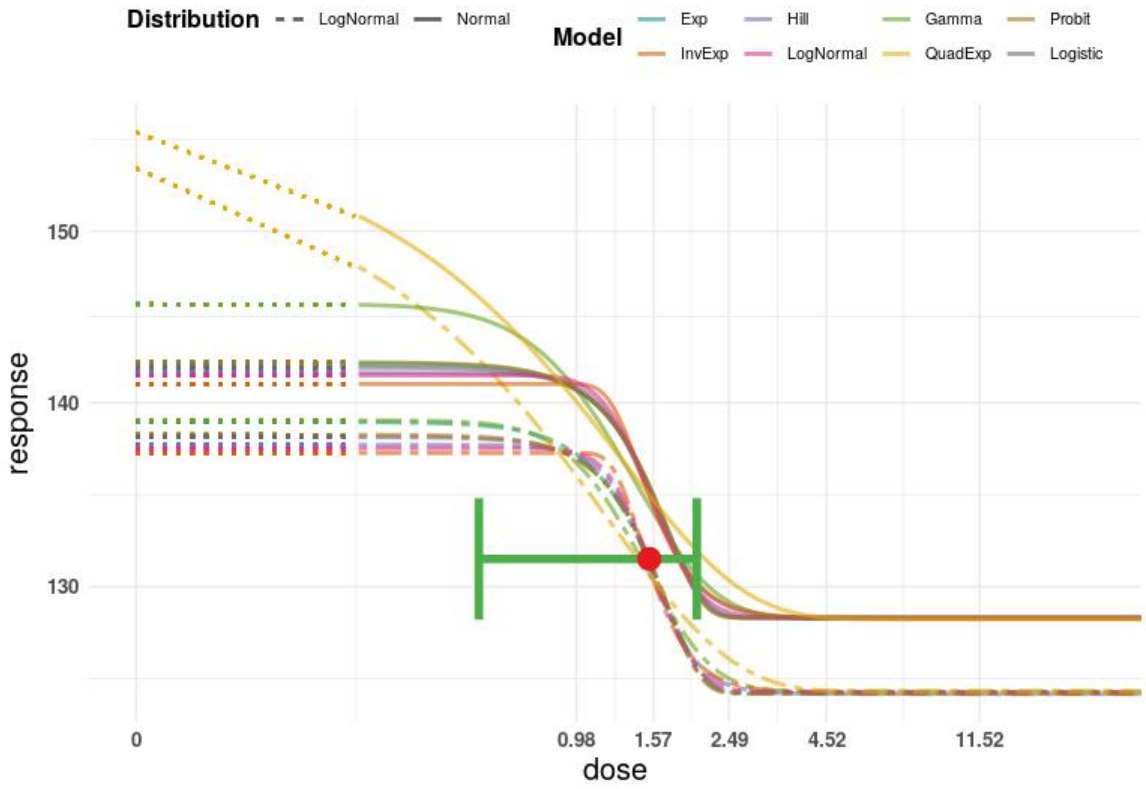


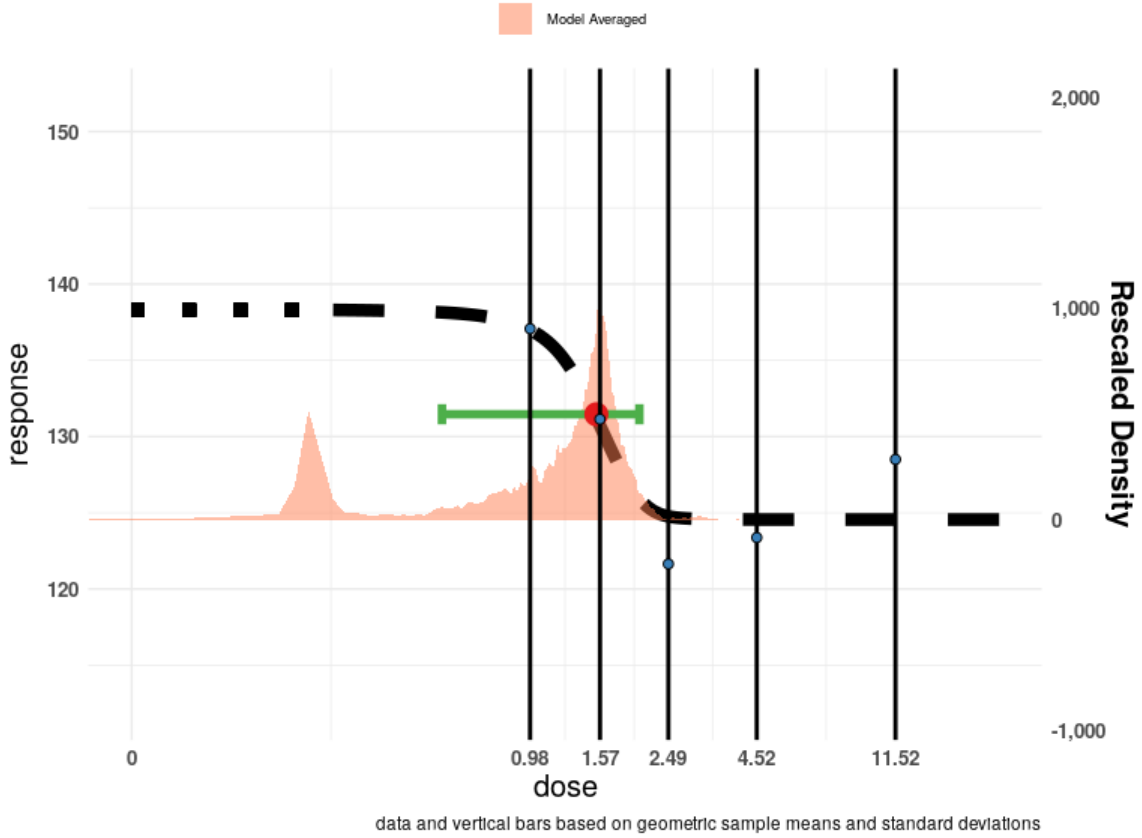
Normal distribution



data and vertical bars based on arithmetic sample means and standard deviations


LogNormal distribution
Model
Exp
Hill
Gamma
Probit
InvExp
LogNormal
QuadExp
Logistic
response
160
140
120
100
0
0.98
1.57
2.49
4.52
11.52
dose
data and vertical bars based on geometric sample means and standard deviations


Distribution
LogNormal
Normal
Model
Exp
Hill
Gamma
Probit
InvExp
LogNormal
QuadExp
Logistic
response
150
140
130
0
0.98
1.57
2.49
4.52
11.52
dose


Model Averaged
150
140
130
120
response
2,000
1,000
0
-1,000
Rescaled Density
0
0.98
1.57
2.49
4.52
11.52
dose
data and vertical bars based on geometric sample means and standard deviations

Wade et al. (2015) ischemic heart disease, relative BMR 5%

Data Description

The endpoint to be analyzed is: Adj.cases for ischemic heart disease

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	N
0.93	124	100735
2.02	146	96324
2.84	15	2941

The 'Value for CES' is set to 6.162e-05.

Extended dose range is applied.

Informative background prior: min: 0.00104631; the most likely: 0.00123095; max: 0.00141560. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 1.07e+00).

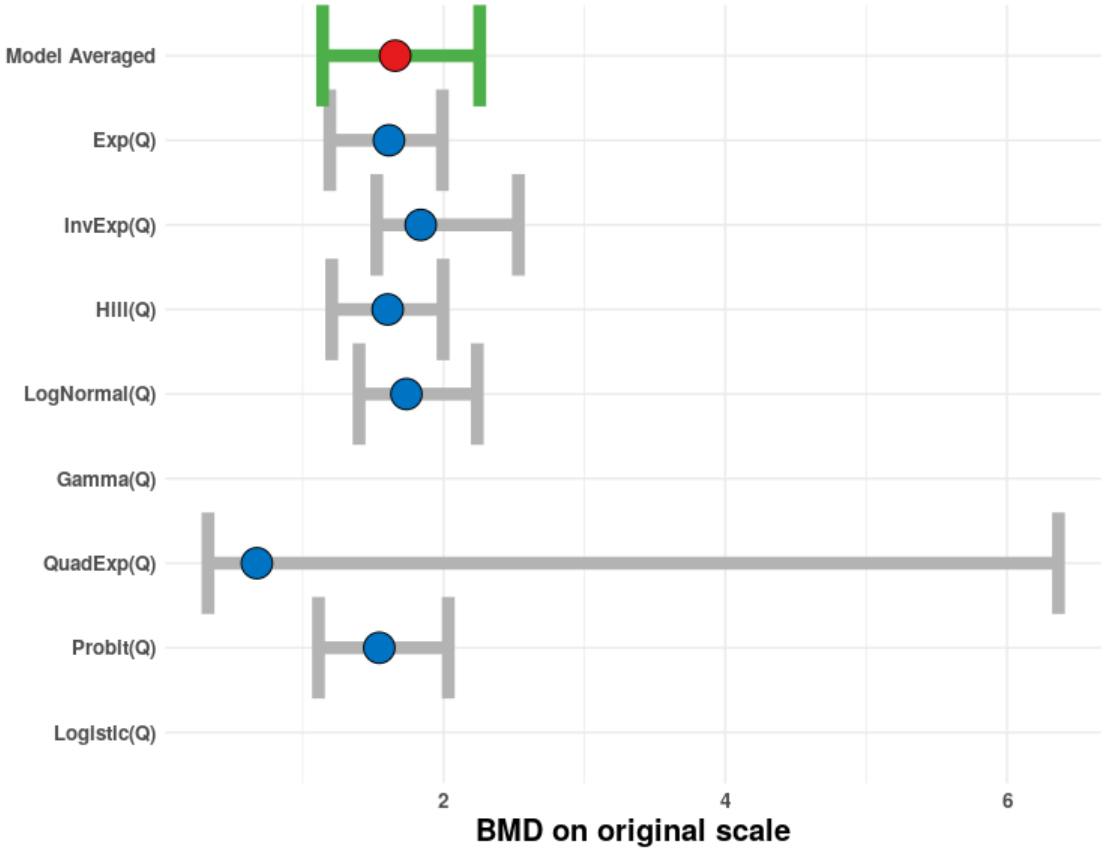
Model Averaged BMD

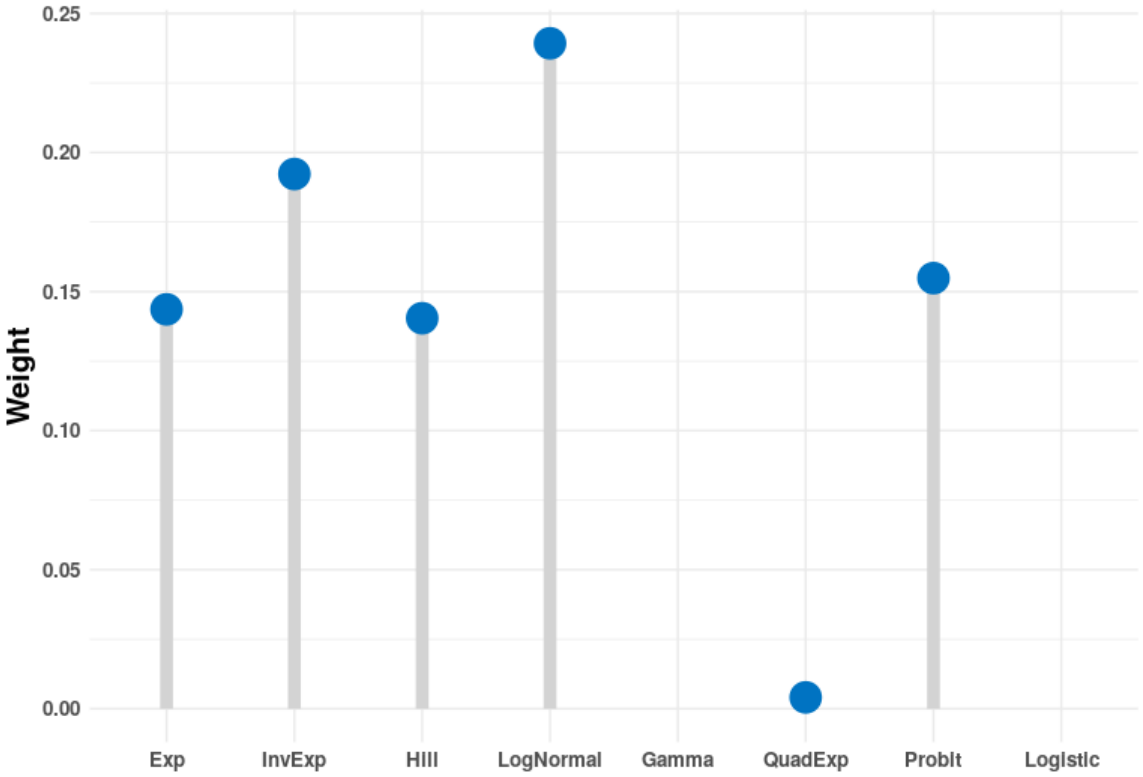
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	1.227	1.667	2.279

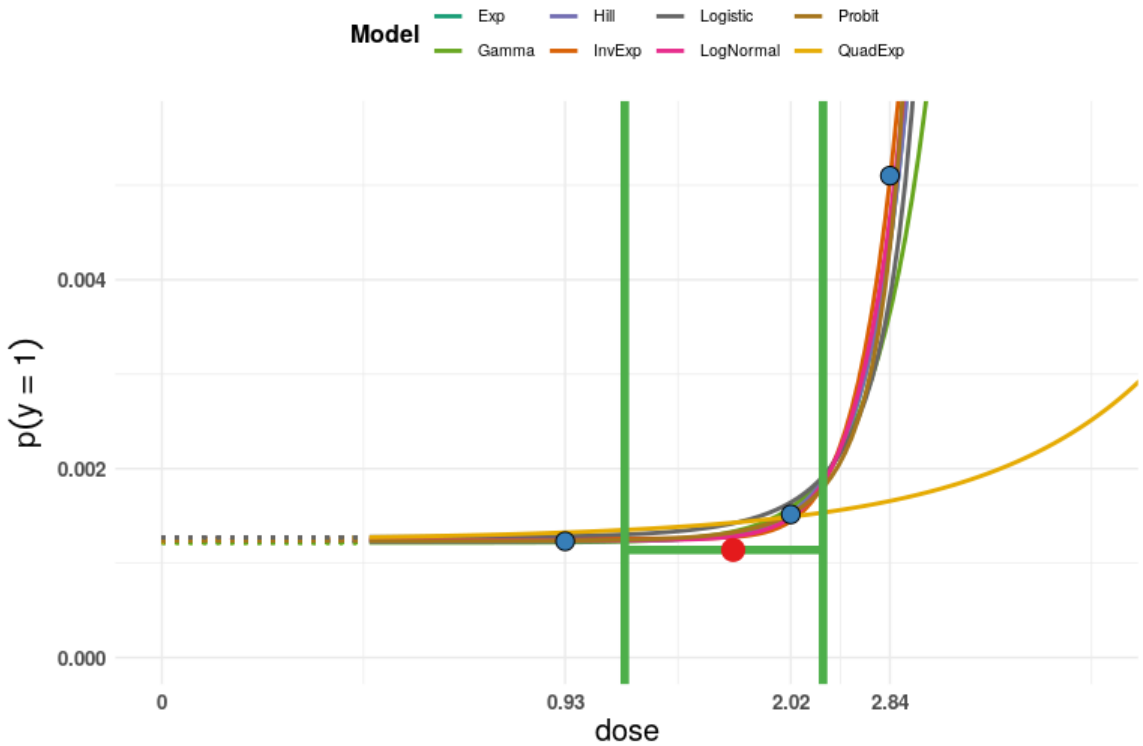
Estimated BMDs per model

Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	1.193	1.613	1.992	0.144	1
IE4_Q	1.526	1.838	2.532	0.192	1
H4_Q	1.207	1.604	1.997	0.140	1
LN4_Q	1.401	1.737	2.240	0.239	1
QE4_Q	0.328	0.675	6.366	0.004	1
P4_Q	1.112	1.544	2.034	0.155	1

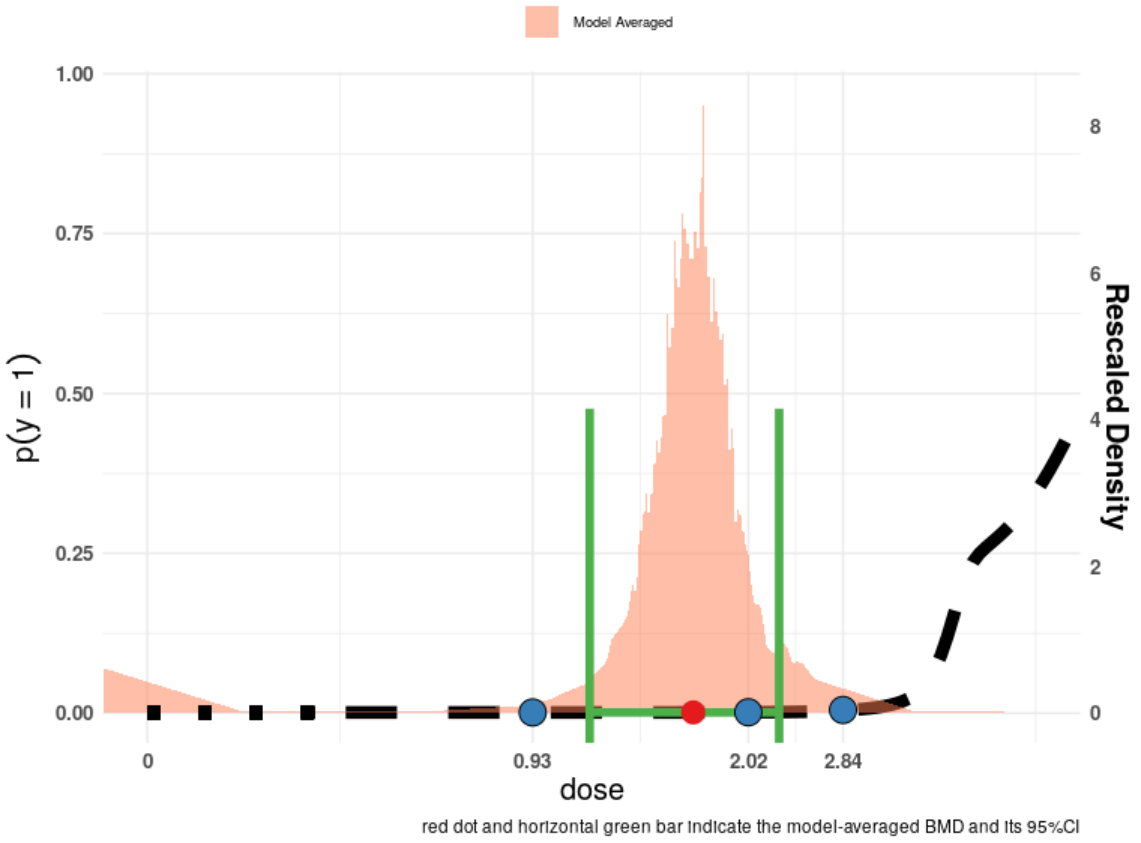
Plots of Fitted Models







red dot and horizontal green bar indicate the model-averaged BMD and its 95%CI


Model Averaged
1.00
0.75
0.50
0.25
0.00
p(y = 1)
8
6
4
2
0
Rescaled Density
0
0.93
2.02
2.84
dose
red dot and horizontal green bar indicate the model-averaged BMD and its 95%CI

Wu et al. (2015) ischemic heart disease, relative BMR 5%

Data Description

The endpoint to be analyzed is: Adj.cases for ischemic heart disease

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	N
1.40	64	453
4.49	83	452
15.00	90	454

The 'Value for CES' is set to 0.00822622.

Extended dose range is not applied.

Informative background prior: min: 0.13986755; the most likely: 0.14128035; max: 0.14269316. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 5.15e+00).

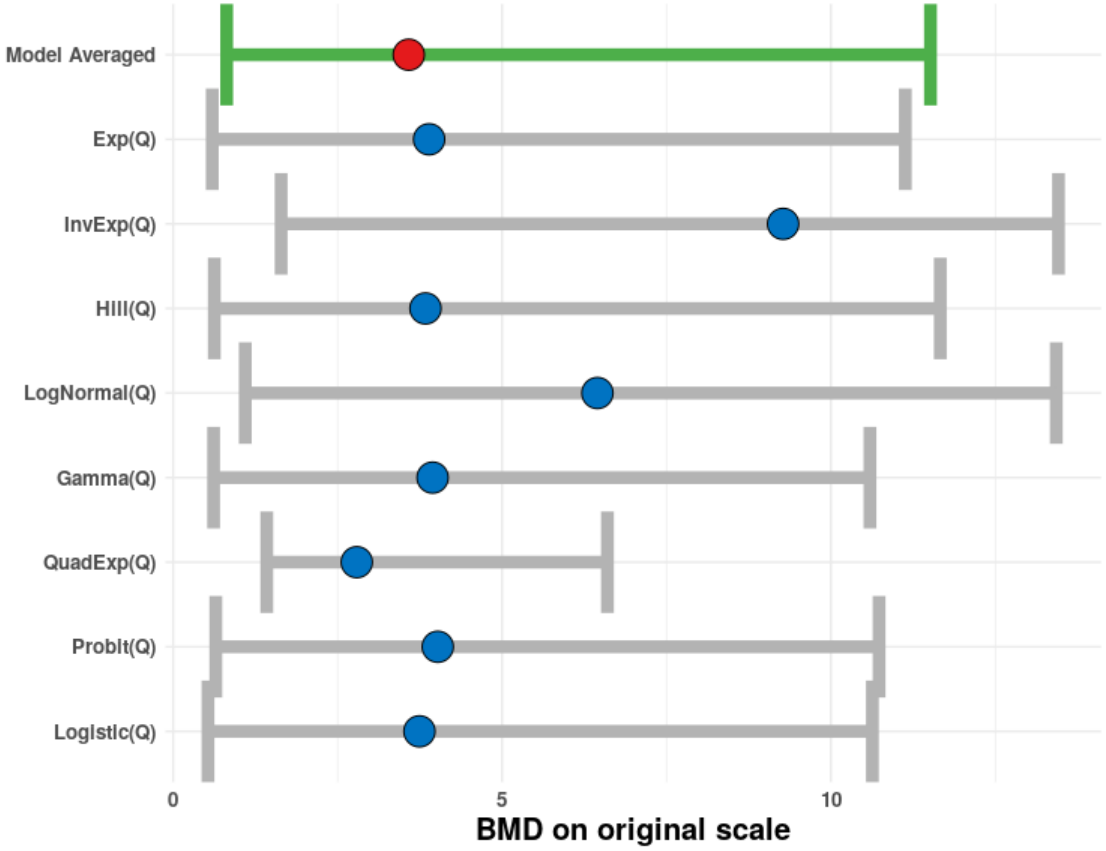
Model Averaged BMD

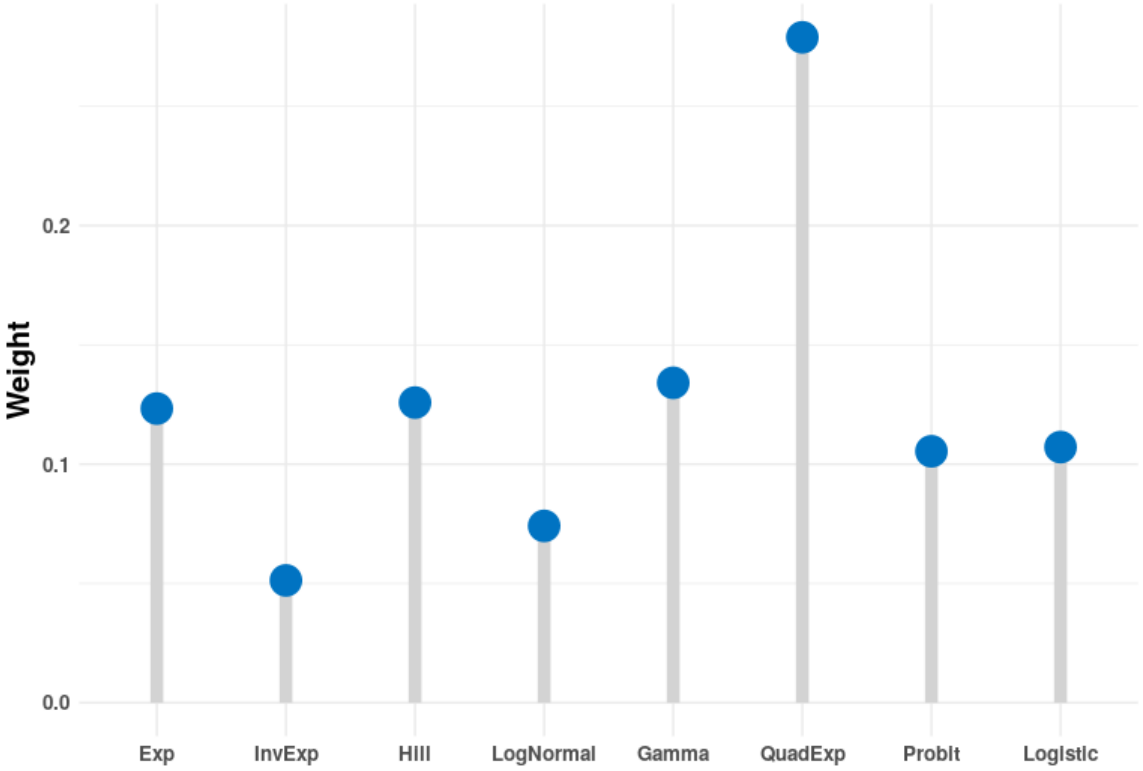
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.813	3.582	11.514

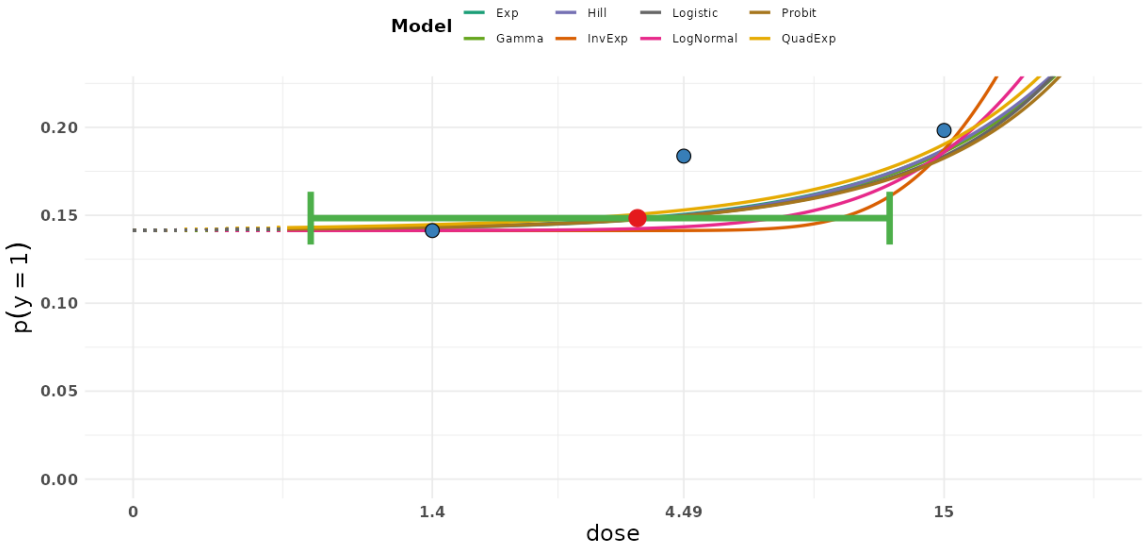
Estimated BMDs per model

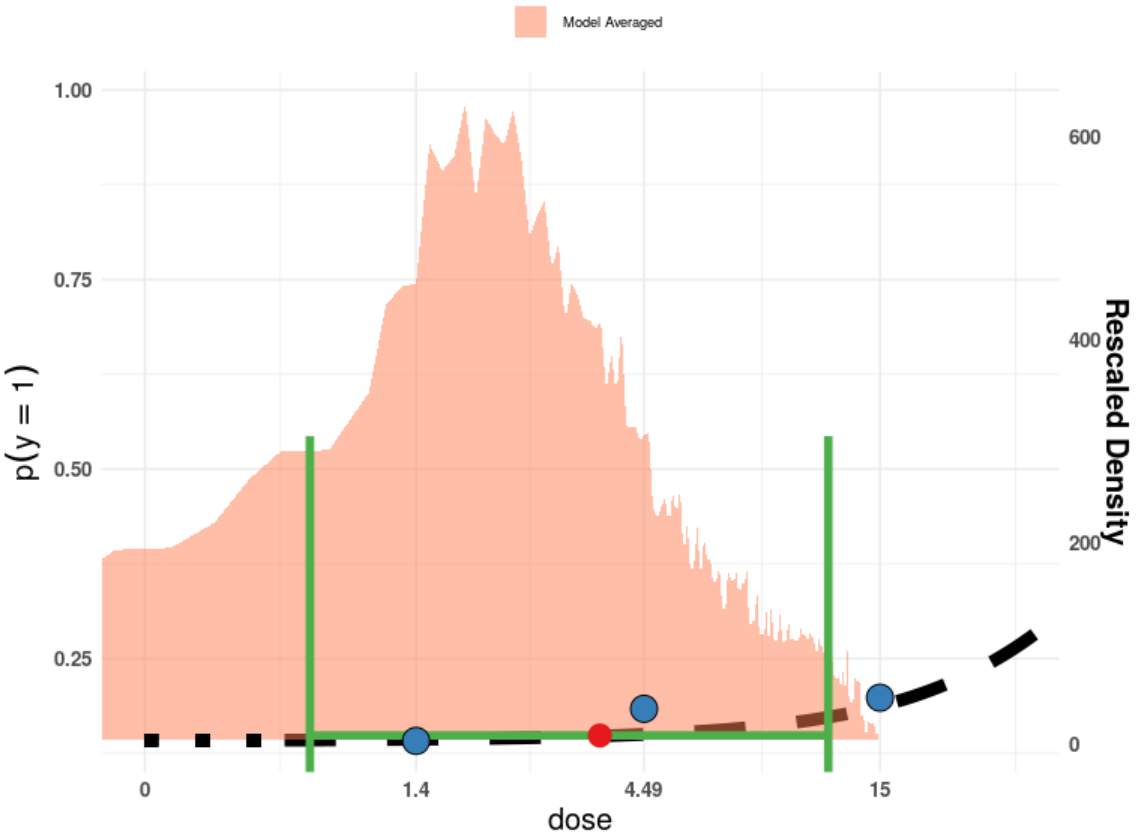
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.595	3.892	11.131	0.123	1
IE4_Q	1.642	9.274	13.460	0.051	0
H4_Q	0.626	3.836	11.663	0.126	1
LN4_Q	1.096	6.450	13.427	0.074	1
G4_Q	0.615	3.945	10.594	0.134	1
QE4_Q	1.423	2.792	6.603	0.279	1
P4_Q	0.649	4.023	10.733	0.105	1
L4_Q	0.530	3.744	10.631	0.107	1

Plots of Fitted Models




Weight
0.2
0.1
0.0
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
p(y = 1)
0.20
0.15
0.10
0.05
0.00
0
1.4
4.49
15
dose


Model Averaged
1.00
0.75
0.50
0.25
p(y = 1)
600
400
200
0
Rescaled Density
0
1.4
4.49
15
dose

Xia et al. (2009) skin lesions, relative BMR 5%

Data Description

The endpoint to be analyzed is: Adj.cases for skin lesions

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	N
0.79	52	3215
1.07	33	845
1.48	56	1277
2.57	206	3429
4.75	137	1537
11.57	127	1021
17.02	10	92

The 'Value for CES' is set to 0.000822.

Extended dose range is applied.

Informative background prior: min: 0.01536547; the most likely: 0.01617418; max: 0.01698289. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 2.00e-03).

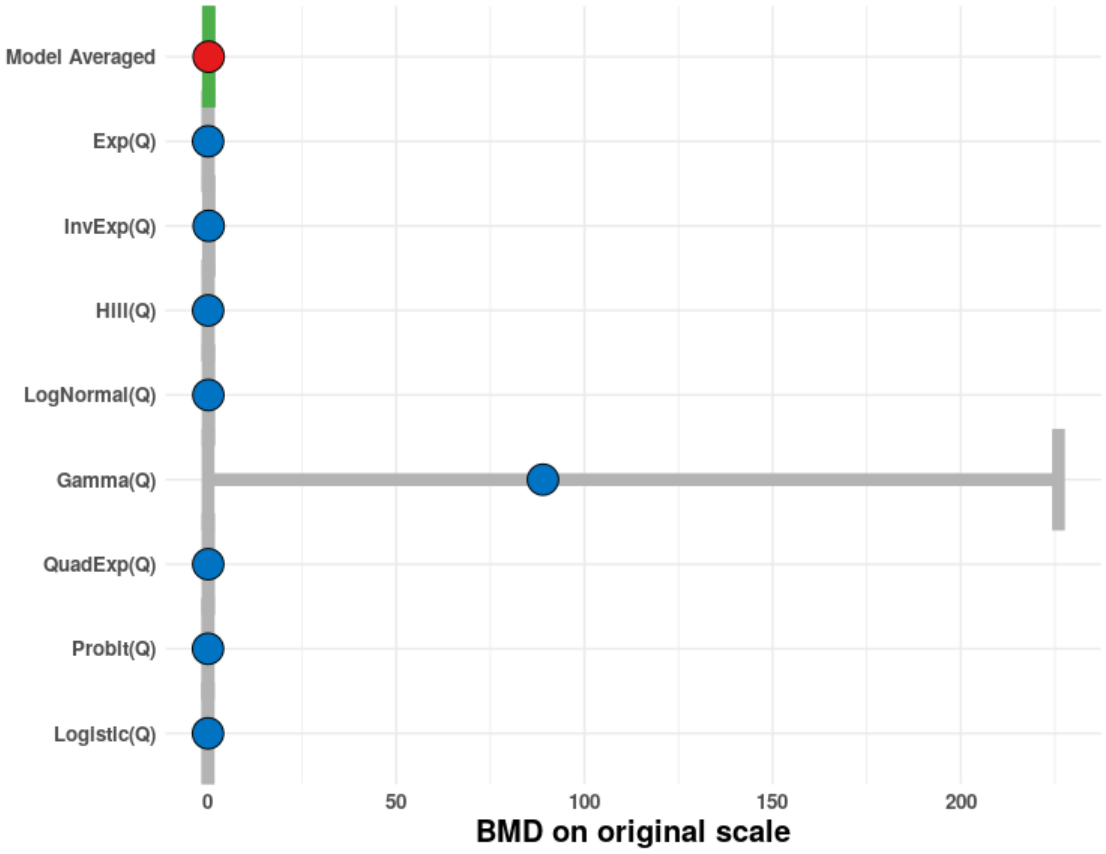
Model Averaged BMD

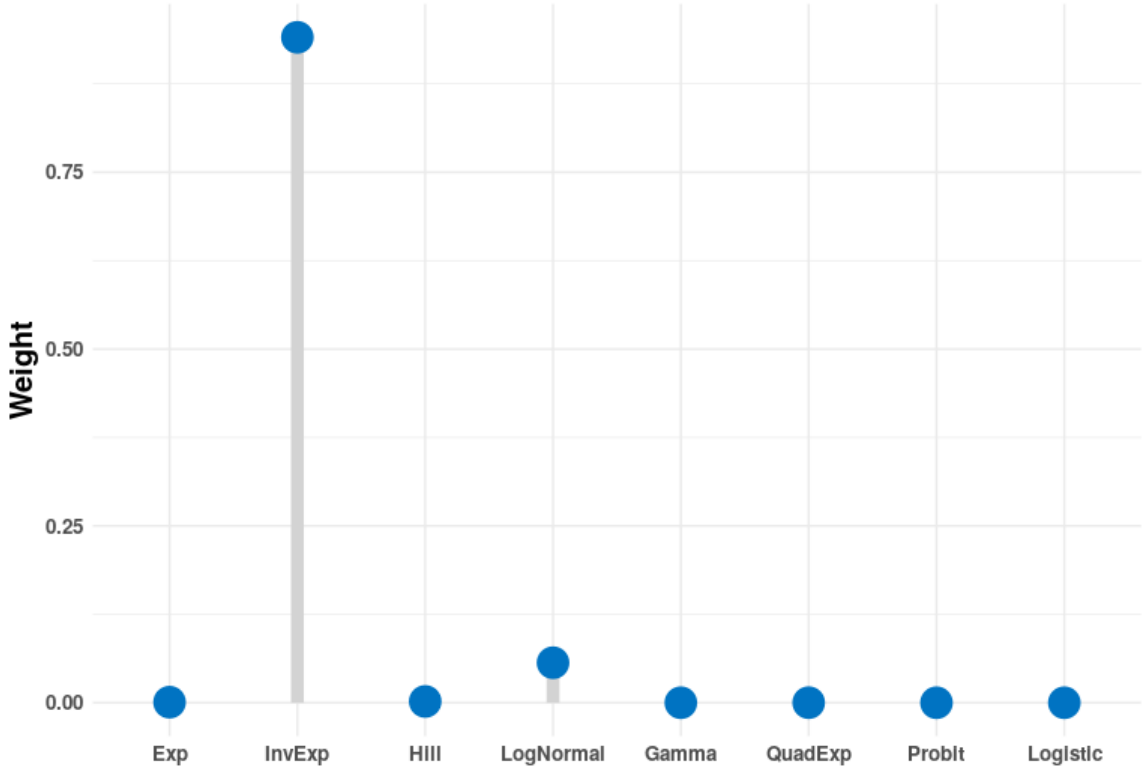
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.106	0.182	0.253

Estimated BMDs per model

Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.015	0.028	0.049	0.001	1
IE4_Q	0.124	0.184	0.253	0.941	1
H4_Q	0.017	0.033	0.056	0.002	1
LN4_Q	0.059	0.097	0.145	0.057	1
G4_Q	0.018	88.990	225.952	0.000	0
QE4_Q	0.058	0.063	0.070	0.000	1
P4_Q	0.001	0.003	0.007	0.000	1
L4_Q	0.001	0.002	0.004	0.000	1

Plots of Fitted Models




Weight
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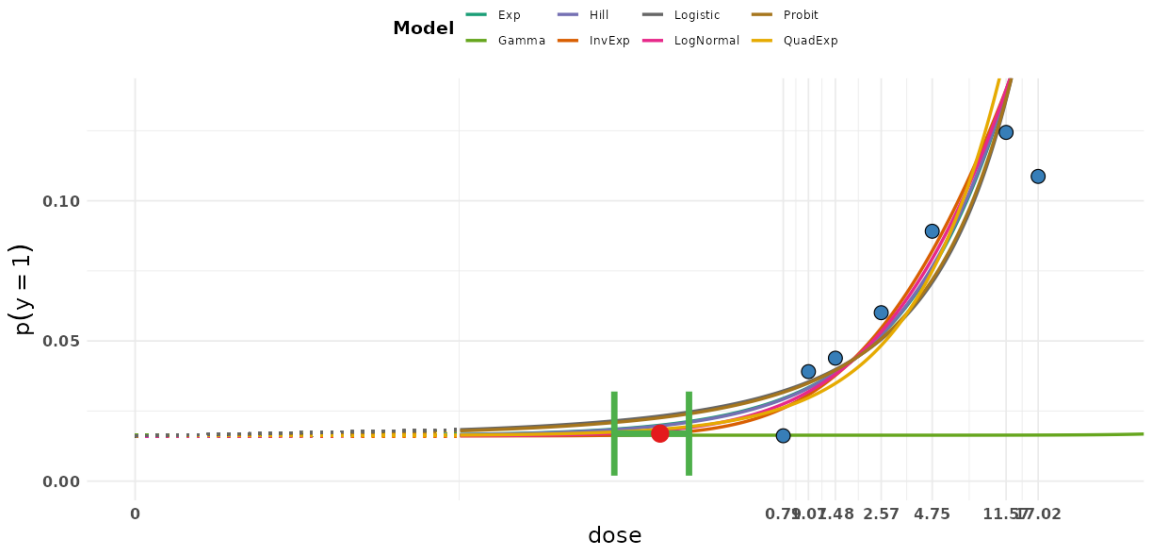
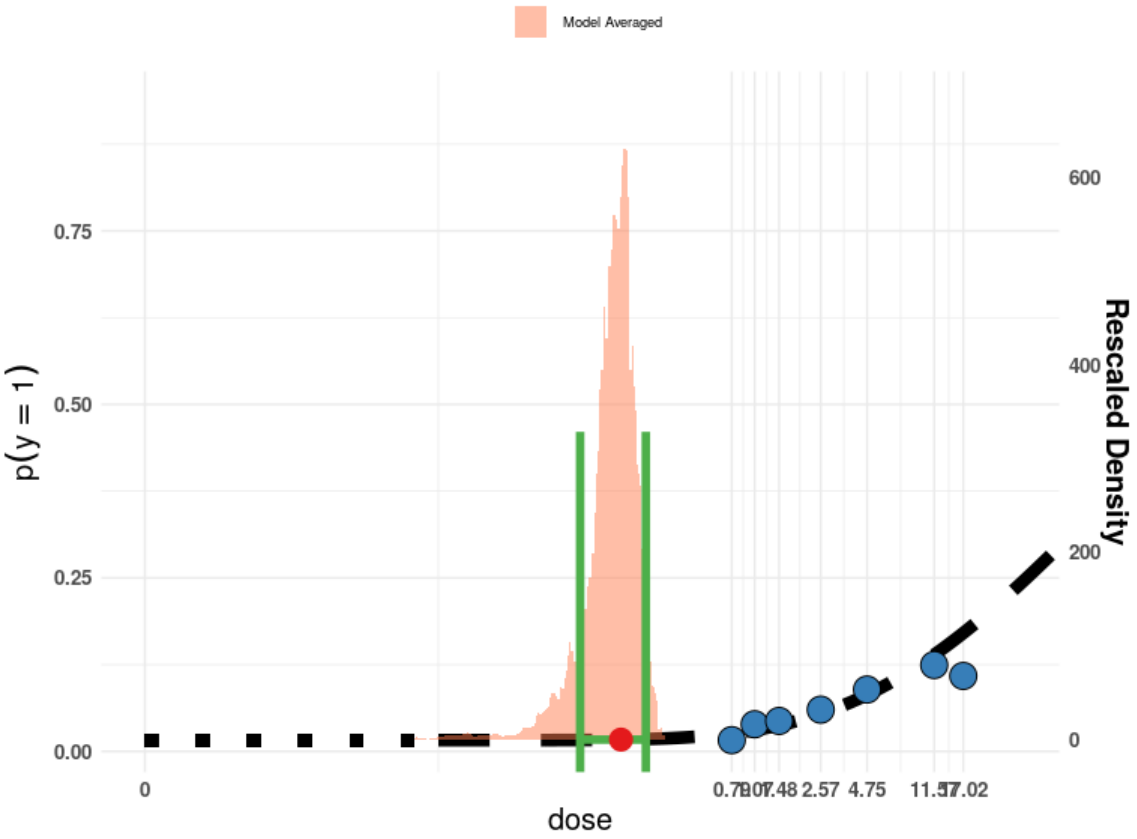
0.50
0.25
0.00
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
p(y = 1)
0.10
0.05
0.00
0
0.79
1.07
1.48
2.57
4.75
11.57
17.02
dose


Model Averaged
p(y = 1)
0.75
0.50
0.25
0.00
600
400
200
0
Rescaled Density
0
0.79
1.07
1.48
2.57
4.75
11.57
17.02
dose

Zheng et al. (2015) chronic kidney disease, relative BMR 5%

Data Description

The endpoint to be analyzed is: Adj.cases for chronic kidney disease

Data used for analysis:

Exposure.µg.kg.bw.per.day	Adj.cases	N
0.061	101	772
0.160	113	781
0.260	124	784
0.350	164	782

The 'Value for CES' is set to 0.00752608.

Extended dose range is not applied.

Informative background prior: min: 0.12952073; the most likely: 0.13082902; max: 0.13213731. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Results

Information pertaining to this endpoint.

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 2.40e-02).

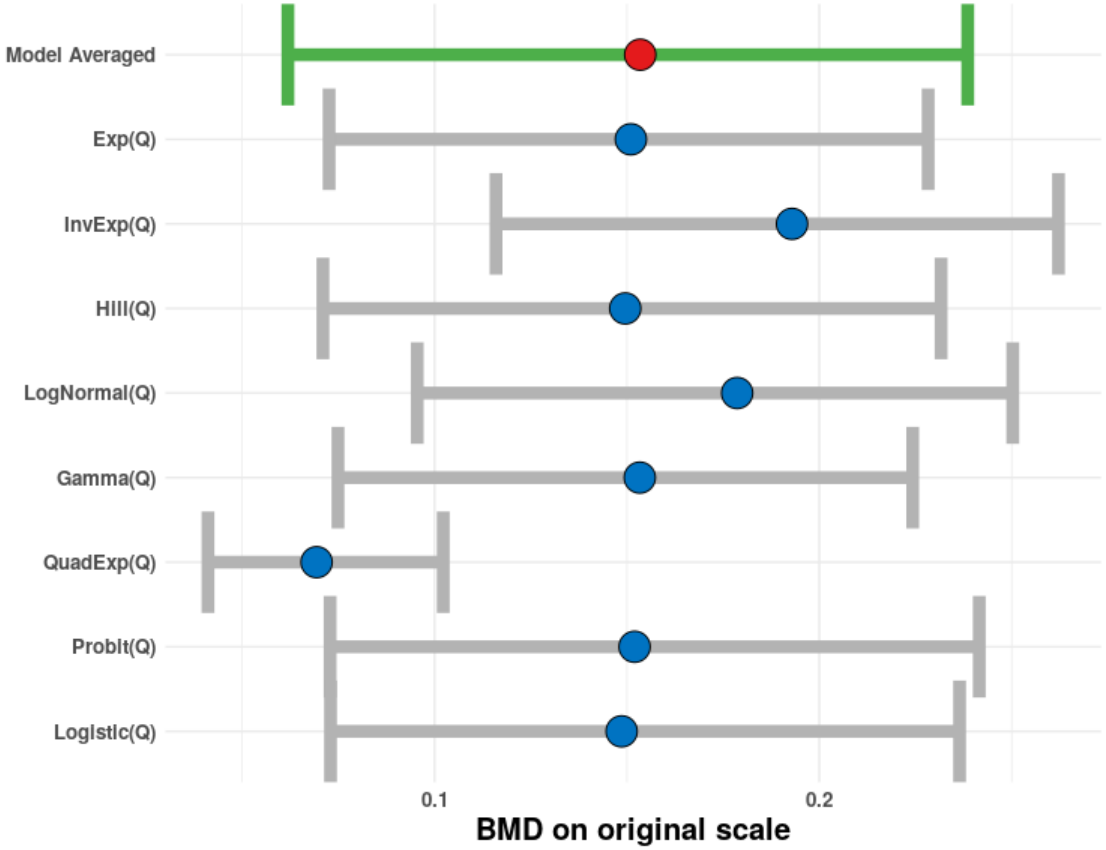
Model Averaged BMD

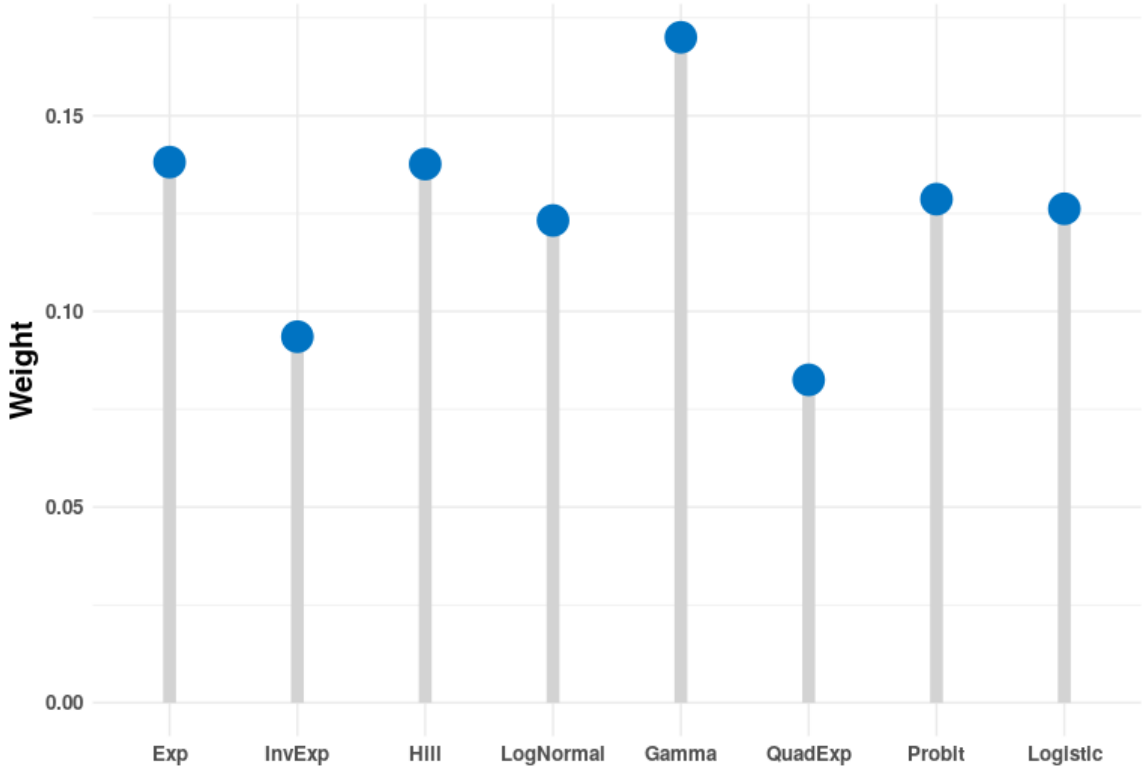
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.062	0.153	0.239

Estimated BMDs per model

Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.073	0.151	0.228	0.138	1
IE4_Q	0.116	0.193	0.262	0.094	1
H4_Q	0.071	0.150	0.232	0.138	1
LN4_Q	0.096	0.179	0.250	0.123	1
G4_Q	0.075	0.153	0.224	0.170	1
QE4_Q	0.041	0.069	0.102	0.083	1
P4_Q	0.073	0.152	0.242	0.129	1
L4_Q	0.073	0.149	0.236	0.126	1

Plots of Fitted Models

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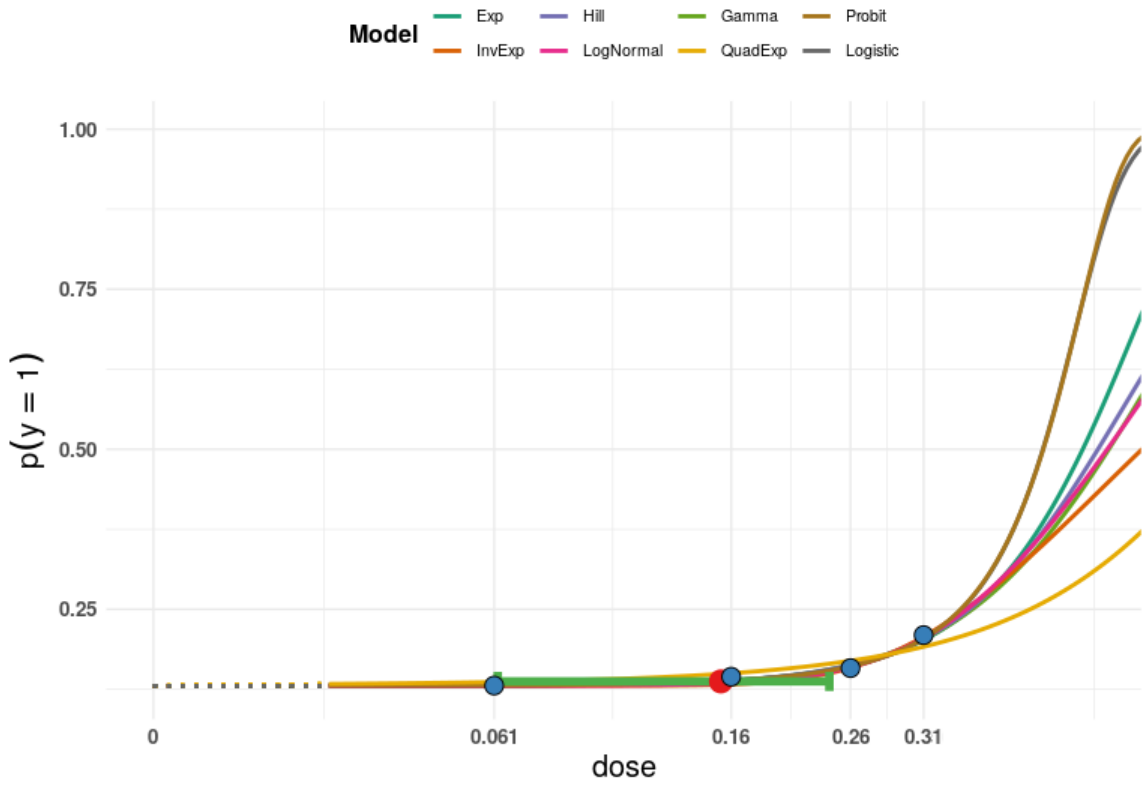
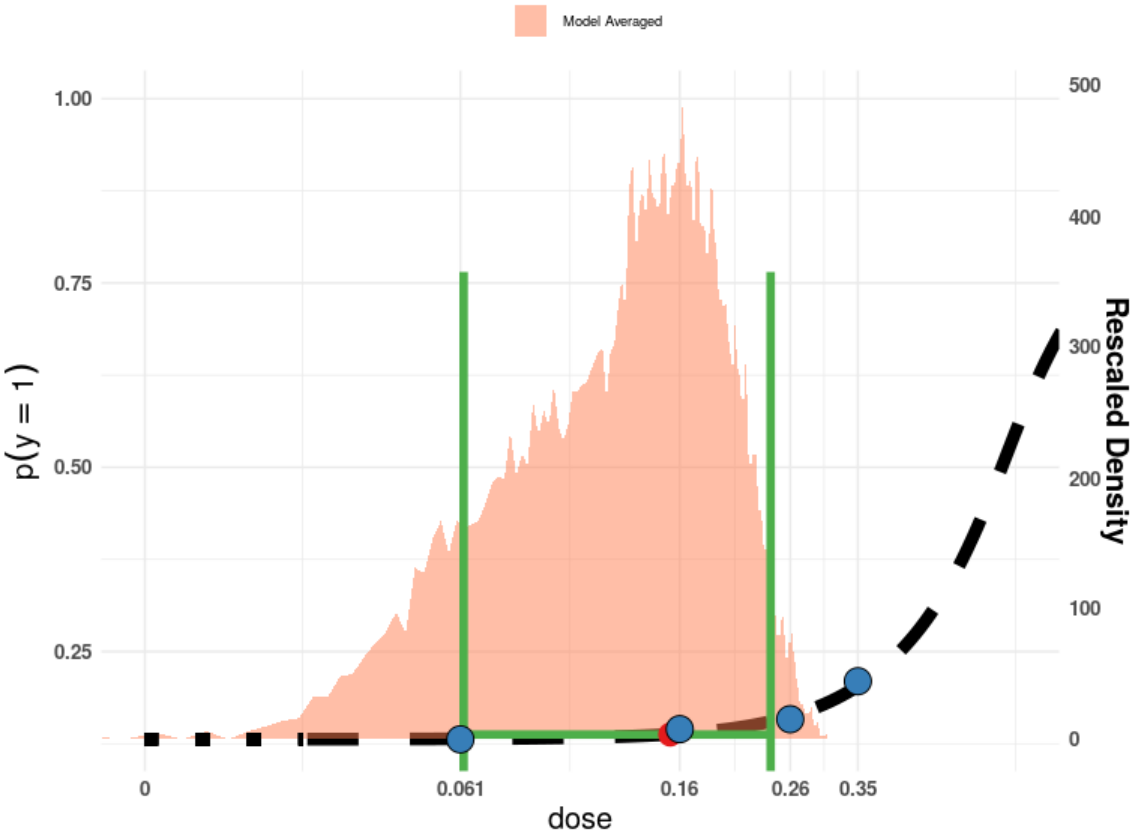
0.00
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic
p(y = 1)
1.00
0.75
0.50
0.25
0
0.061
0.16
0.26
0.31
dose


Model Averaged
1.00
0.75
0.50
0.25
p(y = 1)
500
400
300
200
100
0
Rescaled Density
0
0.061
0.16
0.26
0.35
dose

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