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

Annex E3 Benchmark dose modelling reports

Relative increase of the background incidence after adjustment for confounders by 10%[1]

Annex E3 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) and used in the uncertainty analysis.

E3.1 Selection of the BMR

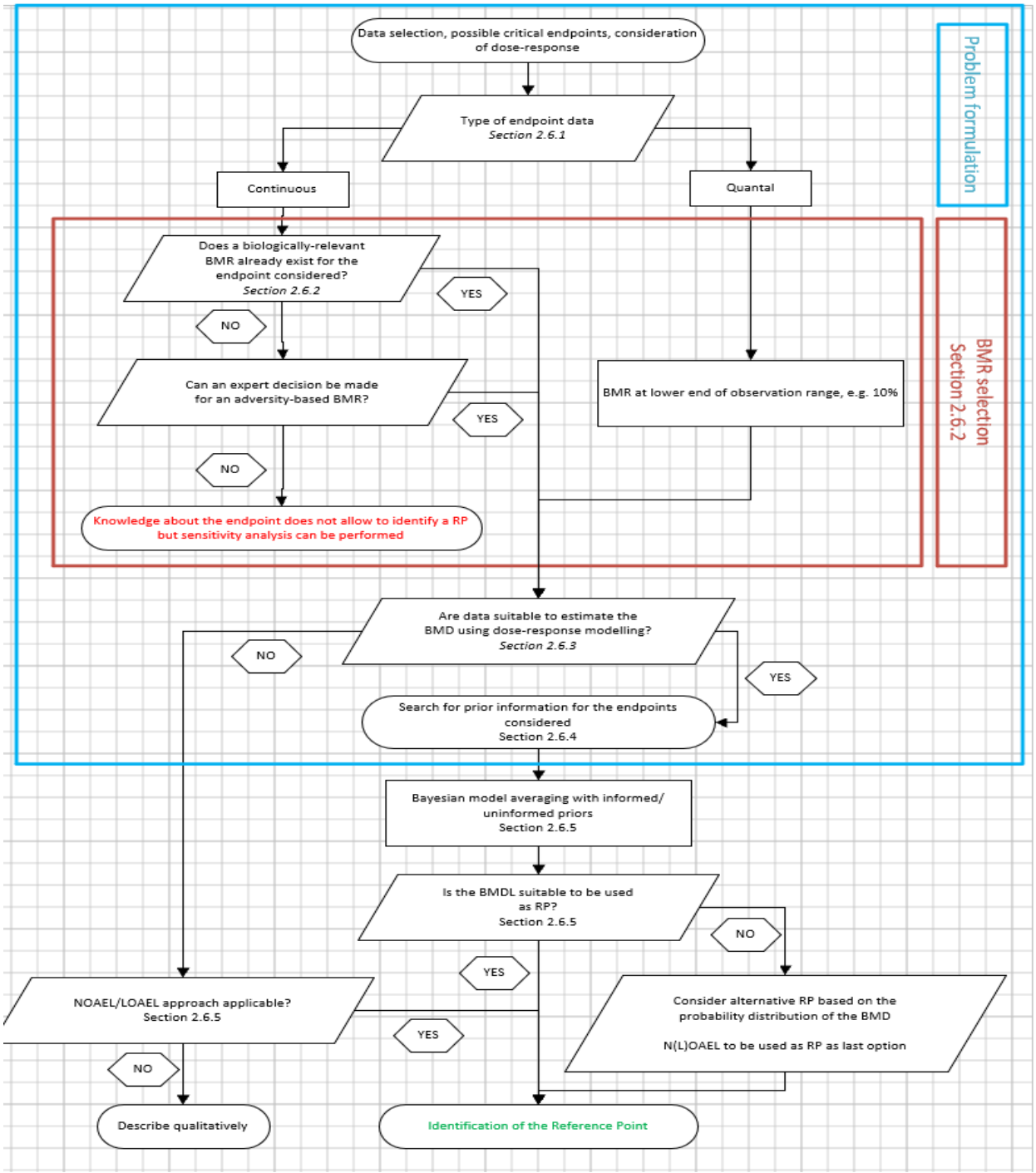
The BMD is identified as the specific dose that corresponds to the desired BMR level. To assess the uncertainty associated with the BMD, a 90% confidence interval is estimated, with the lower bound denoted as BMDL and the upper bound as BMDU. The BMDL and BMDU values help to quantify the range within 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 10%[1].

E3.2 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 (Vahter et al., 2020), an extra risk of 10% 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).

E3.3 BMD modelling reports

Ahsan et al. (2006) skin lesions, relative BMR 10%

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 0.00230978.

Extended dose range is applied.

Informative background prior: min: 0.02235060; the most likely: 0.02257636; max: 0.02280212. 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 2.41e-03).

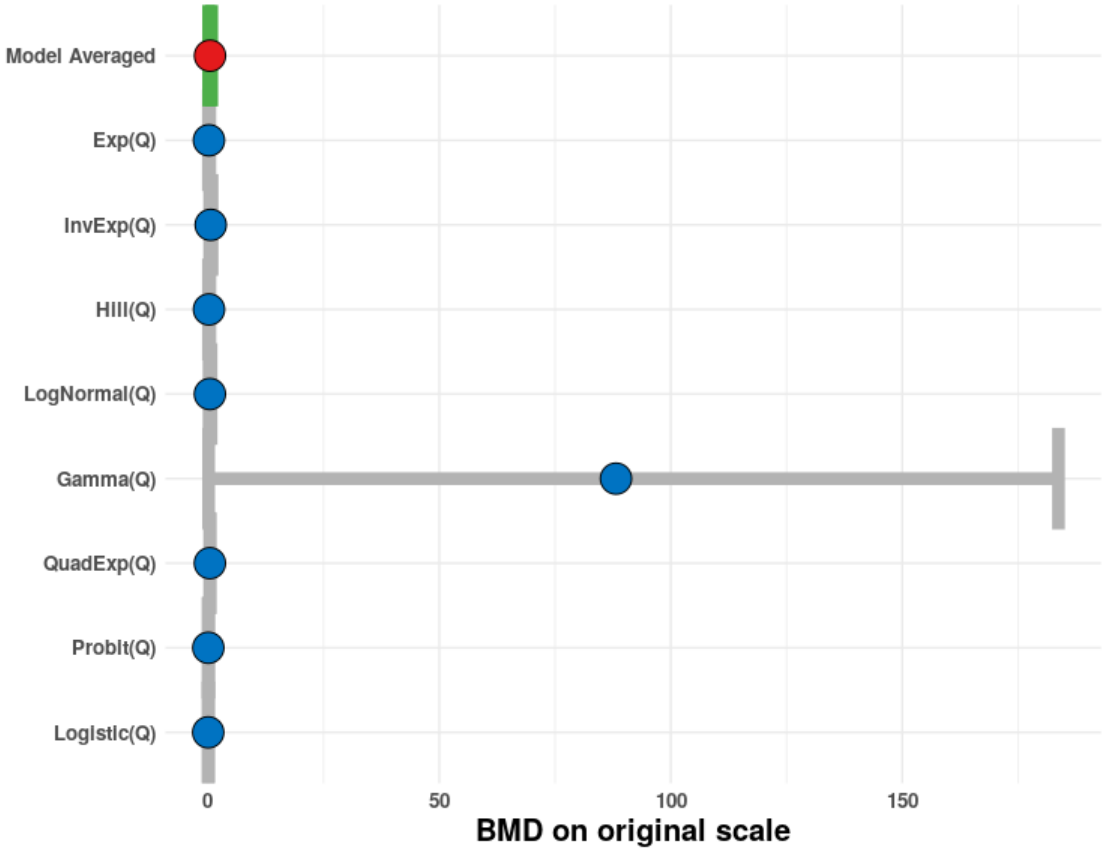
Model Averaged BMD

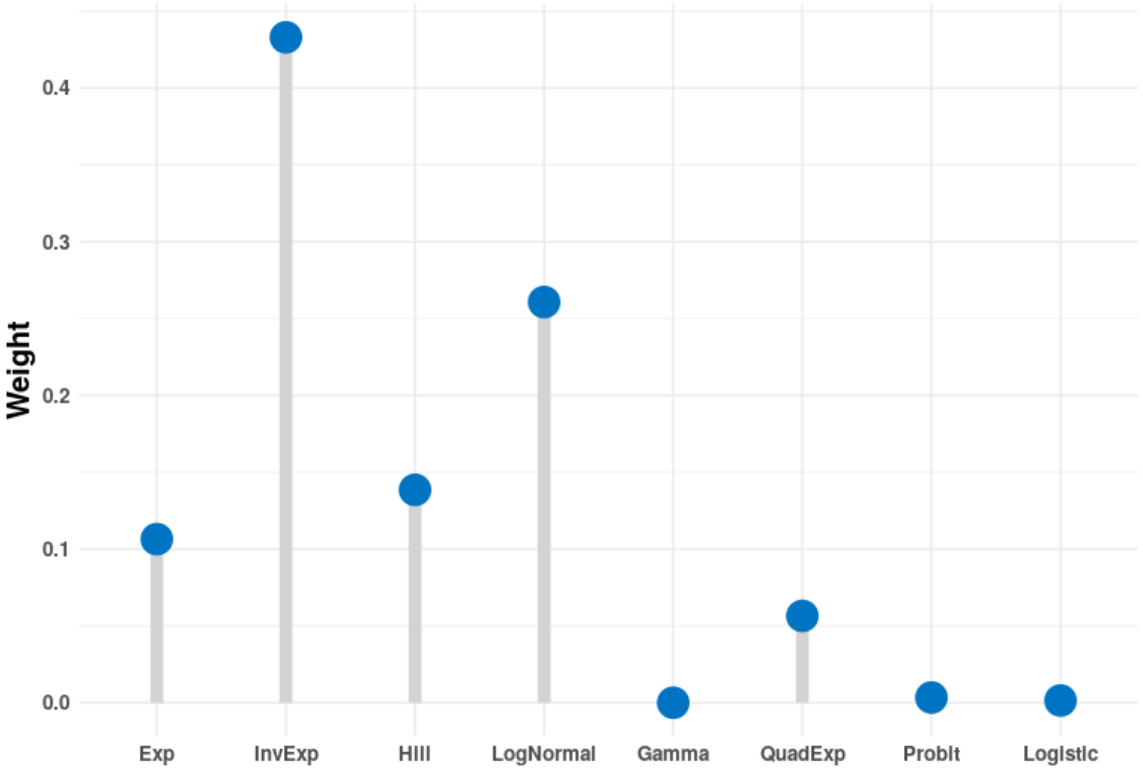
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.175	0.464	0.82

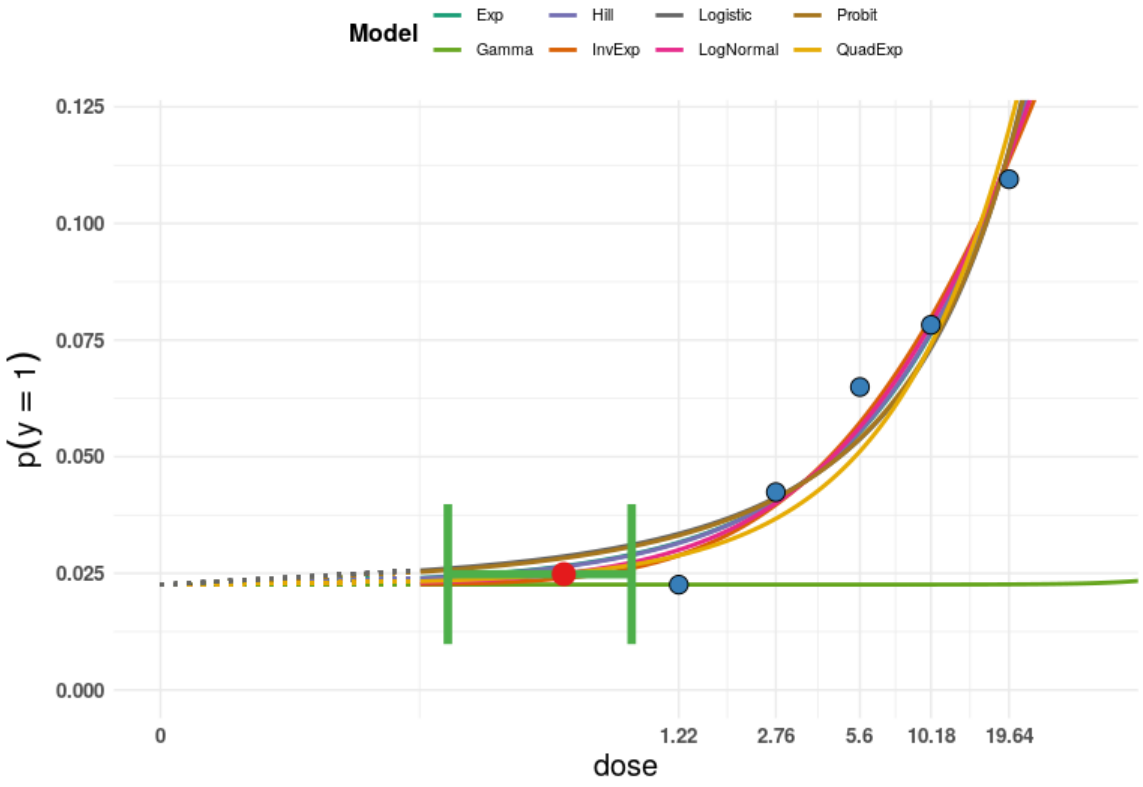
Estimated BMDs per model

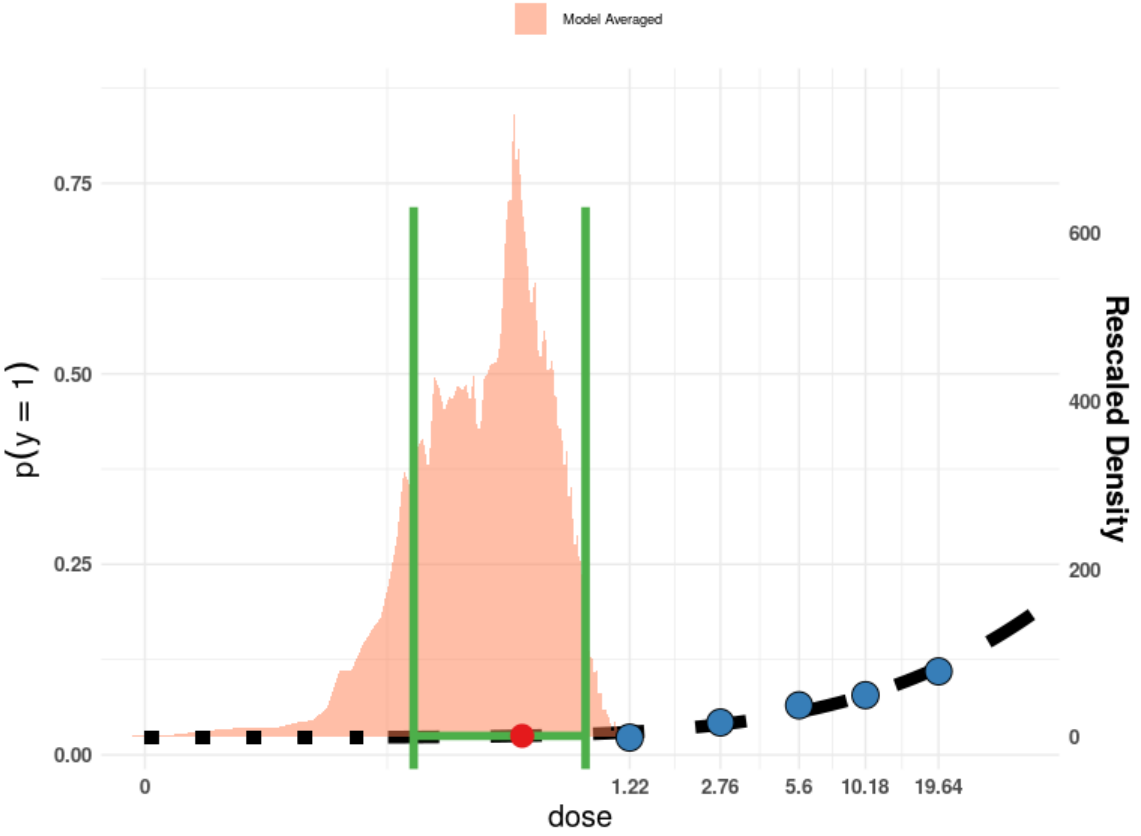
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.123	0.238	0.410	0.106	1
IE4_Q	0.391	0.618	0.904	0.433	1
H4_Q	0.133	0.250	0.429	0.139	1
LN4_Q	0.261	0.441	0.686	0.261	1
G4_Q	0.161	88.169	183.752	0.000	0
QE4_Q	0.396	0.438	0.493	0.056	1
P4_Q	0.043	0.100	0.196	0.003	1
L4_Q	0.031	0.080	0.163	0.001	1

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)
0.125
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)
0.75
0.50
0.25
0.00
Rescaled Density
600
400
200
0
0
1.22
2.76
5.6
10.18
19.64
dose

Chen et al. (2010a) lung cancer, relative BMR 10%

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 0.00214286.

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 2.89e-04).

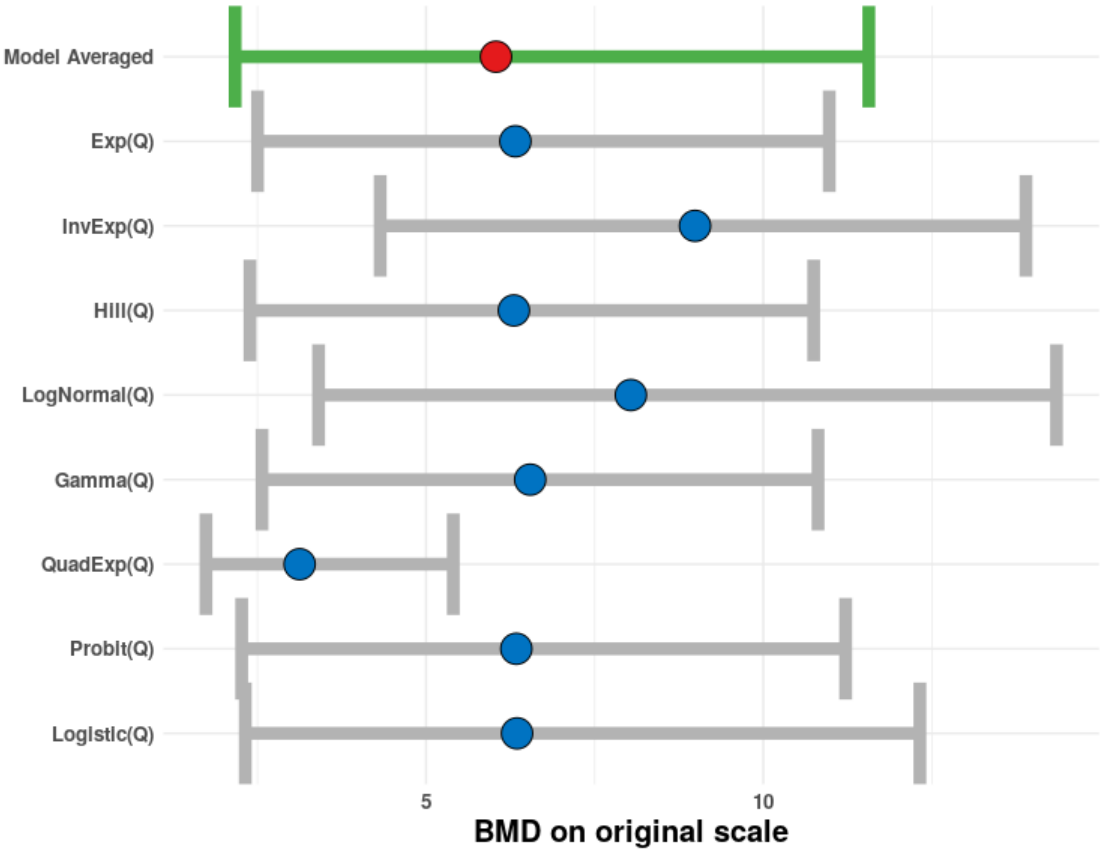
Model Averaged BMD

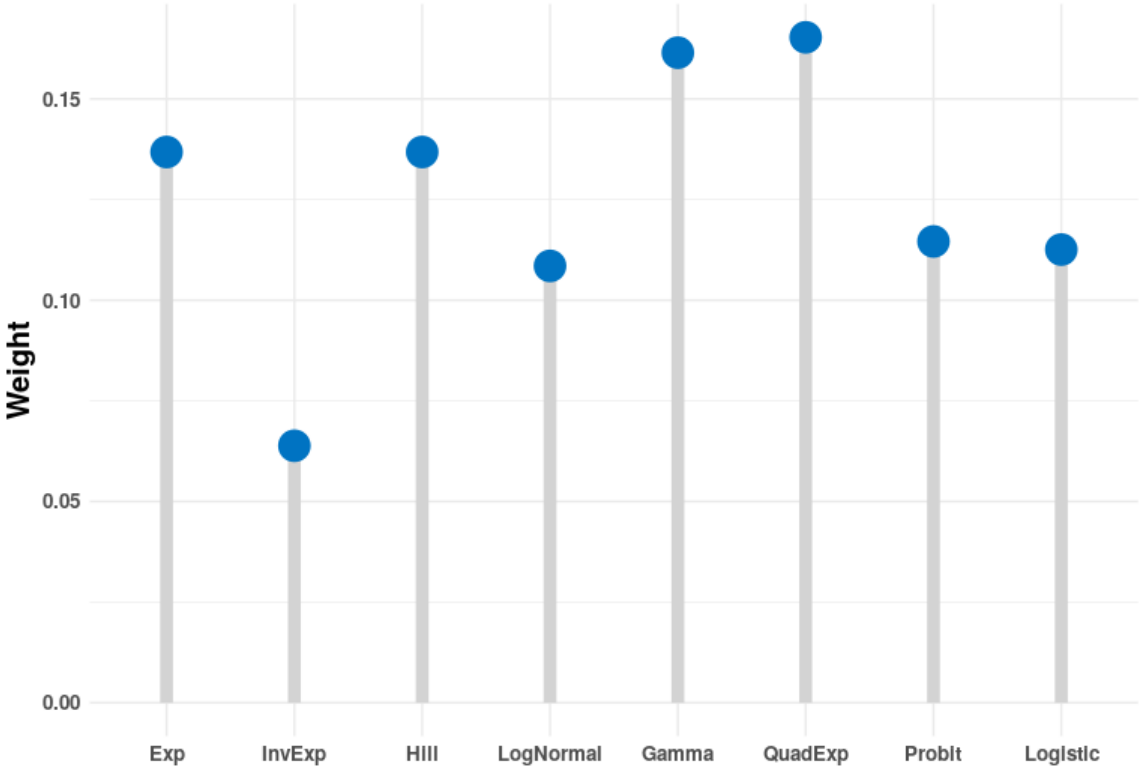
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	2.17	6.037	11.564

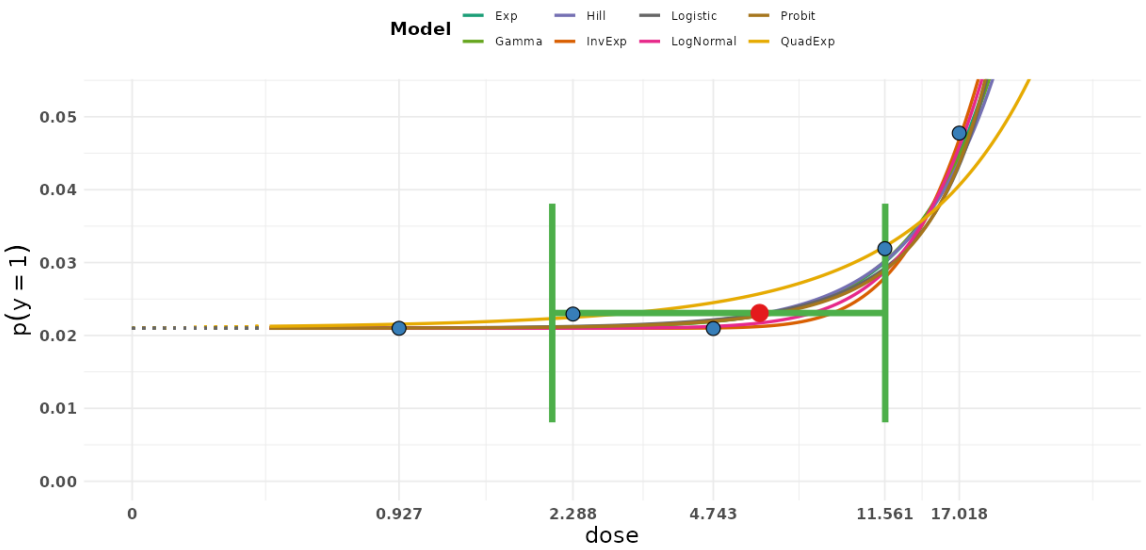
Estimated BMDs per model

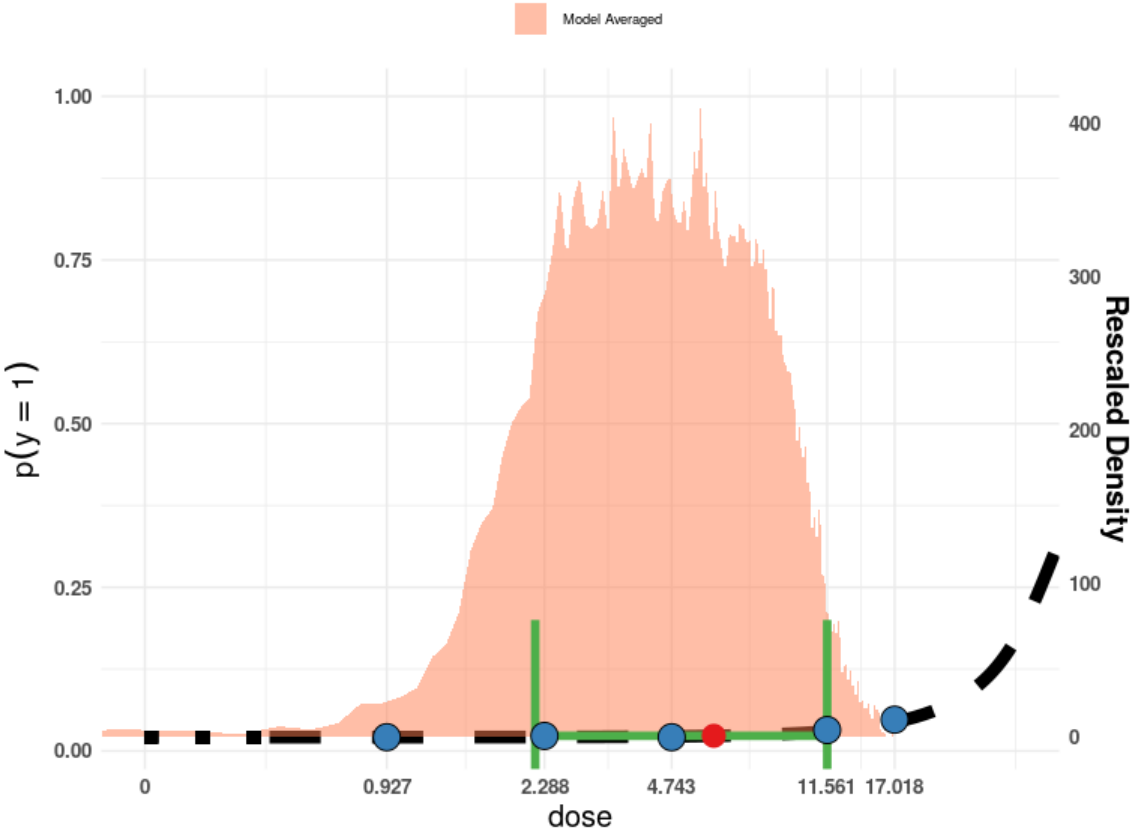
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	2.502	6.325	10.978	0.137	1
IE4_Q	4.321	8.988	13.894	0.064	1
H4_Q	2.389	6.302	10.747	0.137	1
LN4_Q	3.407	8.036	14.347	0.109	1
G4_Q	2.568	6.544	10.812	0.161	1
QE4_Q	1.738	3.126	5.404	0.165	1
P4_Q	2.267	6.338	11.221	0.115	1
L4_Q	2.320	6.349	12.321	0.113	1

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)
0.05
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 10%

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 0.00013129.

Extended dose range is not applied.

Informative background prior: min: 0.00104895; the most likely: 0.00131119; max: 0.00157343. 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 1.62e-04).

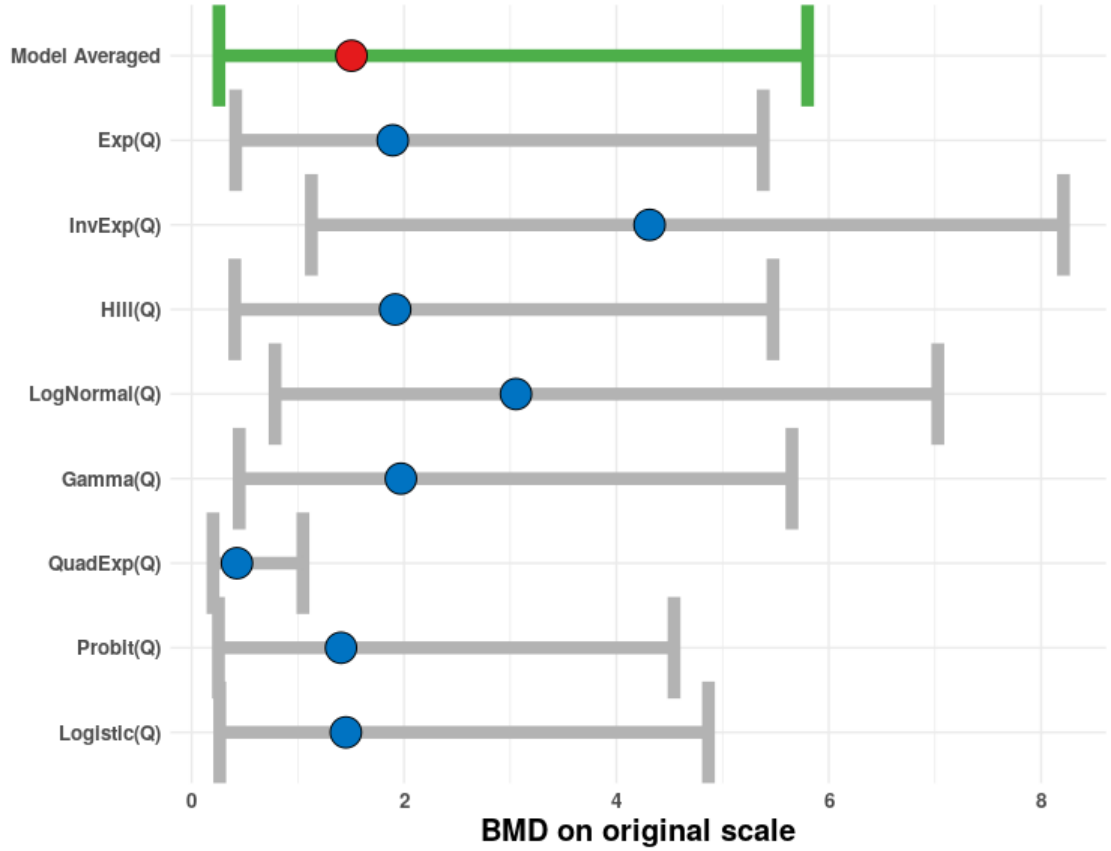
Model Averaged BMD

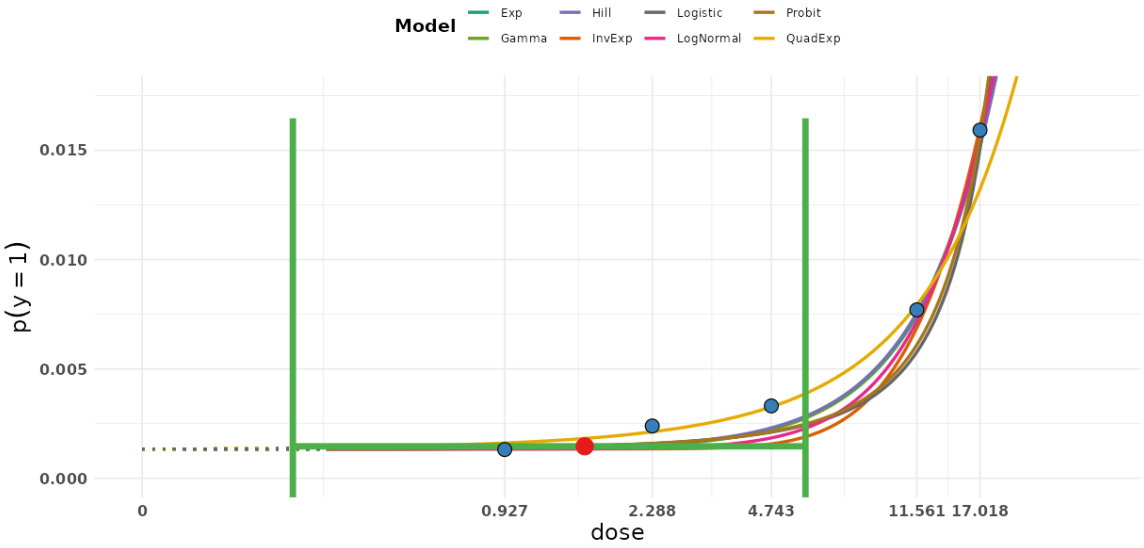
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.257	1.505	5.801

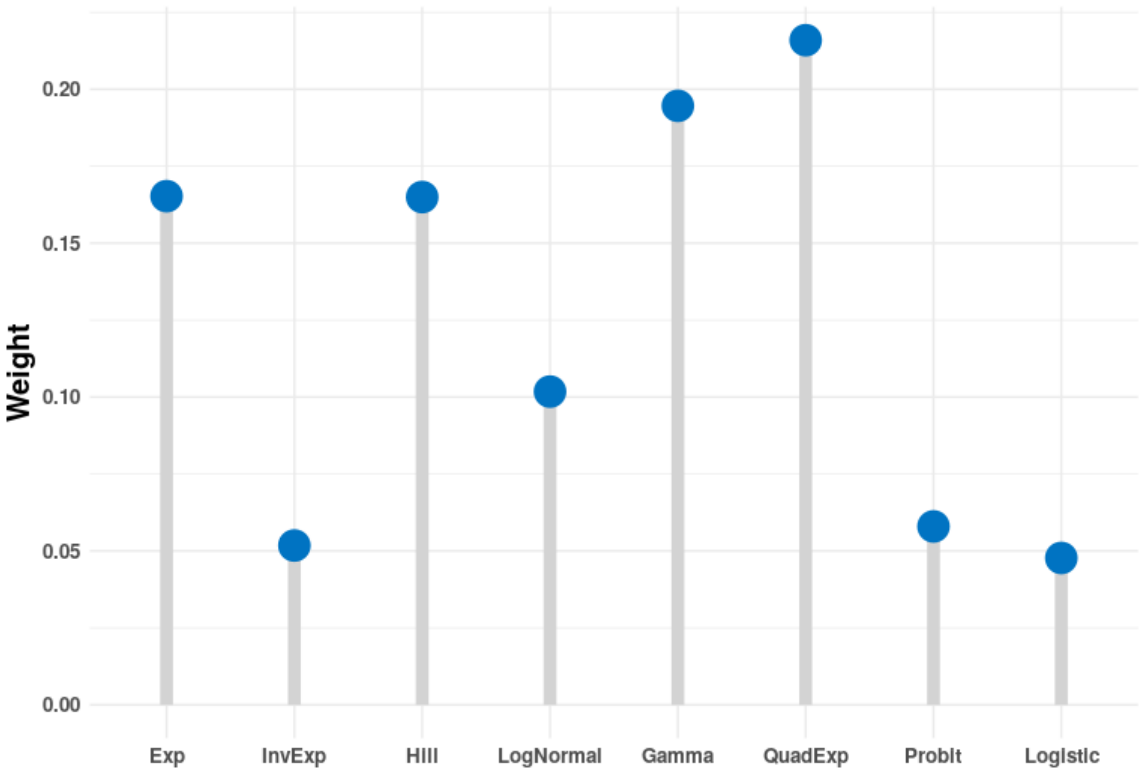
Estimated BMDs per model

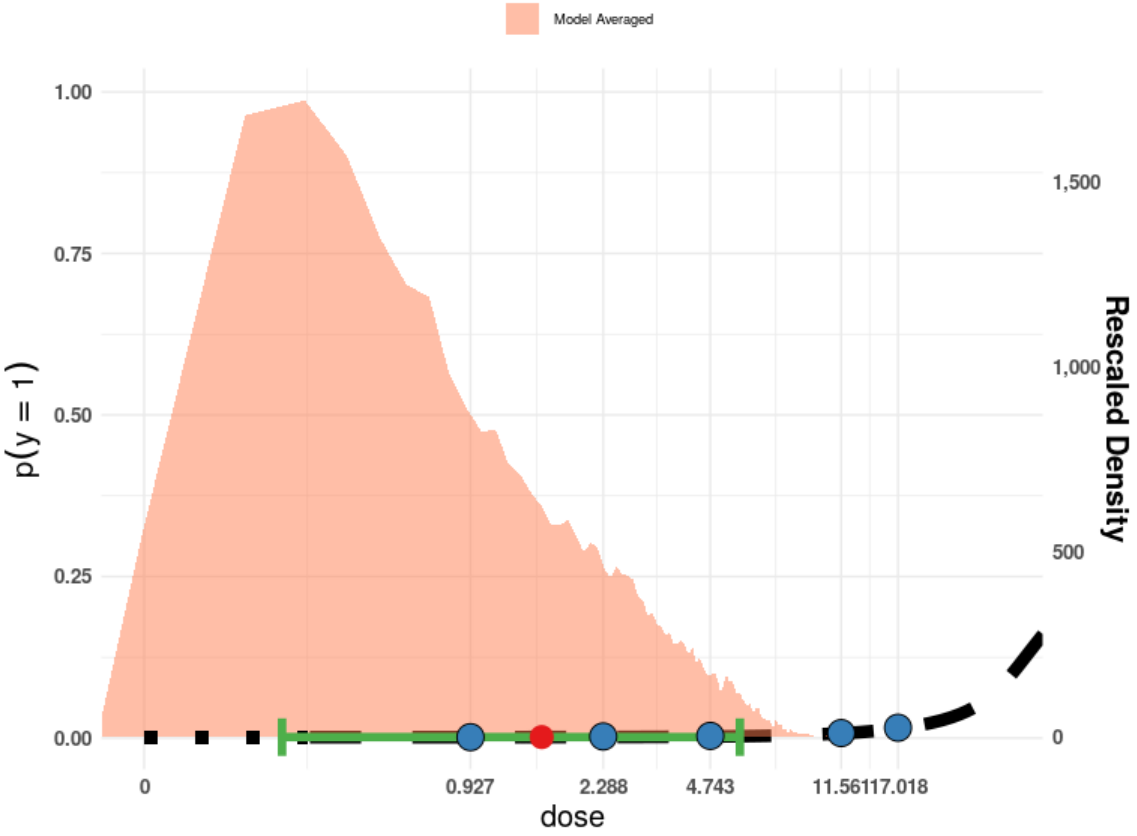
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.415	1.894	5.383	0.165	1
IE4_Q	1.128	4.312	8.211	0.052	1
H4_Q	0.406	1.917	5.475	0.165	1
LN4_Q	0.785	3.055	7.027	0.102	1
G4_Q	0.448	1.971	5.654	0.195	1
QE4_Q	0.201	0.427	1.048	0.216	1
P4_Q	0.253	1.407	4.543	0.058	1
L4_Q	0.264	1.453	4.867	0.048	1

Plots of Fitted Models






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


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

Cherry et al. (2008) stillbirth, relative BMR 10%

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 0.00300587.

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 1.11e+00).

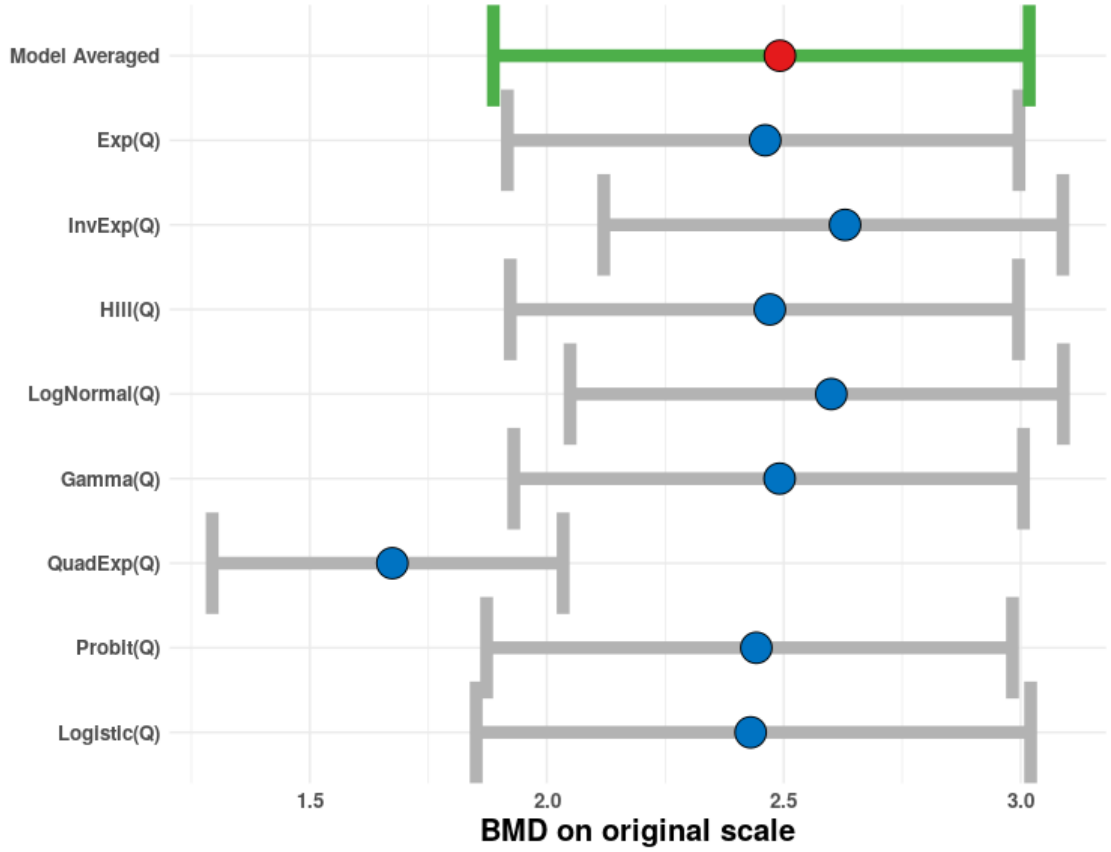
Model Averaged BMD

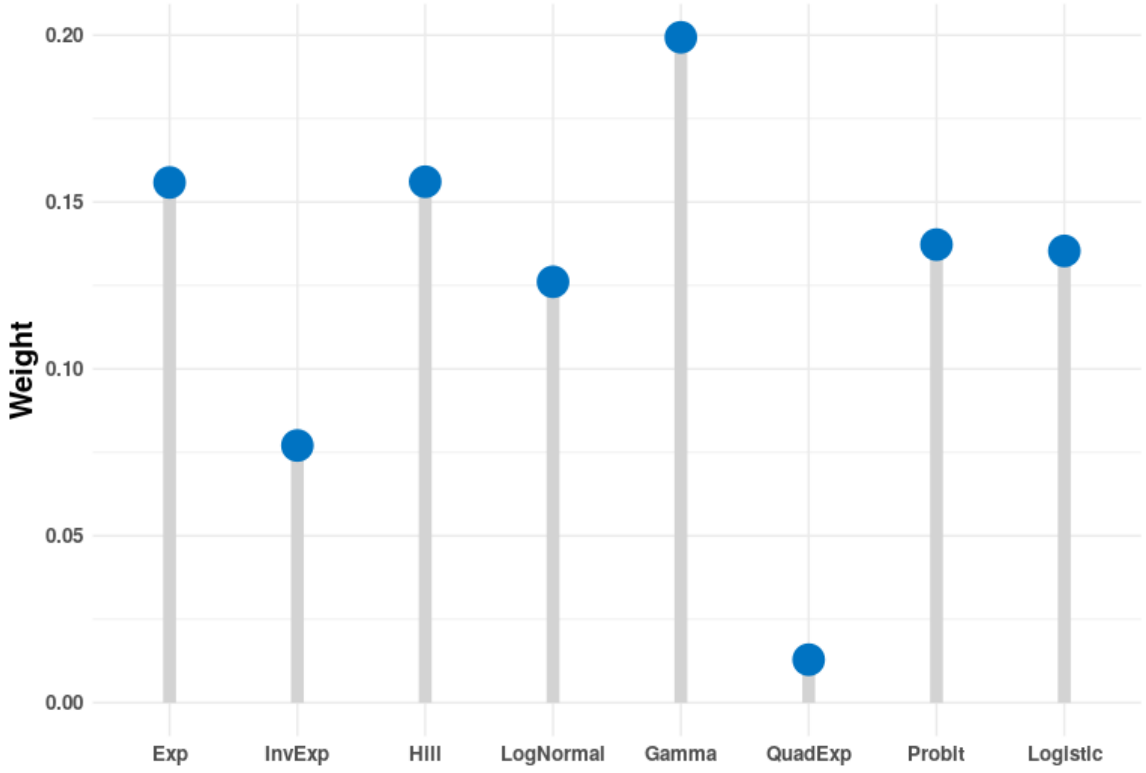
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	1.887	2.492	3.018

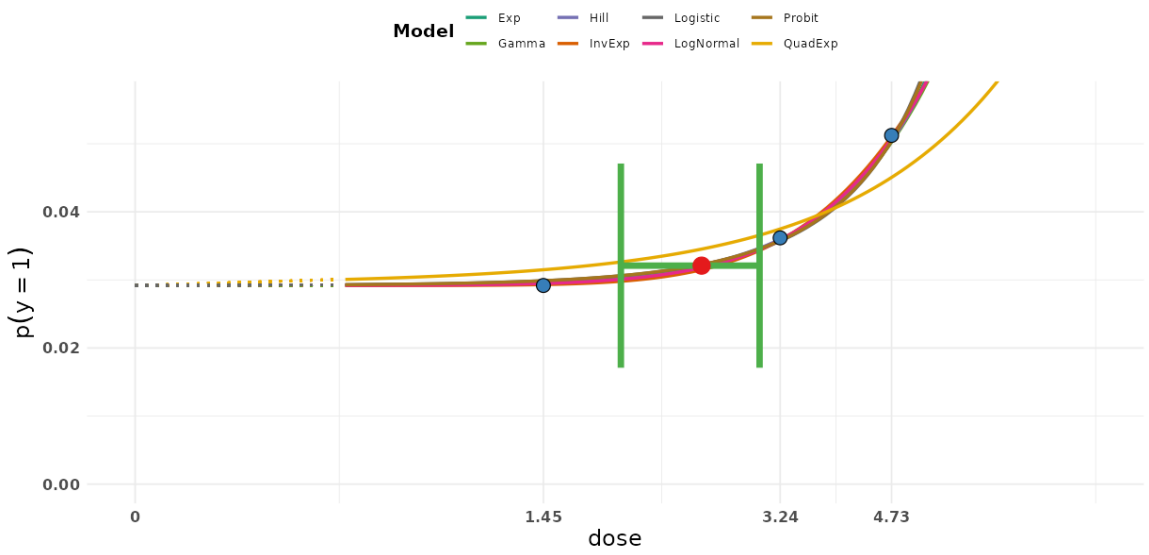
Estimated BMDs per model

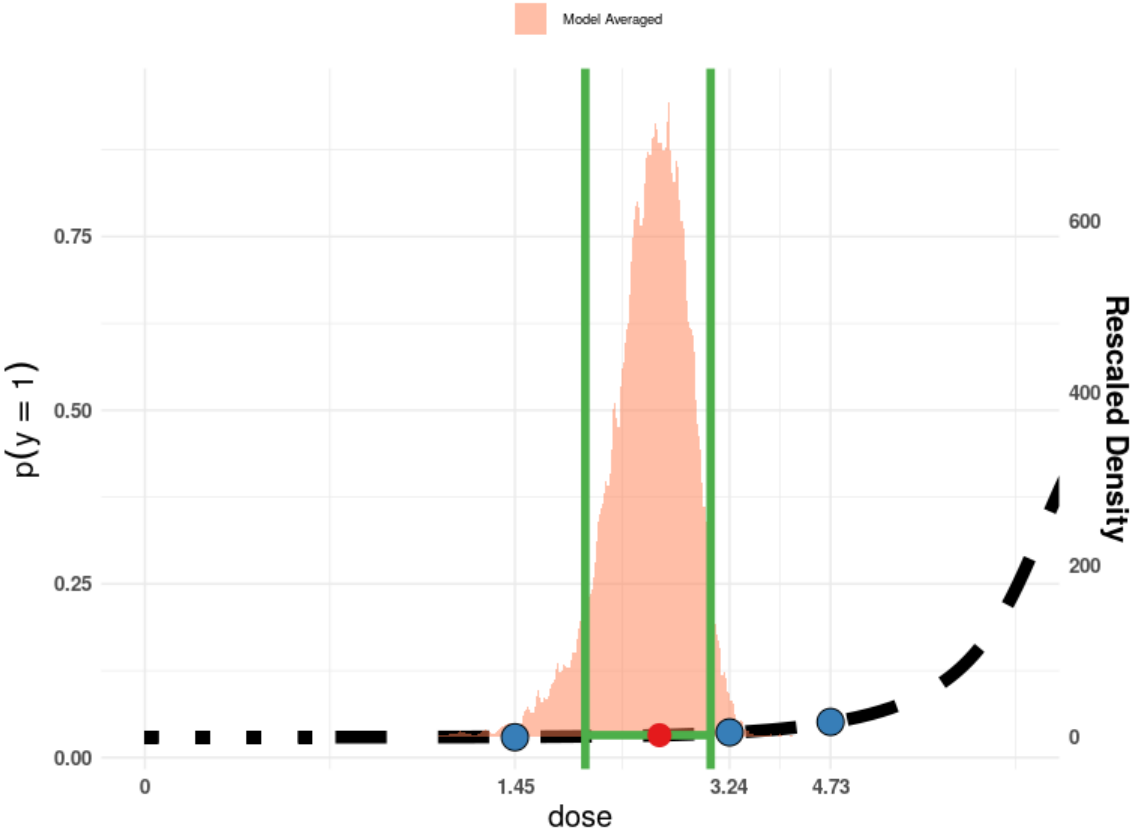
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	1.917	2.461	2.996	0.156	1
IE4_Q	2.120	2.629	3.089	0.077	1
H4_Q	1.923	2.471	2.995	0.156	1
LN4_Q	2.049	2.600	3.090	0.126	1
G4_Q	1.930	2.491	3.006	0.199	1
QE4_Q	1.294	1.674	2.035	0.013	1
P4_Q	1.873	2.442	2.983	0.137	1
L4_Q	1.851	2.430	3.021	0.135	1

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 10%

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 0.00003647.

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 2.04e+00).

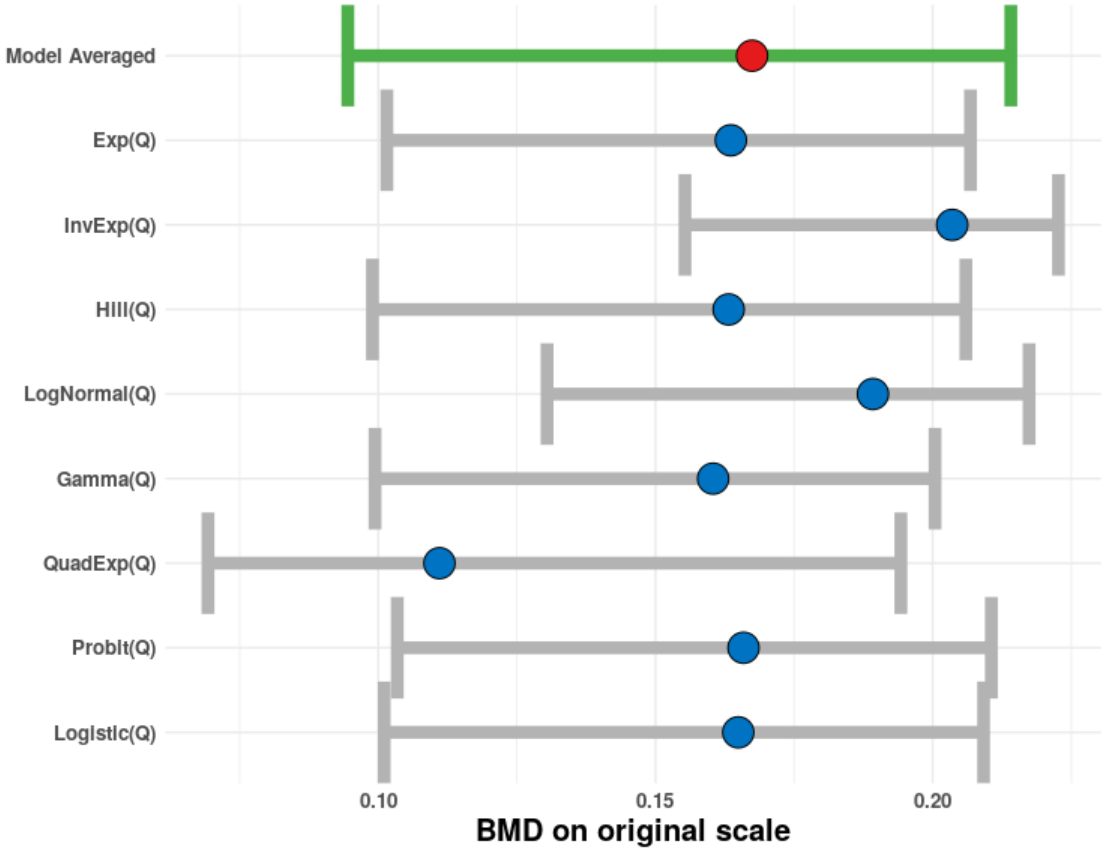
Model Averaged BMD

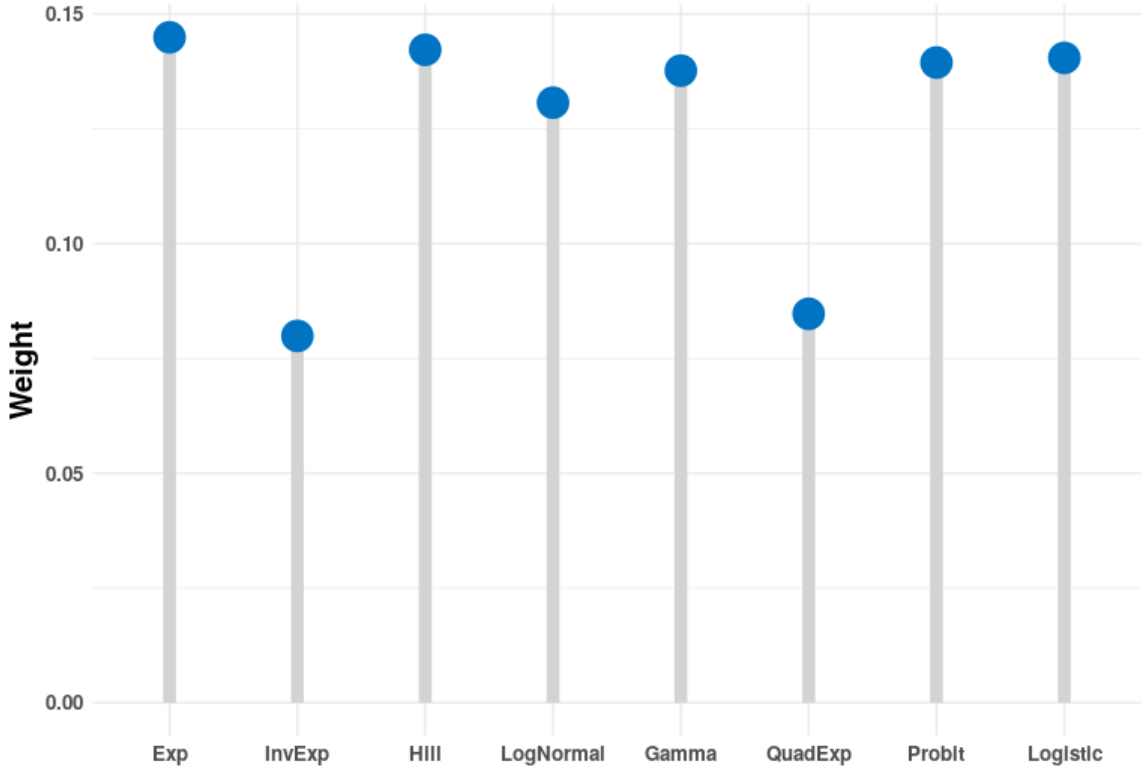
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.095	0.167	0.214

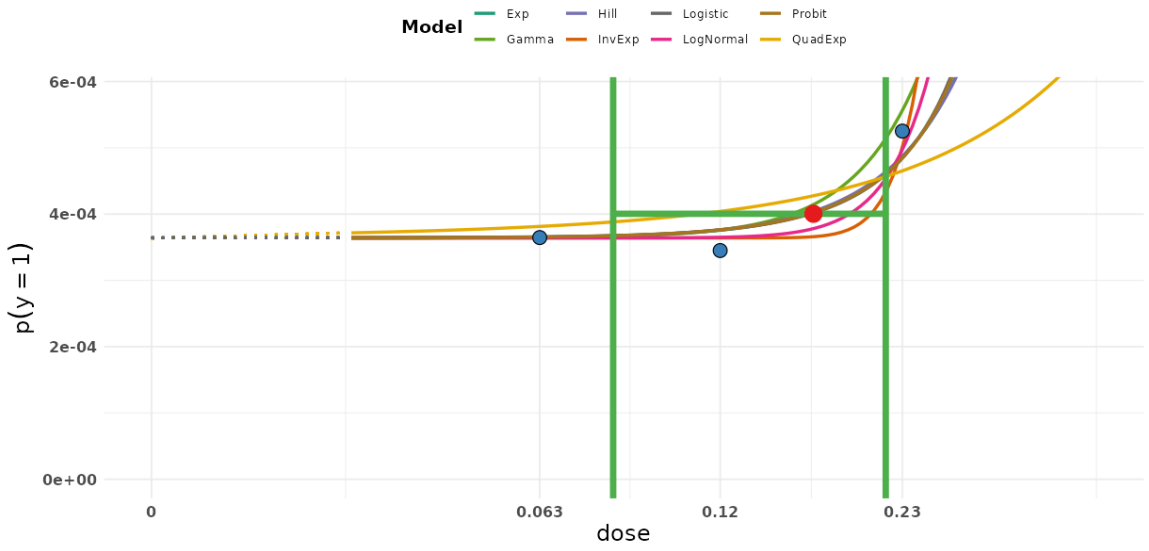
Estimated BMDs per model

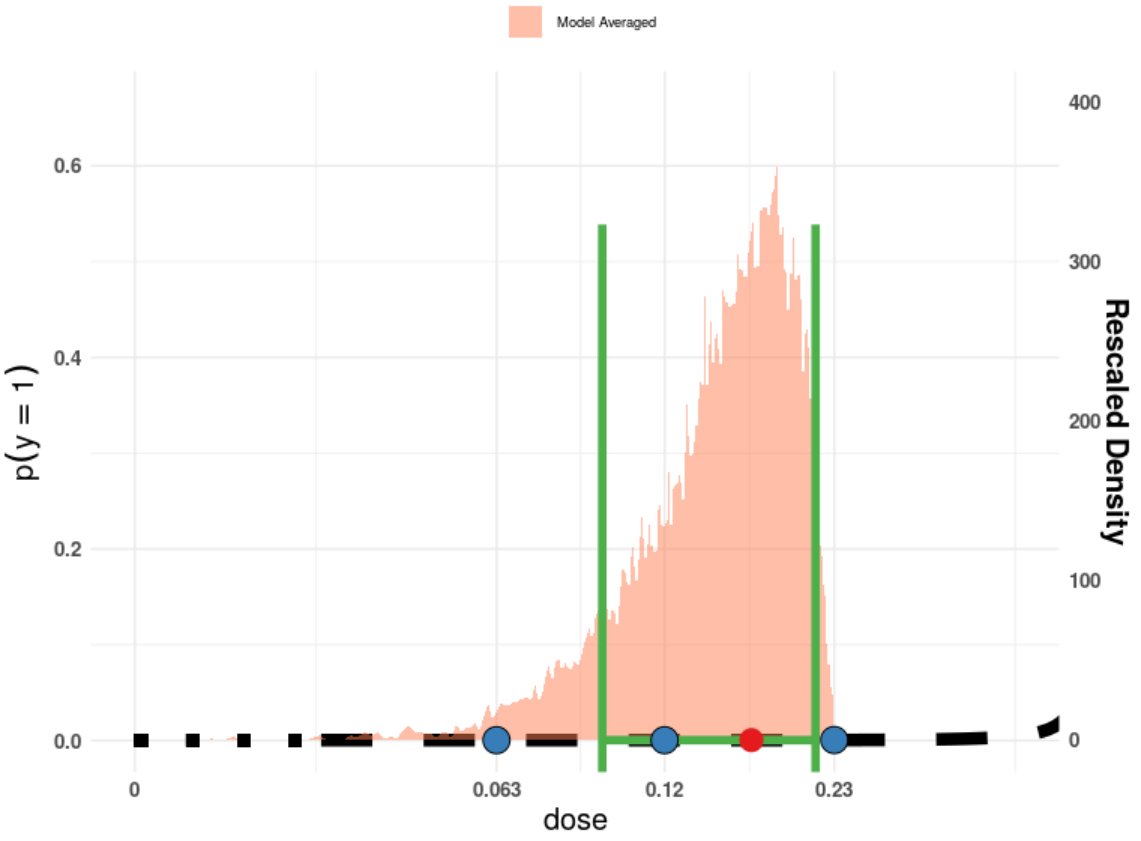
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.102	0.164	0.207	0.145	1
IE4_Q	0.155	0.204	0.223	0.080	1
H4_Q	0.099	0.163	0.206	0.142	1
LN4_Q	0.130	0.189	0.217	0.131	1
G4_Q	0.099	0.160	0.200	0.138	1
QE4_Q	0.069	0.111	0.194	0.085	1
P4_Q	0.103	0.166	0.211	0.139	1
L4_Q	0.101	0.165	0.209	0.140	1

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
p(y = 1)
0.6
0.4
0.2
0.0
400
300
200
100
0
Rescaled Density
0
0.063
0.12
0.23
dose

Hsueh et al. (2009) chronic kidney disease, relative BMR 10%

Data Description

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

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 2.75e-06.

Extended dose range is not applied.

Informative background prior: min: 0.00002721; the most likely: 0.00002748; max: 0.00002775.

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 4.66e-01).

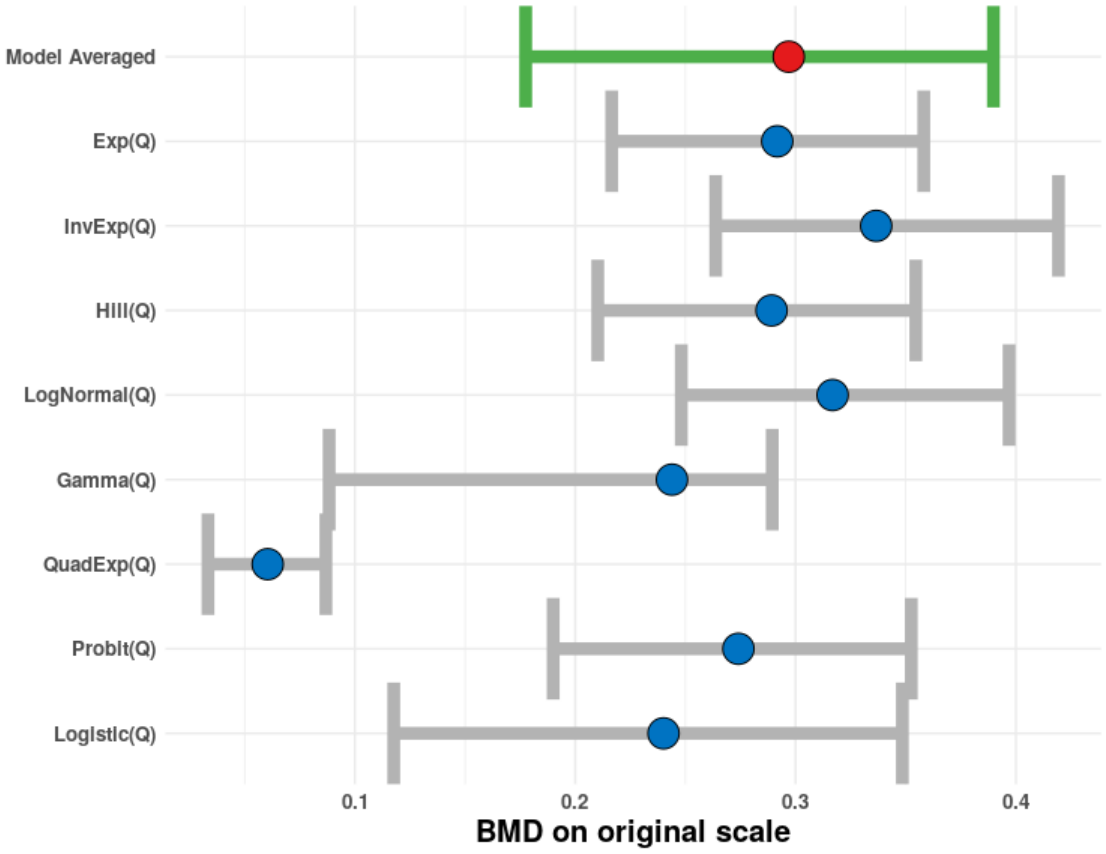
Model Averaged BMD

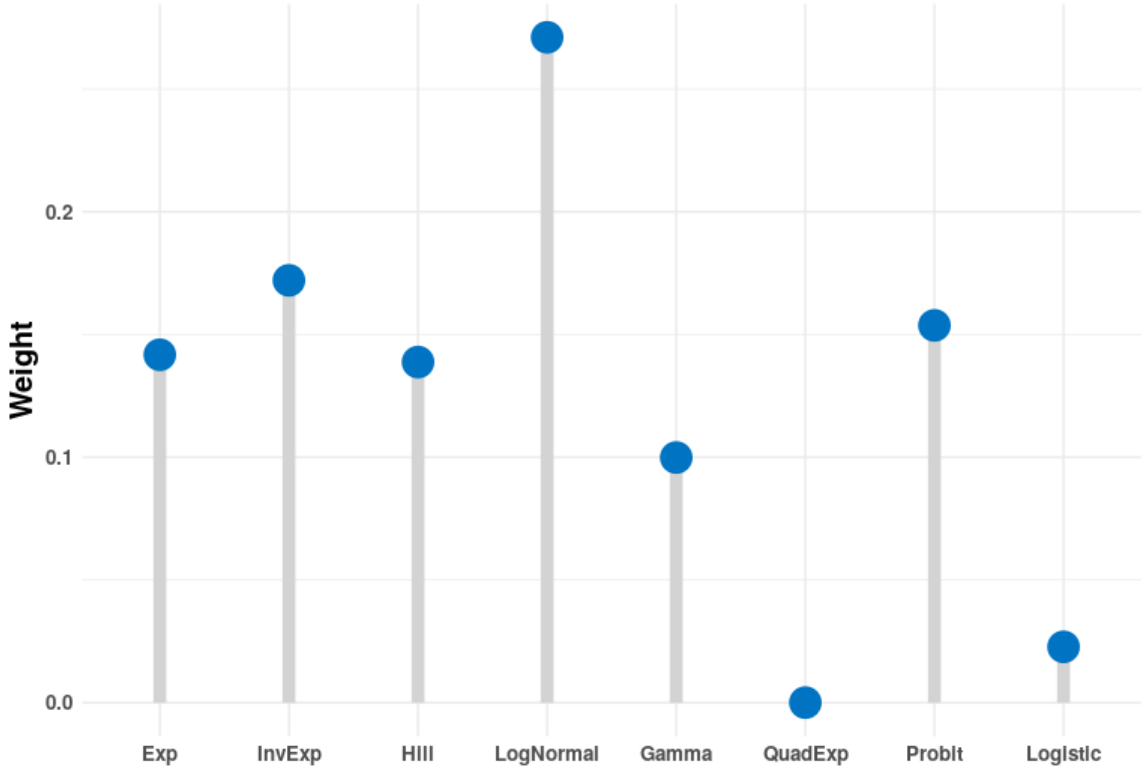
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.178	0.297	0.39

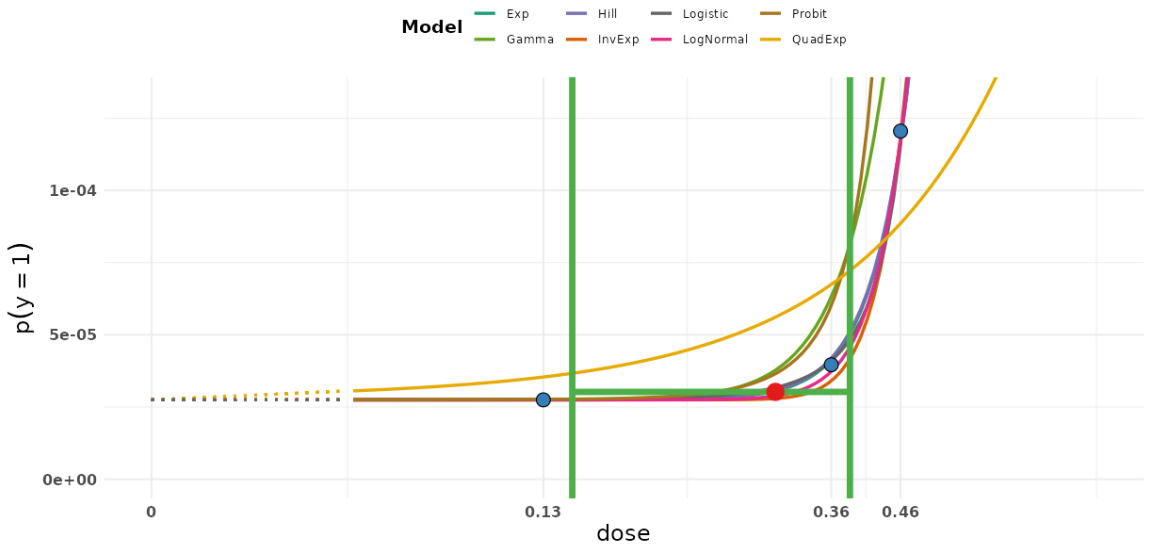
Estimated BMDs per model

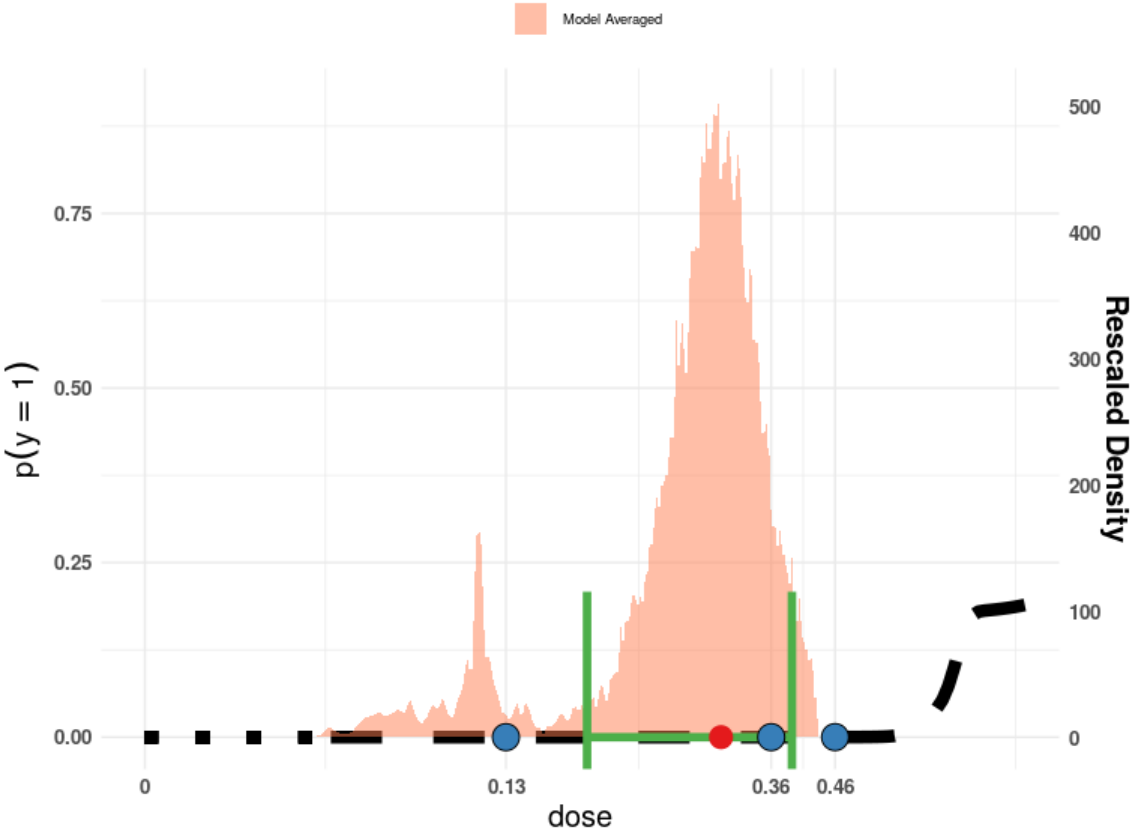
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.217	0.292	0.358	0.142	1
IE4_Q	0.264	0.337	0.419	0.172	1
H4_Q	0.210	0.289	0.355	0.139	1
LN4_Q	0.248	0.317	0.397	0.271	1
G4_Q	0.088	0.244	0.289	0.100	0
QE4_Q	0.033	0.060	0.087	0.000	1
P4_Q	0.190	0.274	0.353	0.154	1
L4_Q	0.118	0.240	0.348	0.023	0

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)
1e-04
5e-05
0e+00
0
0.13
0.36
0.46
dose


Model Averaged
p(y = 1)
0.75
0.50
0.25
0.00
0
0.13
0.36
0.46
dose
500
400
300
200
100
0
Rescaled Density

James et al. (2015) ischemic heart disease, relative BMR 10%

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 0.00122157.

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 2.51e-02).

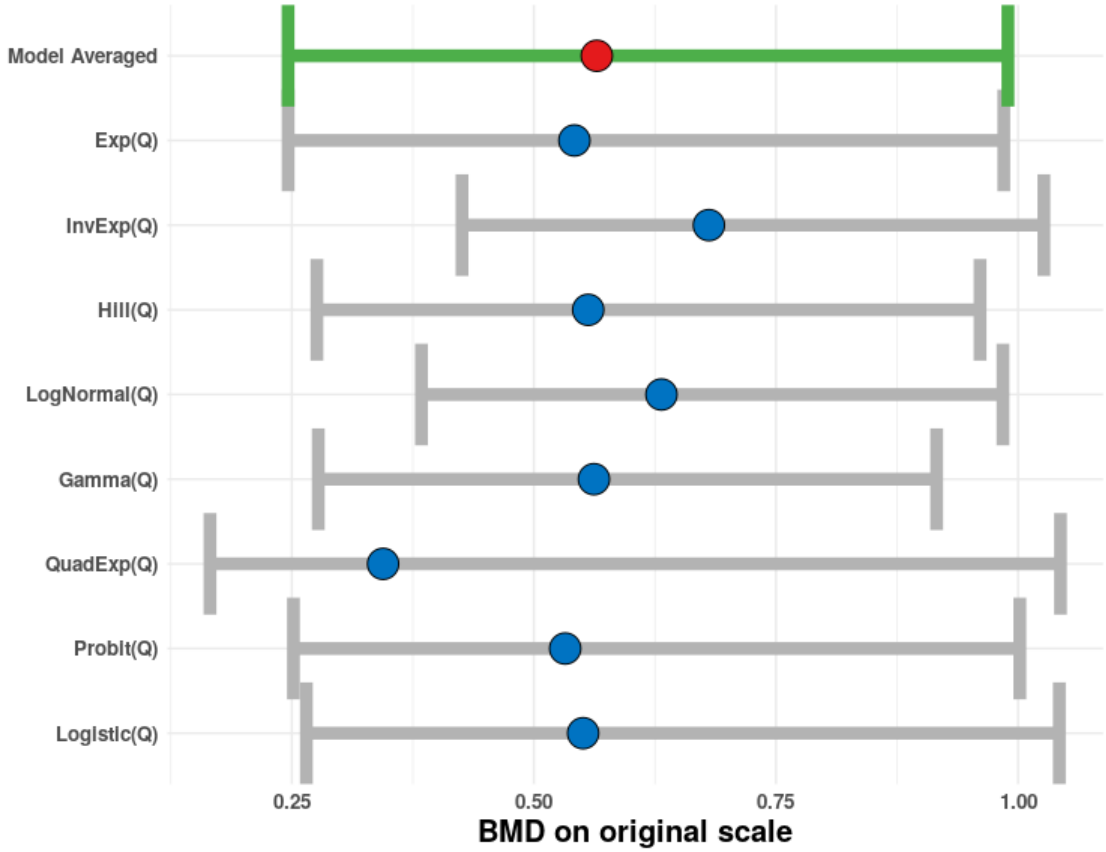
Model Averaged BMD

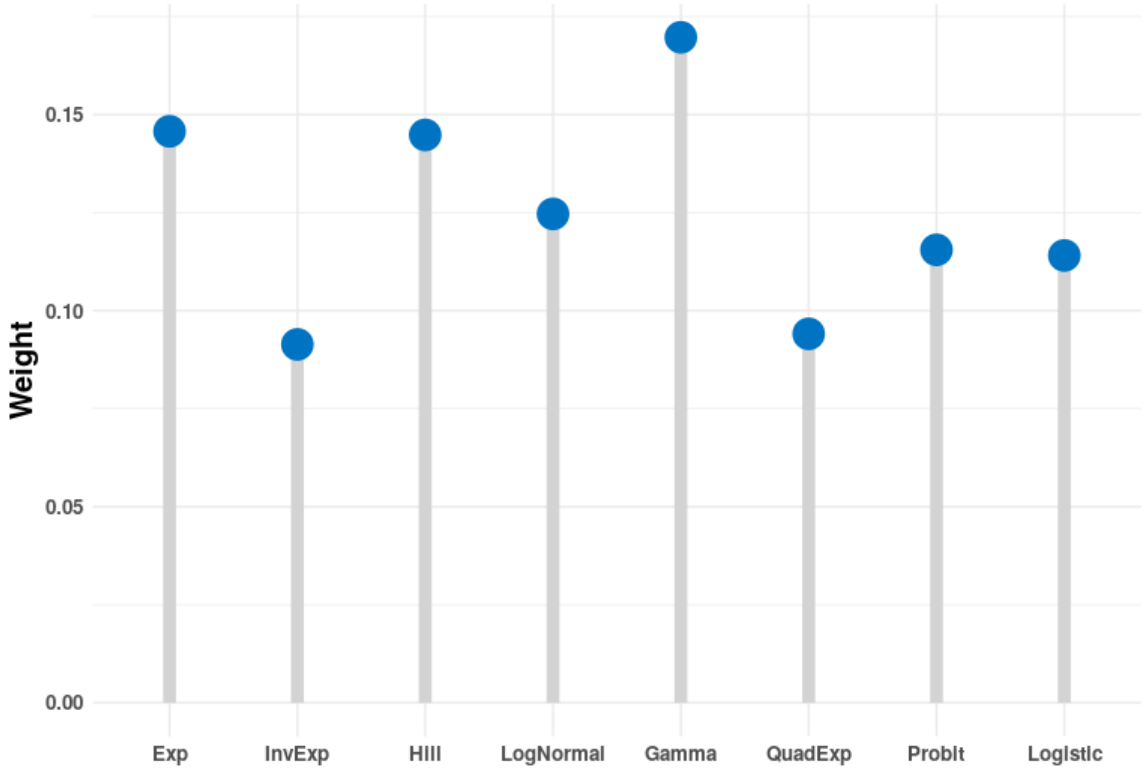
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.246	0.565	0.99

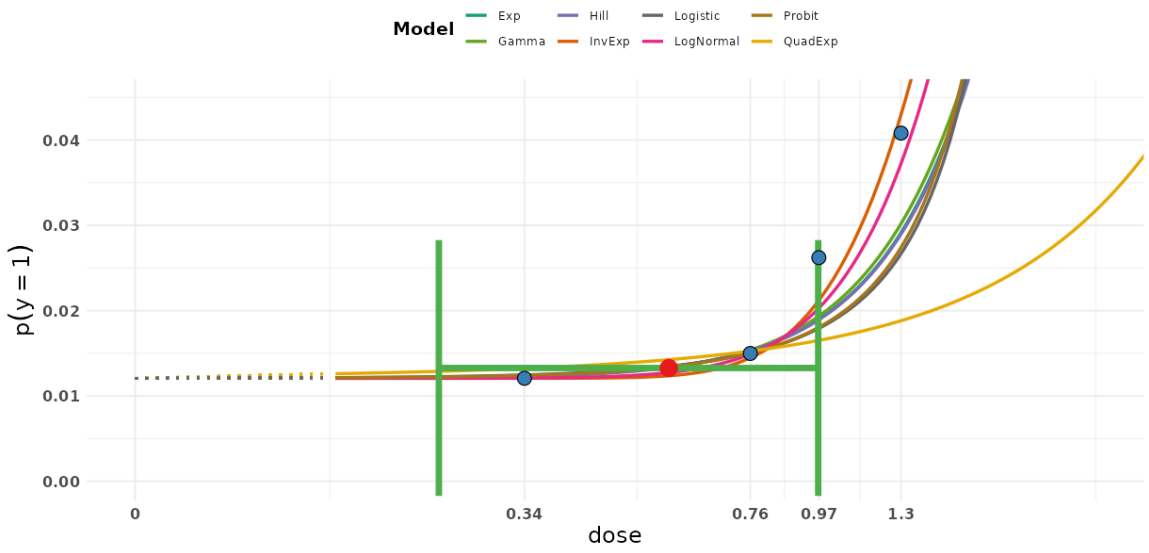
Estimated BMDs per model

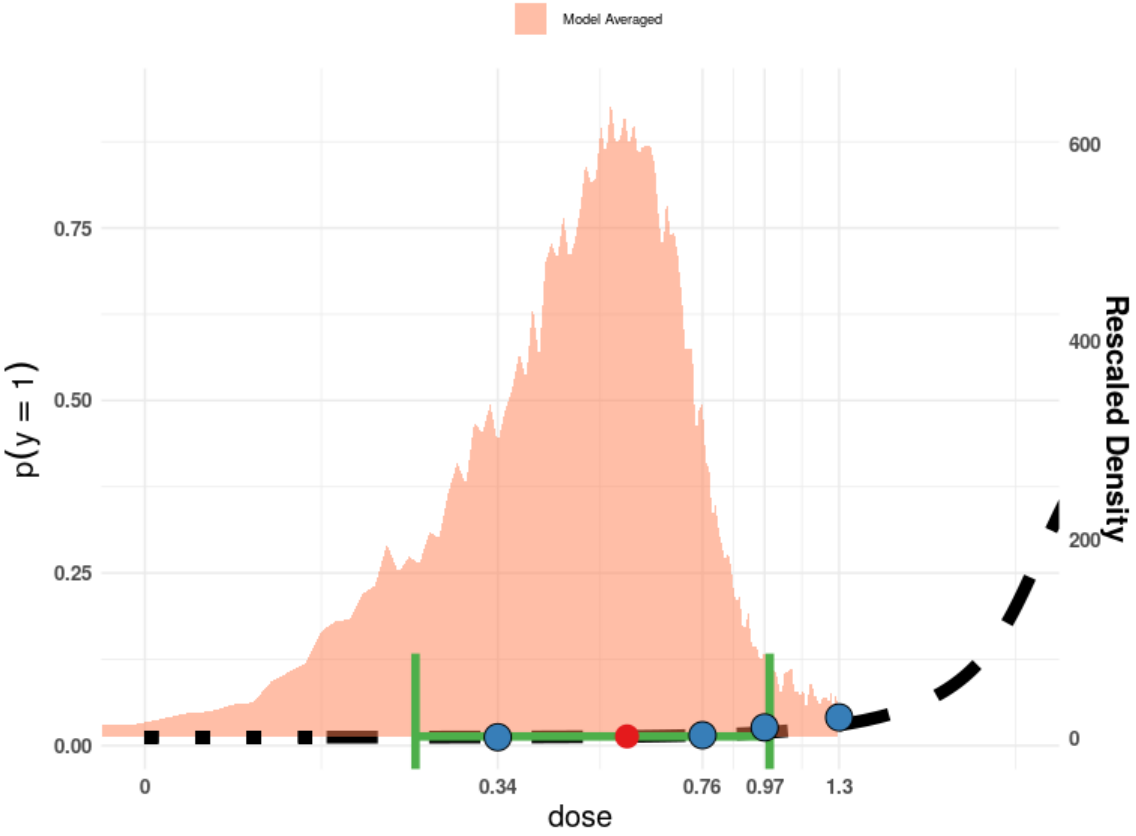
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.246	0.542	0.985	0.146	1
IE4_Q	0.426	0.681	1.027	0.091	1
H4_Q	0.276	0.556	0.961	0.145	1
LN4_Q	0.384	0.632	0.984	0.125	1
G4_Q	0.277	0.562	0.916	0.170	1
QE4_Q	0.165	0.344	1.044	0.094	1
P4_Q	0.252	0.532	1.002	0.116	1
L4_Q	0.265	0.551	1.043	0.114	1

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)
0.75
0.50
0.25
0.00
600
400
200
0
Rescaled Density
0
0.34
0.76
0.97
1.3
dose

Leonardi et al. (2012) skin cancer, relative BMR 10%

Data Description

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 1.475e-05

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 1.01e-05).

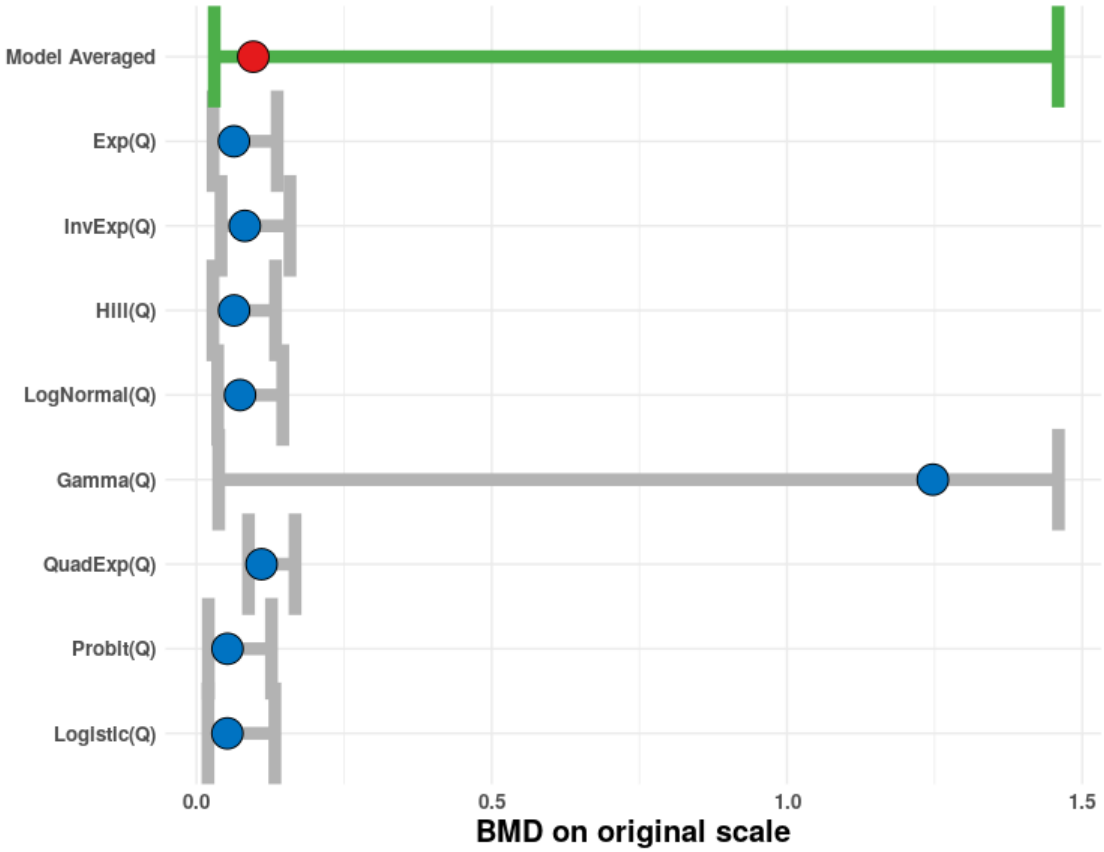
Model Averaged BMD

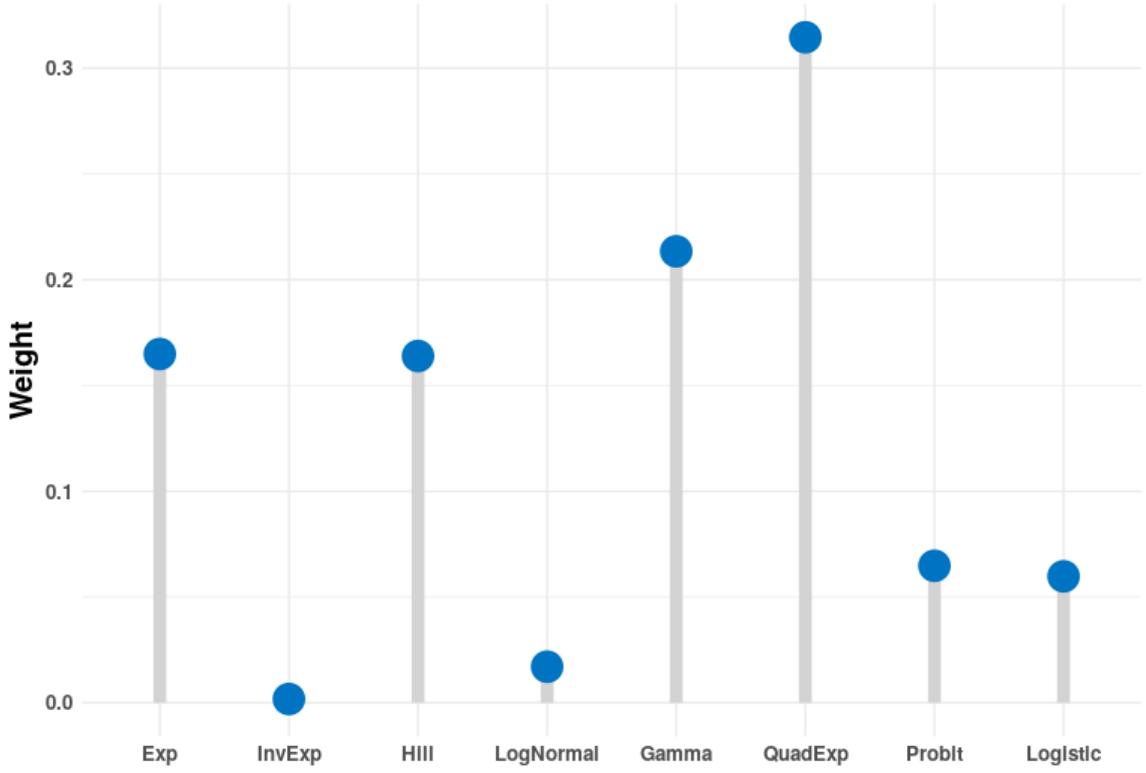
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.03	0.096	1.459

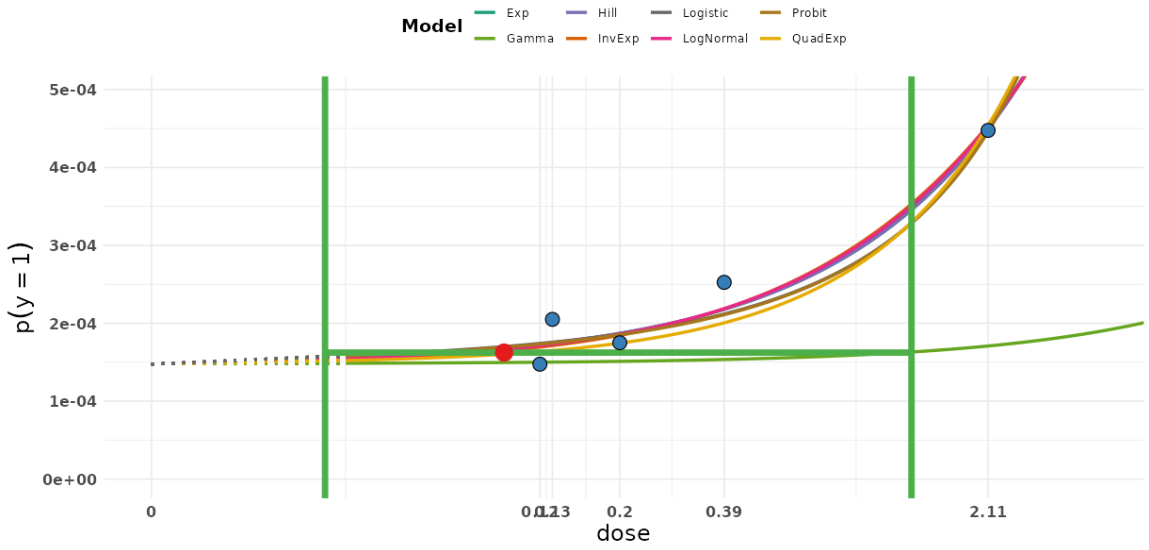
Estimated BMDs per model

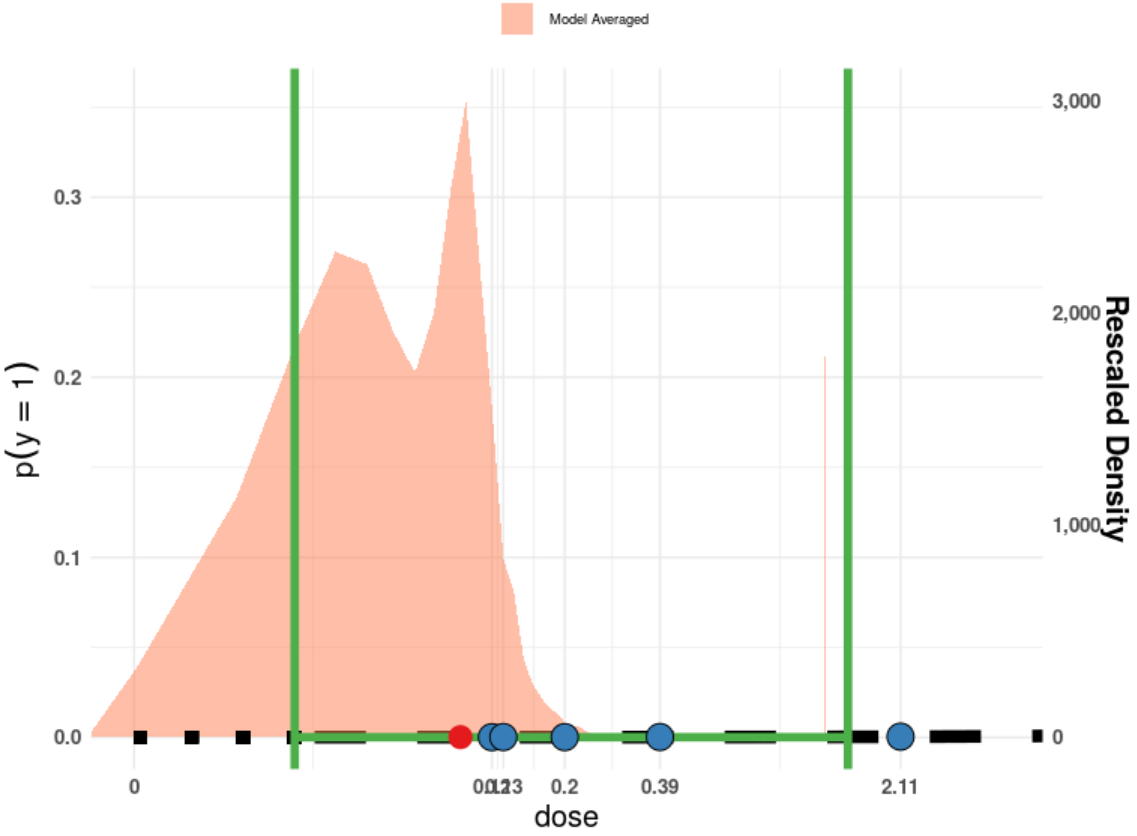
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.028	0.063	0.137	0.165	1
IE4_Q	0.042	0.082	0.158	0.002	1
H4_Q	0.028	0.064	0.134	0.164	1
LN4_Q	0.036	0.074	0.146	0.017	1
G4_Q	0.038	1.247	1.460	0.213	0
QE4_Q	0.088	0.110	0.167	0.315	1
P4_Q	0.020	0.052	0.127	0.065	1
L4_Q	0.019	0.052	0.133	0.060	1

Plots of Fitted Models




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


Model
Exp
Gamma
Hill
InvExp
Logistic
LogNormal
Probit
QuadExp
p(y = 1)
5e-04
4e-04
3e-04
2e-04
1e-04
0e+00
0
0.13
0.2
0.39
2.11
dose


Model Averaged
p(y = 1)
0.3
0.2
0.1
0.0
3,000
2,000
1,000
0
Rescaled Density
0
0.2
0.39
2.11
dose

Milton et al. (2005) spontaneous abortion, relative BMR 10%

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 0.01069182.

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 1.59e+00).

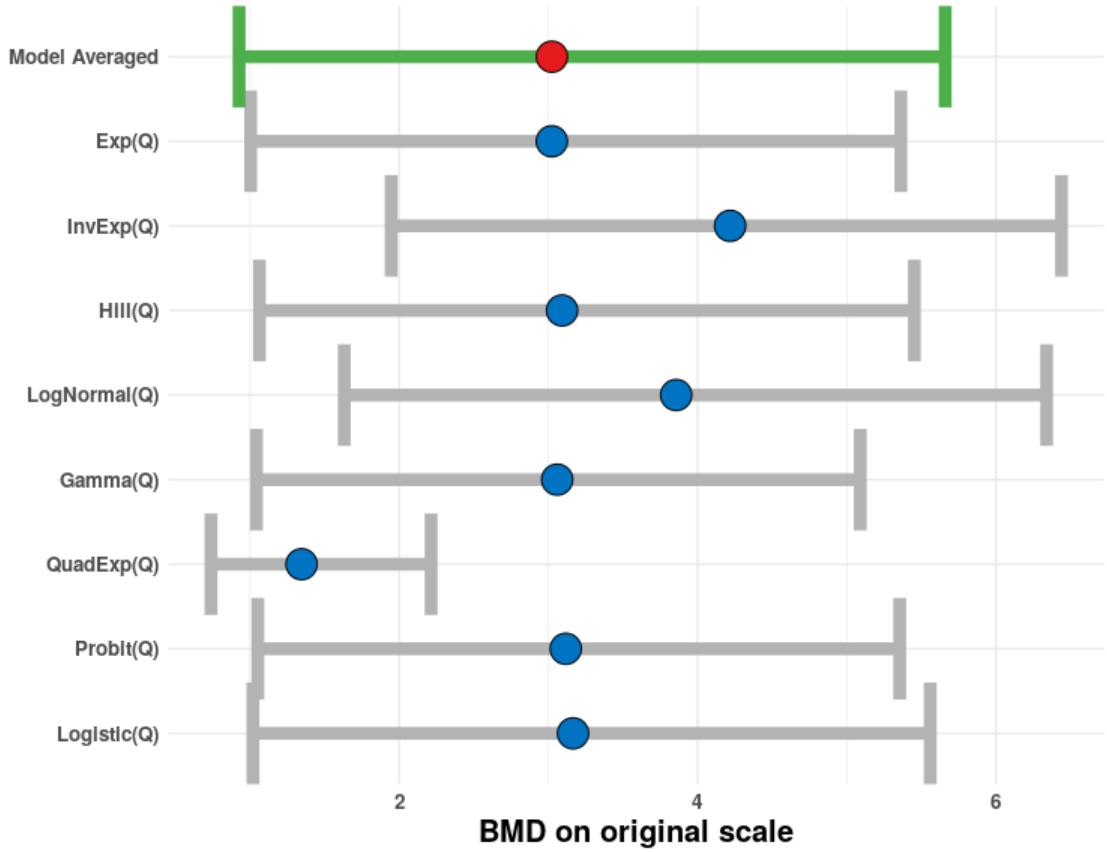
Model Averaged BMD

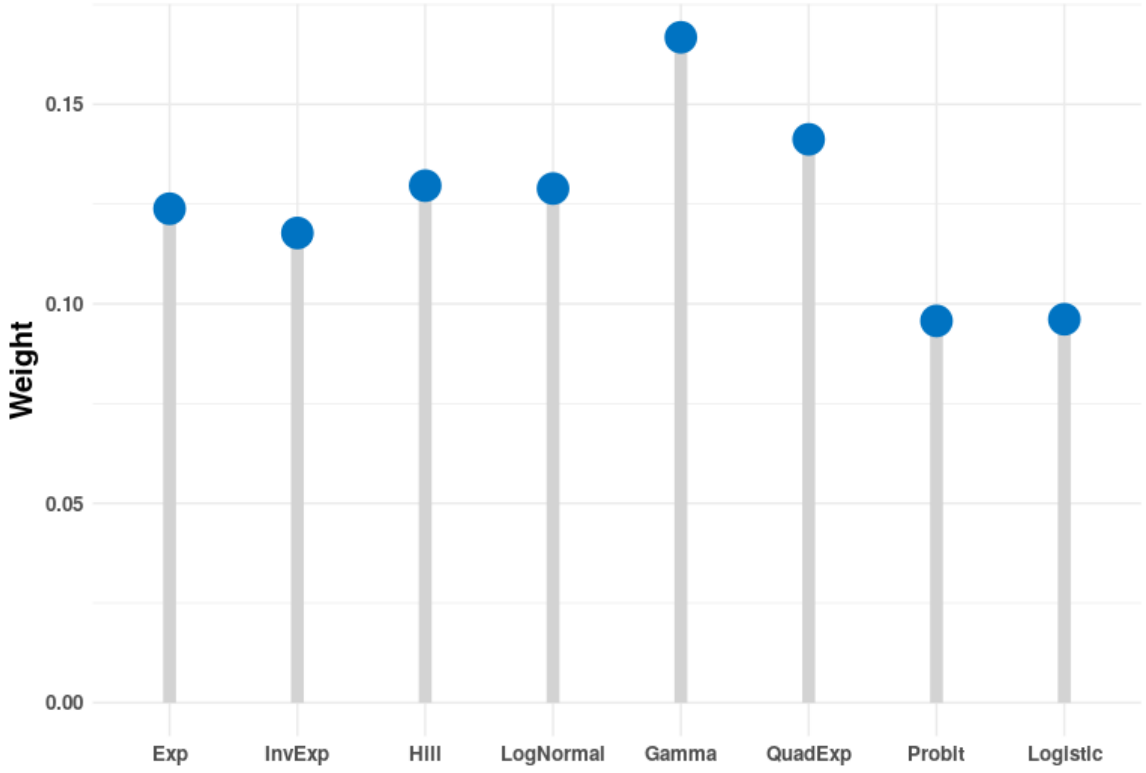
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.927	3.024	5.66

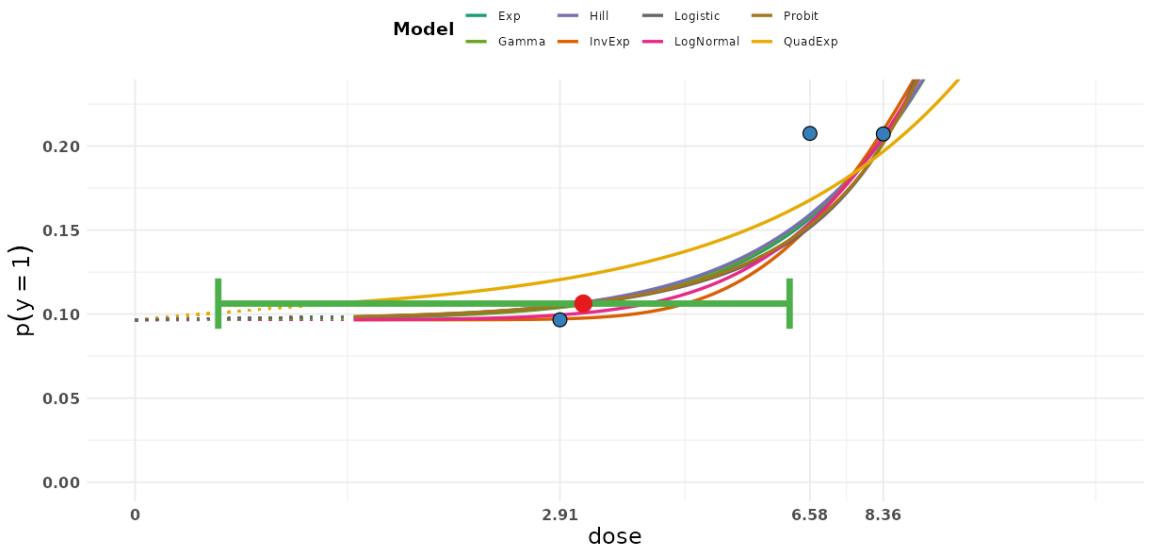
Estimated BMDs per model

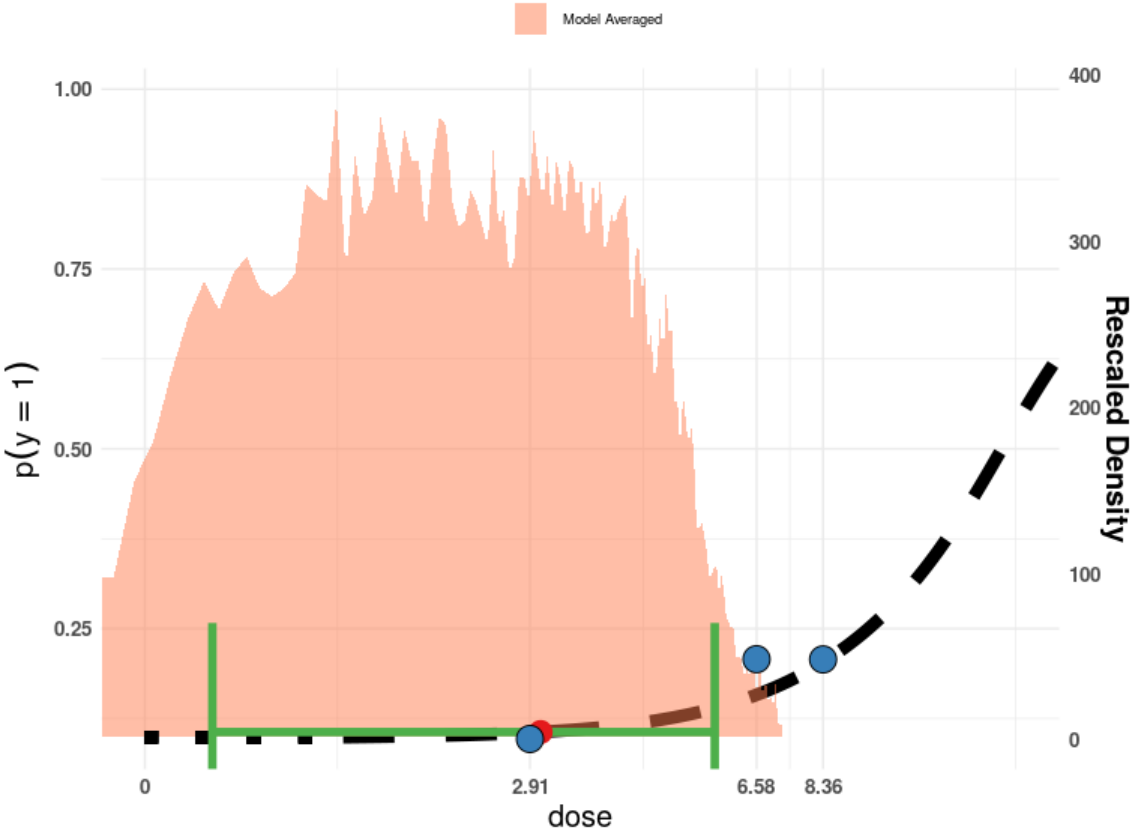
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	1.005	3.023	5.363	0.124	1
IE4_Q	1.947	4.219	6.440	0.118	1
H4_Q	1.063	3.092	5.453	0.130	1
LN4_Q	1.632	3.857	6.340	0.129	1
G4_Q	1.044	3.059	5.091	0.167	1
QE4_Q	0.739	1.346	2.214	0.141	1
P4_Q	1.053	3.117	5.355	0.096	1
L4_Q	1.020	3.166	5.560	0.096	1

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 10%

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 0.00666667.

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 9.95e-01).

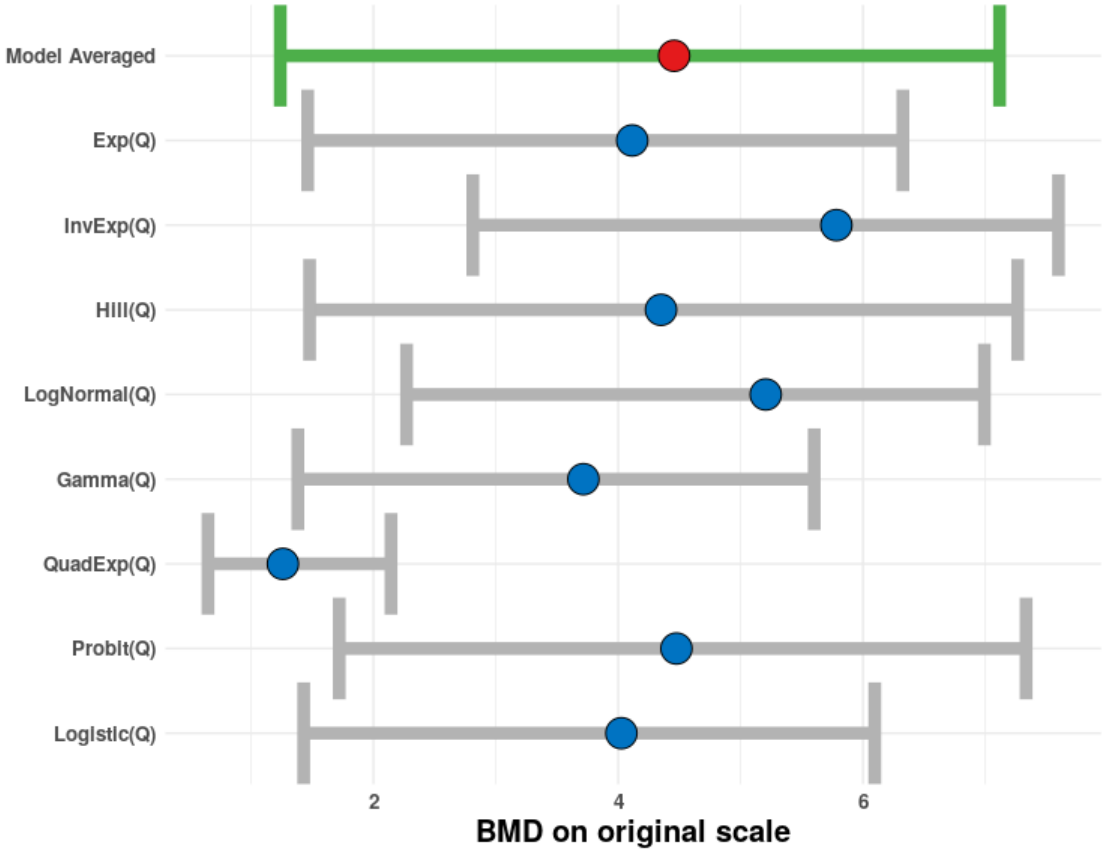
Model Averaged BMD

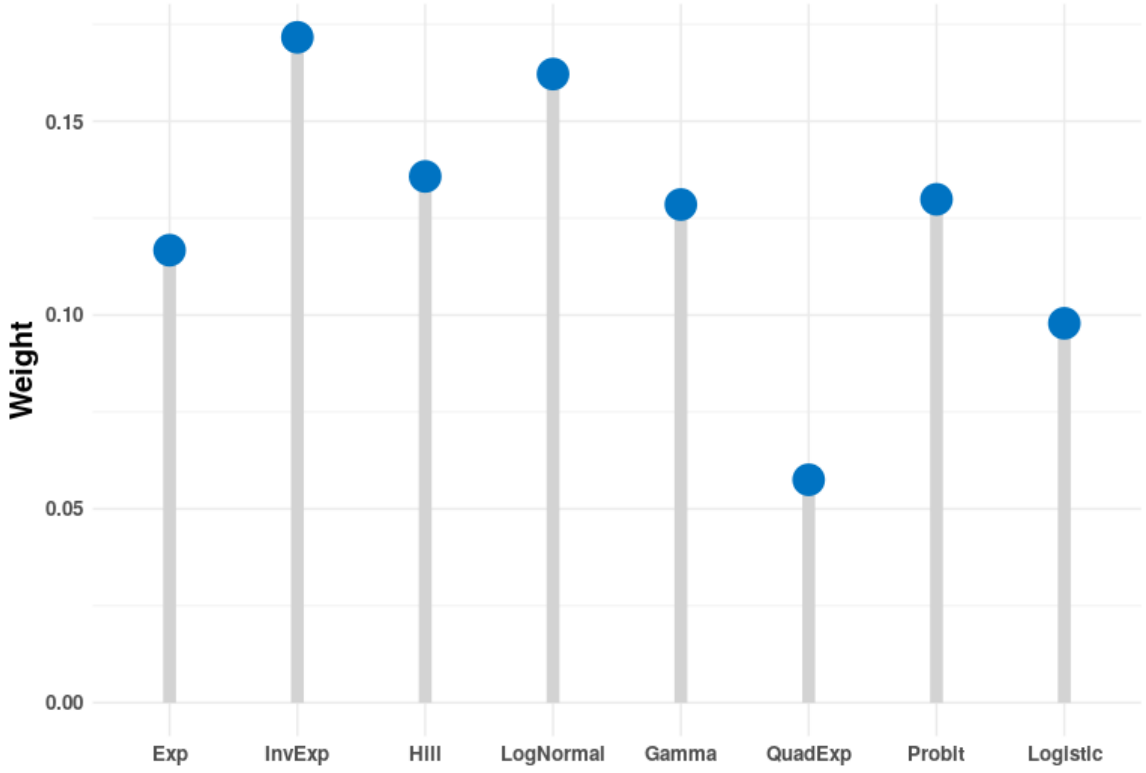
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	1.238	4.457	7.116

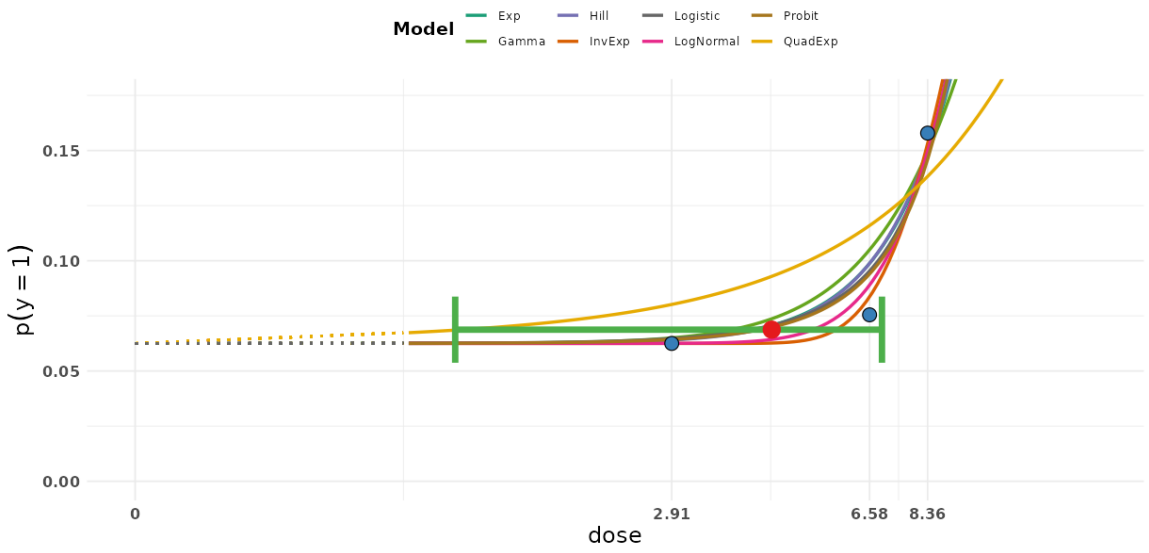
Estimated BMDs per model

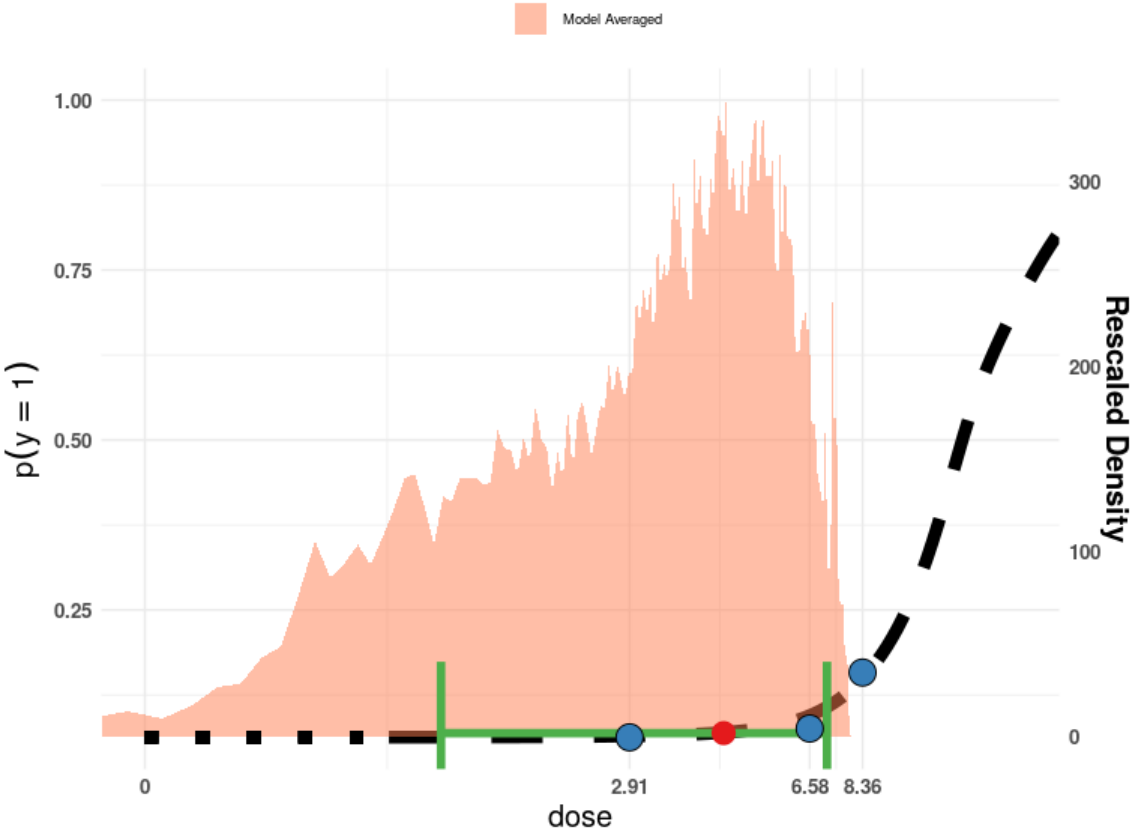
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	1.462	4.114	6.326	0.117	1
IE4_Q	2.812	5.783	7.598	0.172	1
H4_Q	1.478	4.350	7.265	0.136	0
LN4_Q	2.271	5.206	6.992	0.162	1
G4_Q	1.382	3.715	5.602	0.129	1
QE4_Q	0.648	1.260	2.143	0.058	1
P4_Q	1.720	4.476	7.333	0.130	0
L4_Q	1.430	4.026	6.096	0.098	1

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 10%

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 0.00169118.

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 1.00e-02).

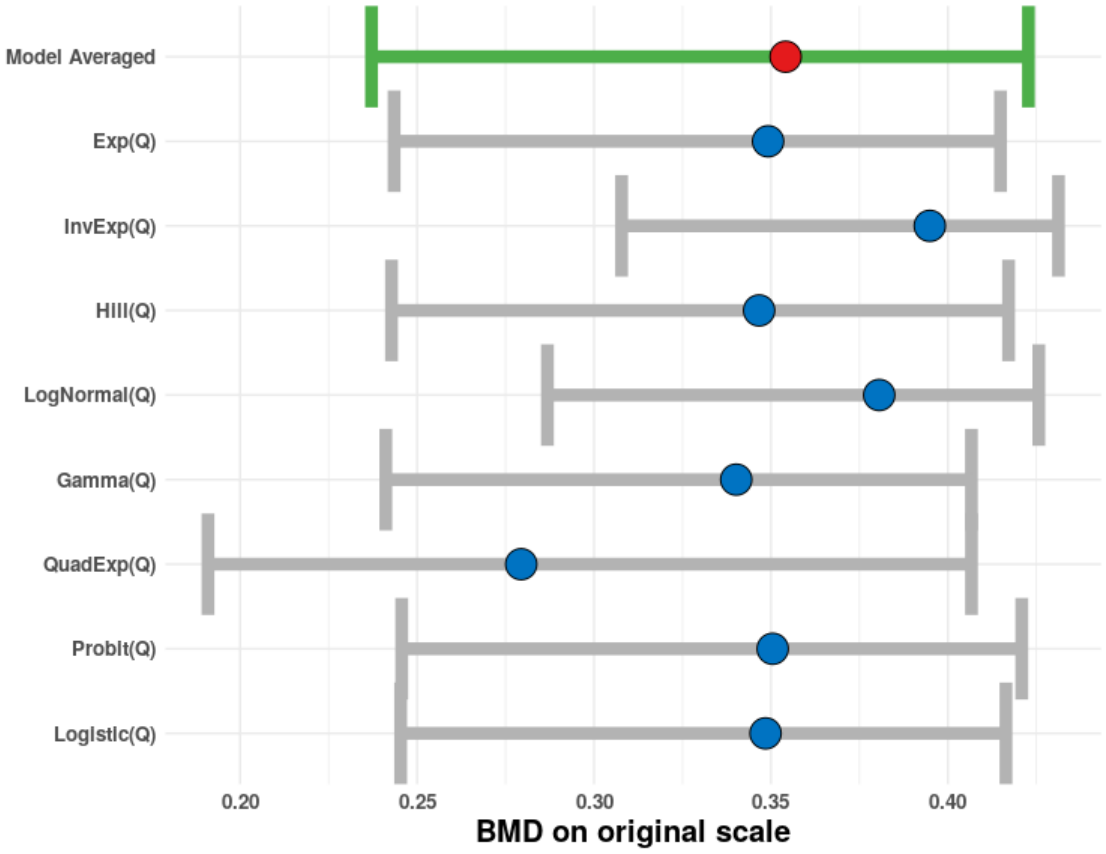
Model Averaged BMD

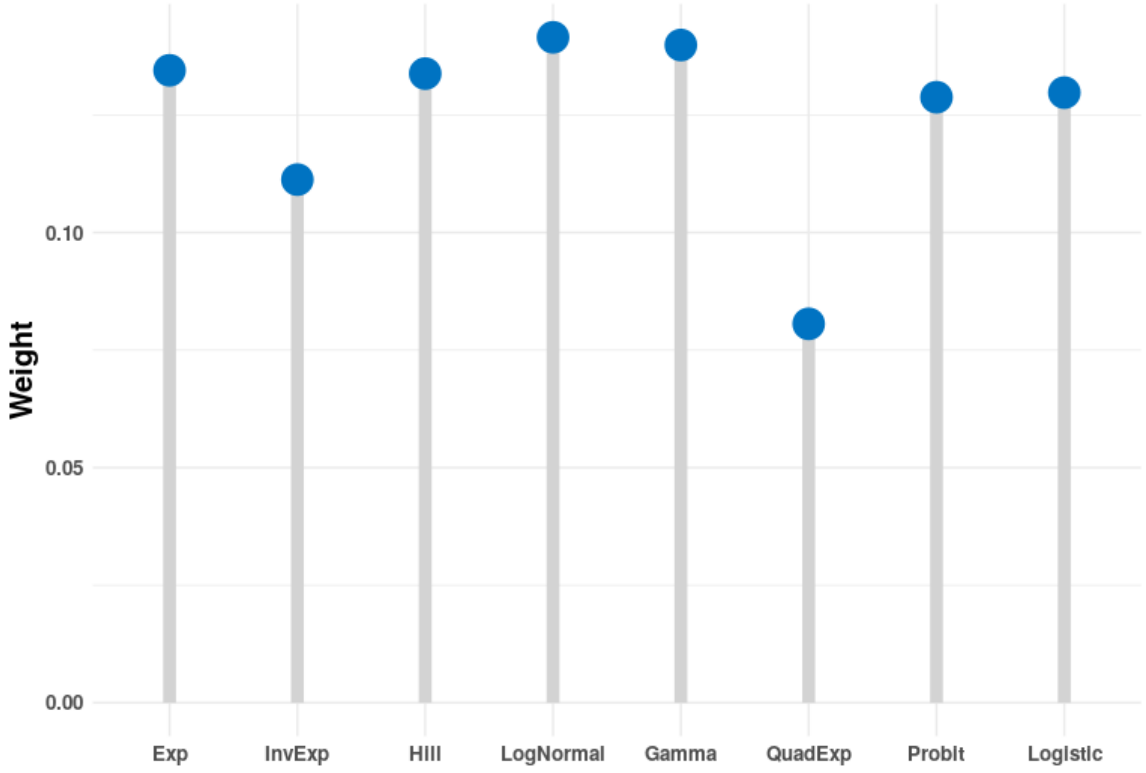
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.237	0.354	0.423

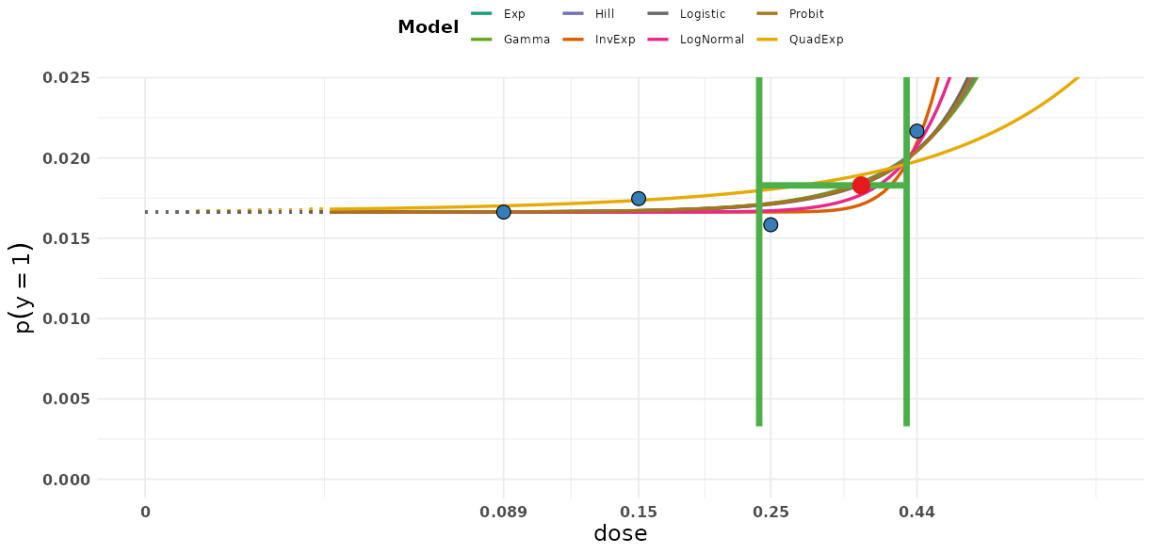
Estimated BMDs per model

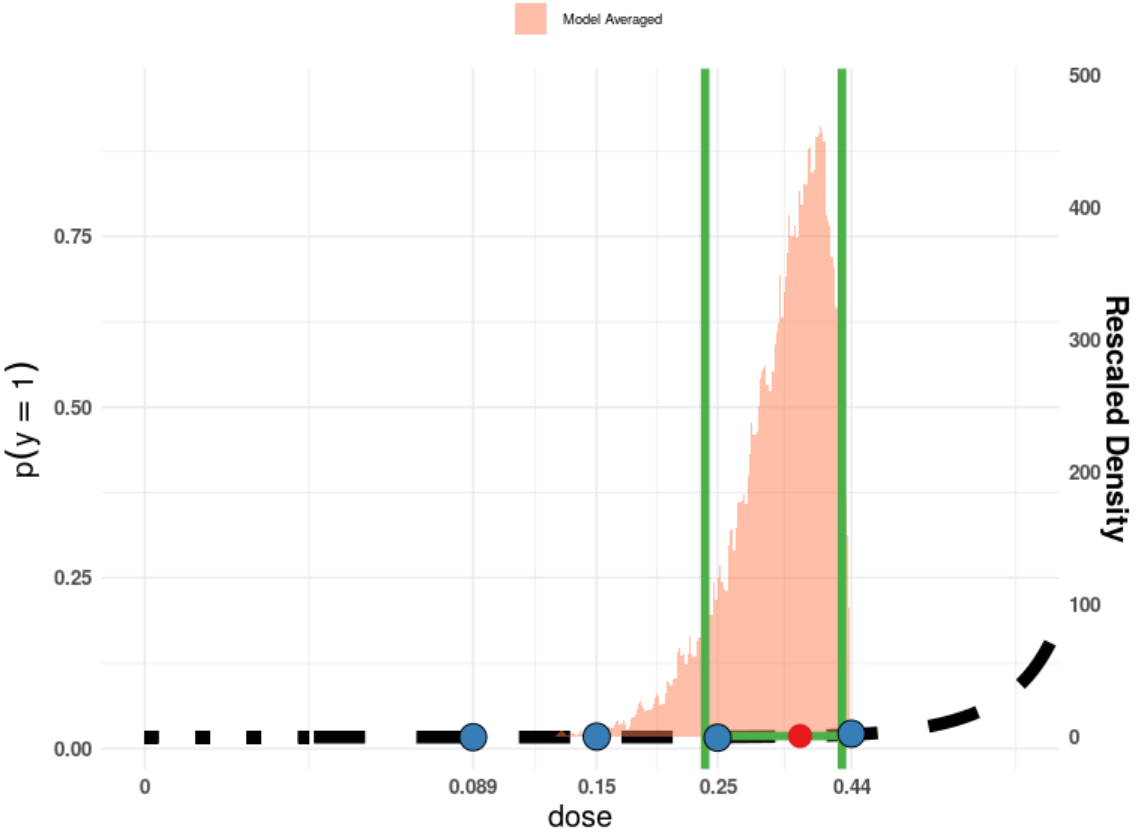
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.244	0.349	0.415	0.134	1
IE4_Q	0.308	0.395	0.431	0.111	1
H4_Q	0.243	0.347	0.417	0.134	1
LN4_Q	0.287	0.381	0.426	0.142	1
G4_Q	0.241	0.340	0.407	0.140	1
QE4_Q	0.191	0.279	0.407	0.081	1
P4_Q	0.246	0.350	0.421	0.129	1
L4_Q	0.245	0.348	0.416	0.130	1

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
0.025
0.020
0.015
0.010
0.005
0.000
p(y = 1)
0
0.089
0.15
0.25
0.44
dose


Model Averaged
p(y = 1)
0.00
0.25
0.50
0.75
0
0.089
0.15
0.25
0.44
dose
Rescaled Density
0
100
200
300
400
500

Pierce et al. (2011) skin lesions, relative BMR 10%

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 0.00522088.

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 7.06e-03).

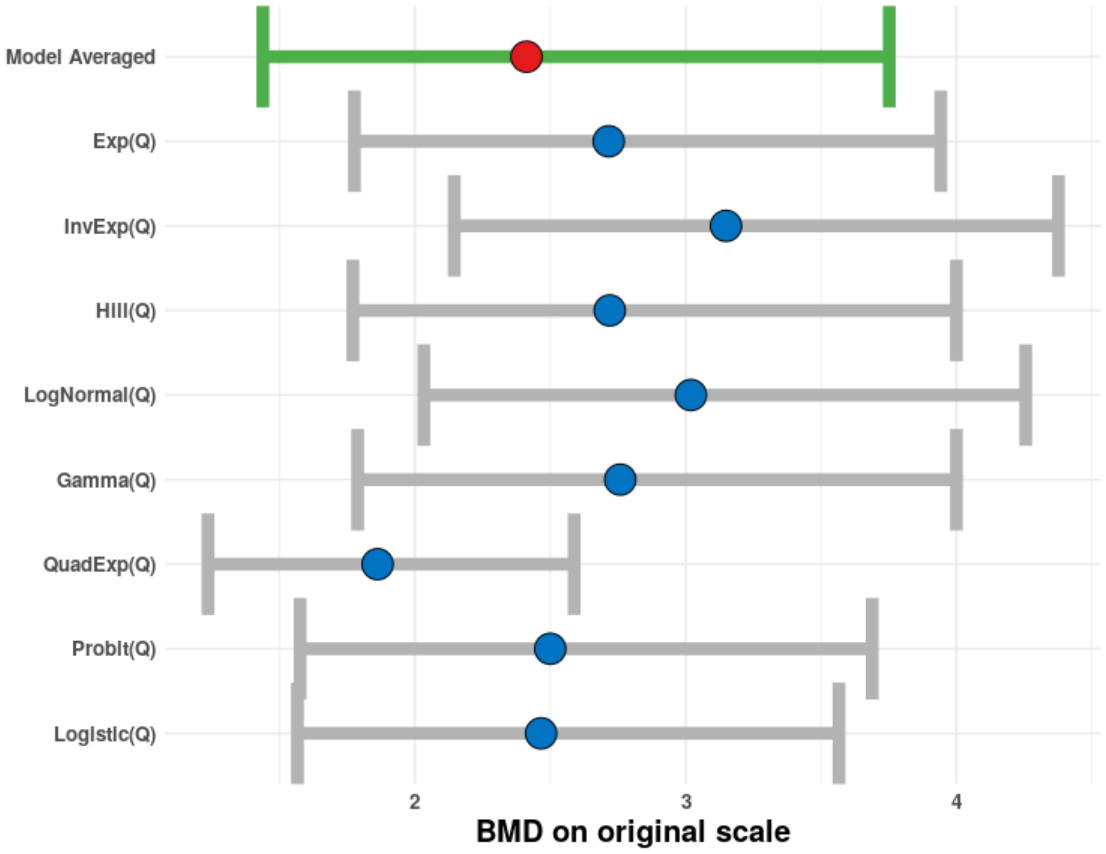
Model Averaged BMD

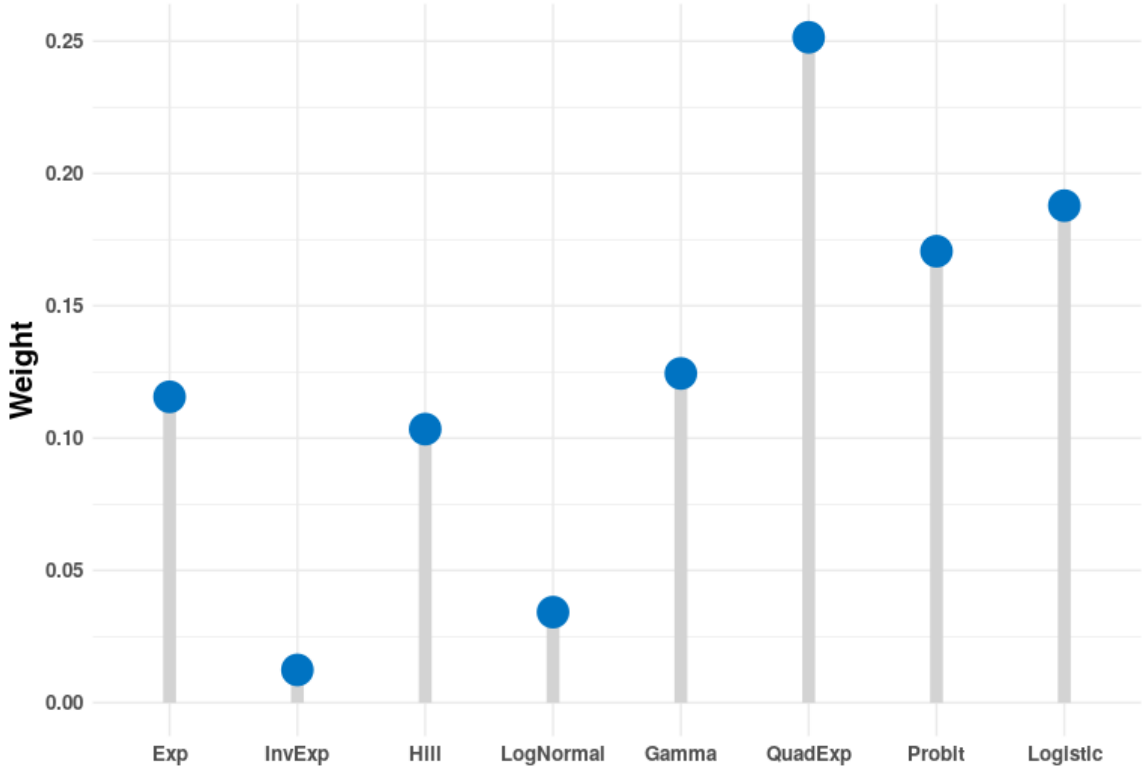
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	1.438	2.412	3.752

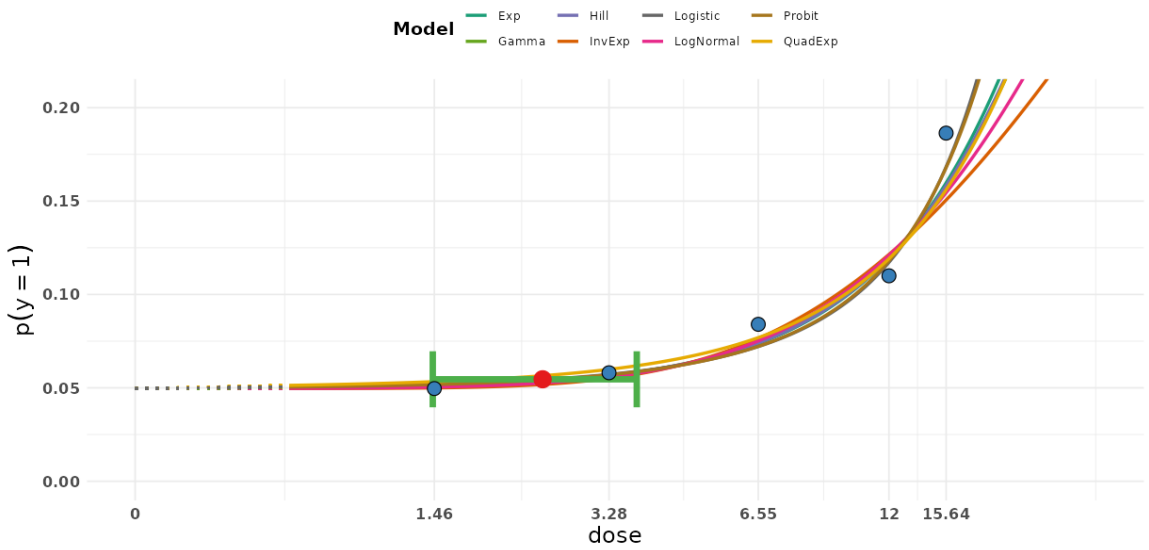
Estimated BMDs per model

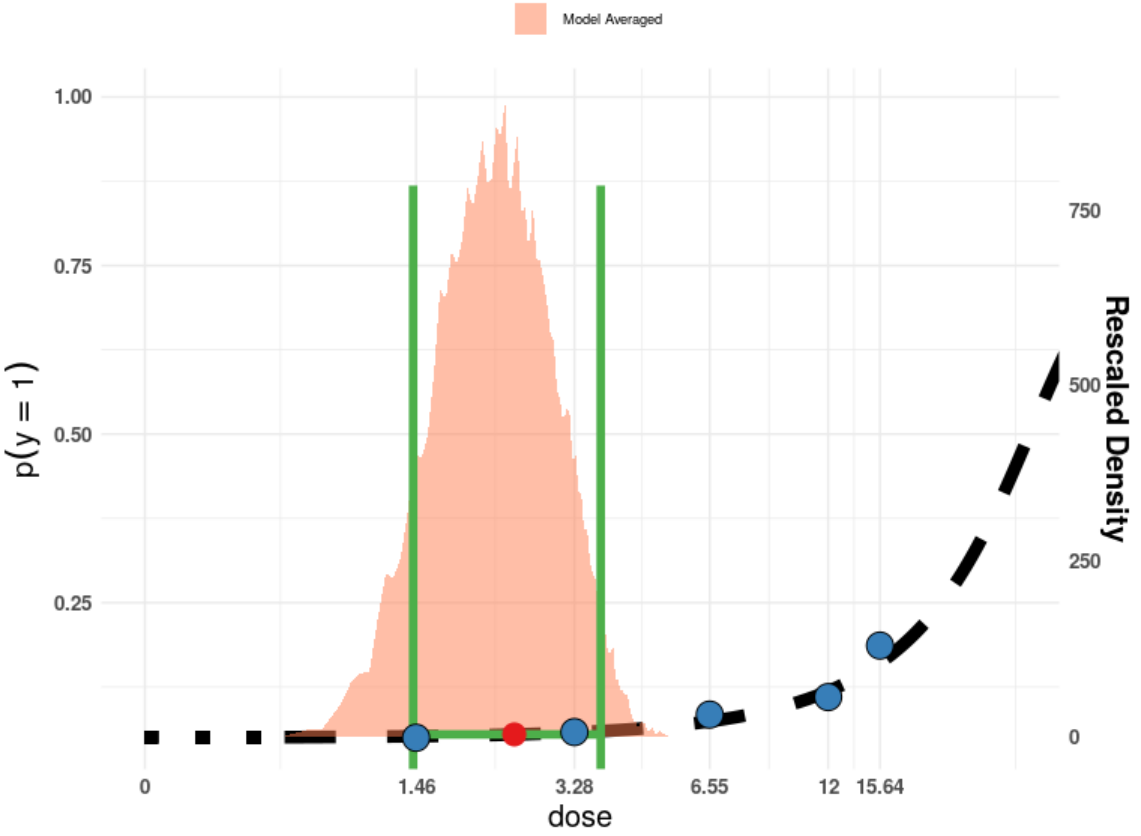
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	1.777	2.716	3.942	0.116	1
IE4_Q	2.145	3.149	4.377	0.012	1
H4_Q	1.771	2.720	4.000	0.103	1
LN4_Q	2.033	3.019	4.256	0.034	1
G4_Q	1.788	2.758	4.000	0.124	1
QE4_Q	1.236	1.862	2.588	0.251	1
P4_Q	1.576	2.500	3.689	0.171	1
L4_Q	1.566	2.466	3.566	0.188	1

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
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
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)
750
500
250
0
Rescaled Density
0
1.46
3.28
6.55
12
15.64
dose

Powers et al. (2019) airflow obstruction, relative BMR 10%

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 0.02984563.

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 1.79e+00).

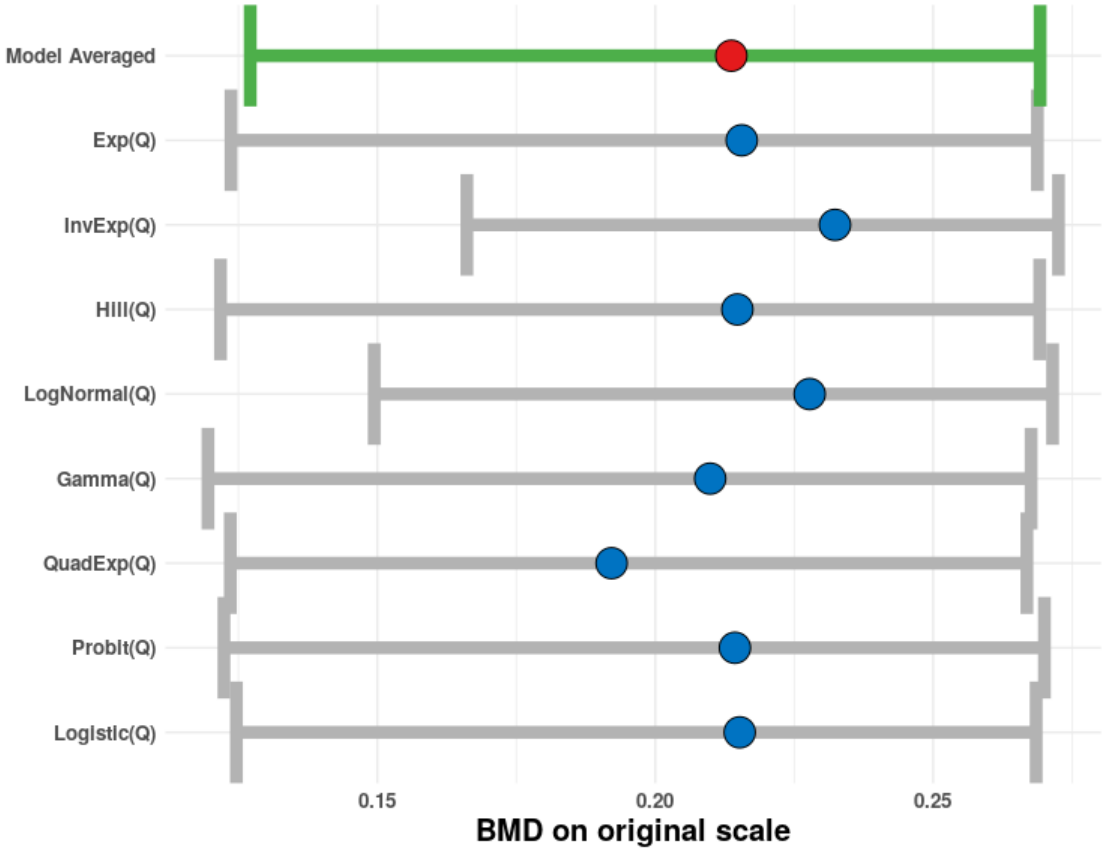
Model Averaged BMD

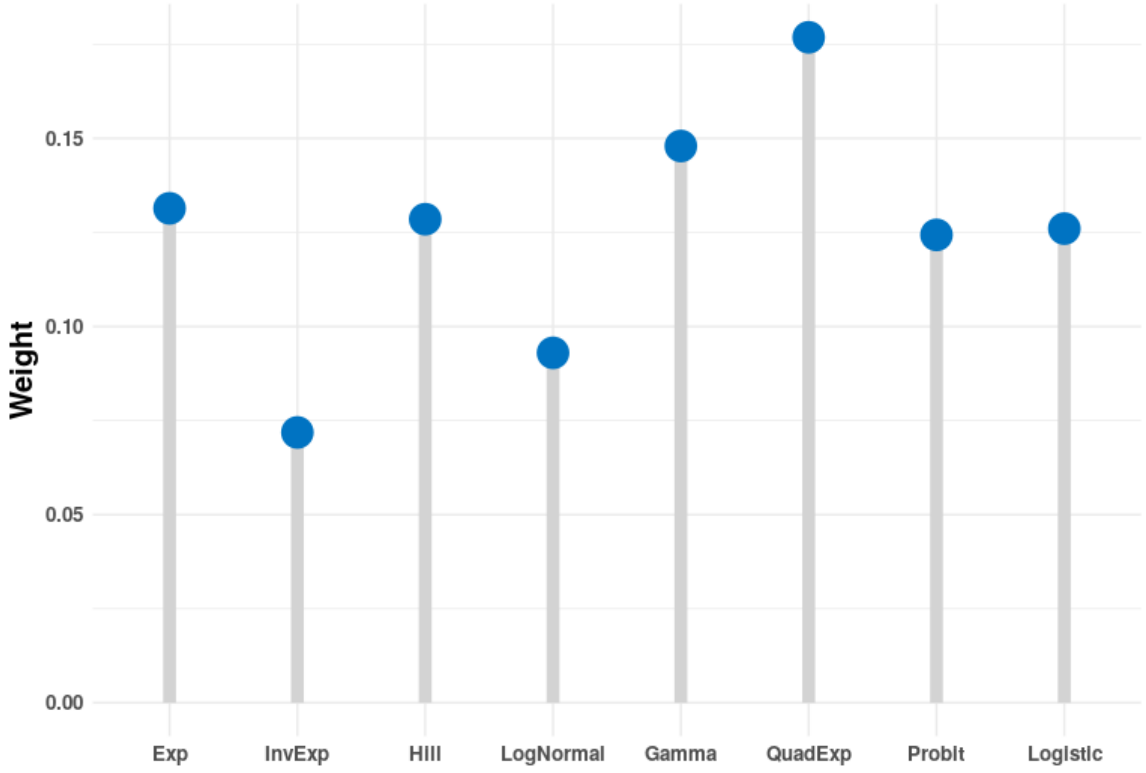
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.127	0.214	0.269

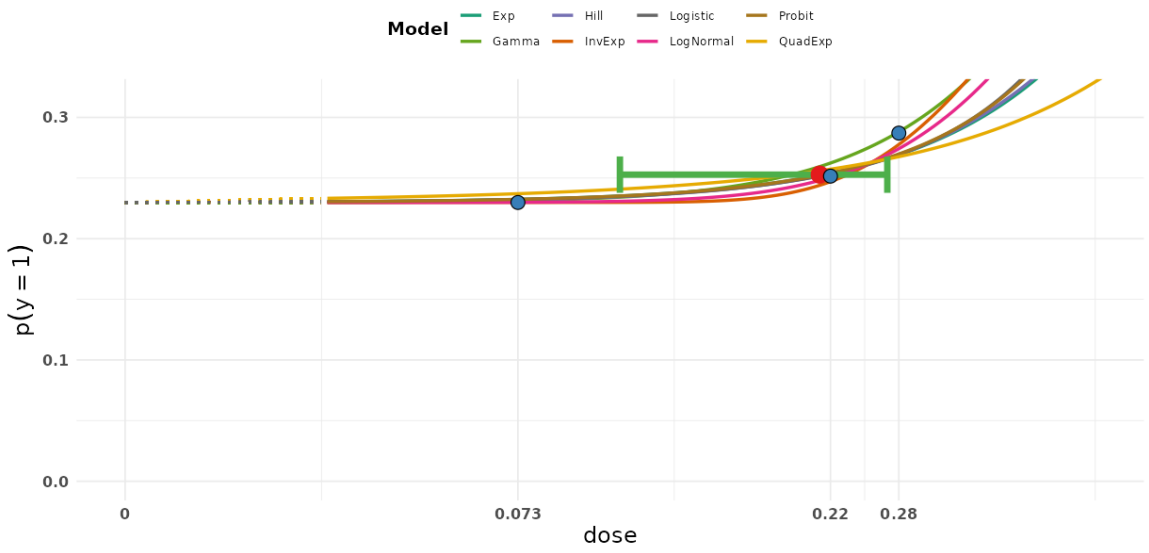
Estimated BMDs per model

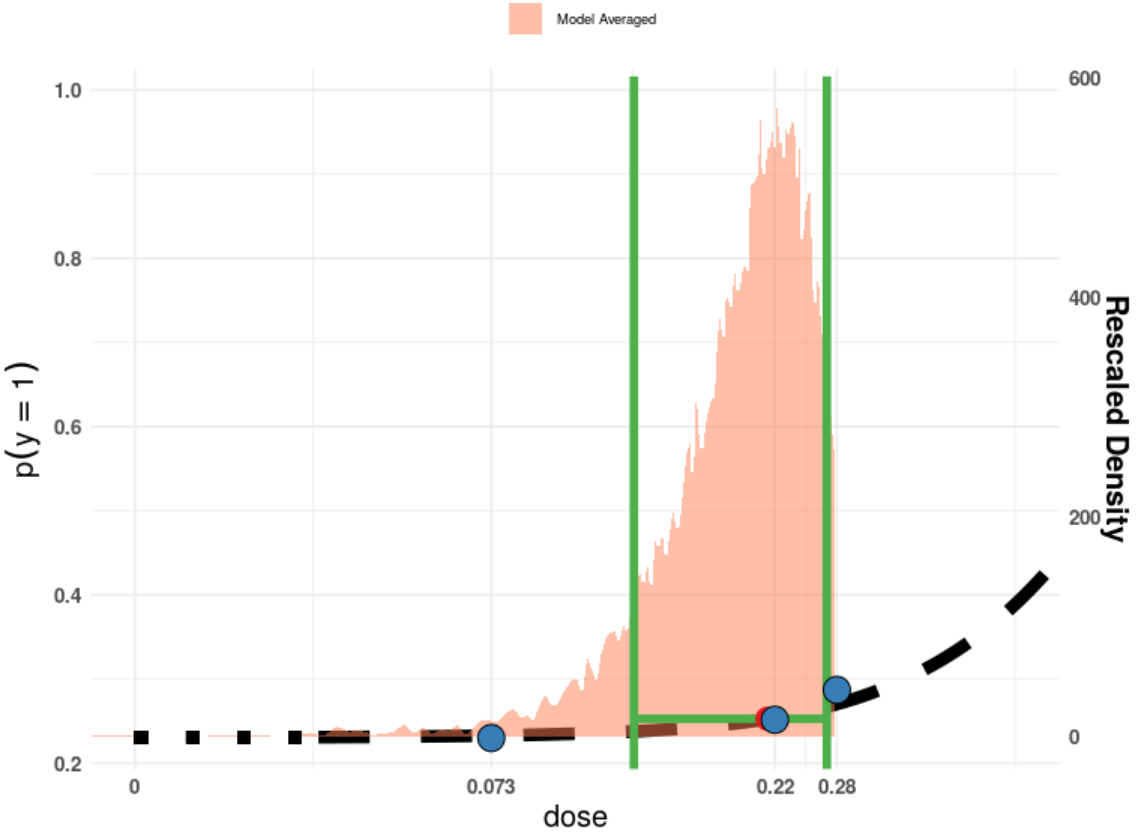
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.124	0.216	0.269	0.131	1
IE4_Q	0.166	0.232	0.273	0.072	1
H4_Q	0.122	0.215	0.269	0.129	1
LN4_Q	0.149	0.228	0.271	0.093	1
G4_Q	0.120	0.210	0.268	0.148	1
QE4_Q	0.124	0.192	0.267	0.177	1
P4_Q	0.122	0.214	0.270	0.124	1
L4_Q	0.125	0.215	0.269	0.126	1

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)
600
400
200
0
Rescaled Density
0
0.073
0.22
0.28
dose

Powers et al. (2019) emphysema, relative BMR 10%

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 0.0030445.

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 2.91e+00).

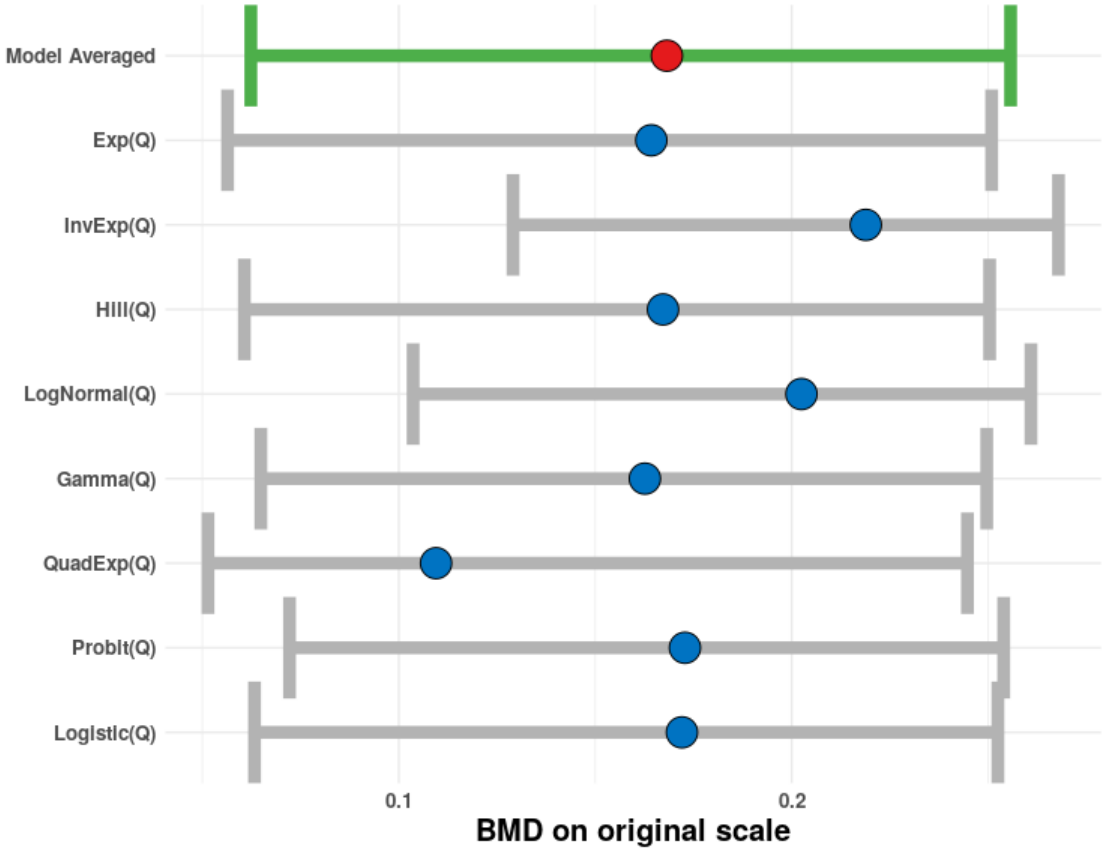
Model Averaged BMD

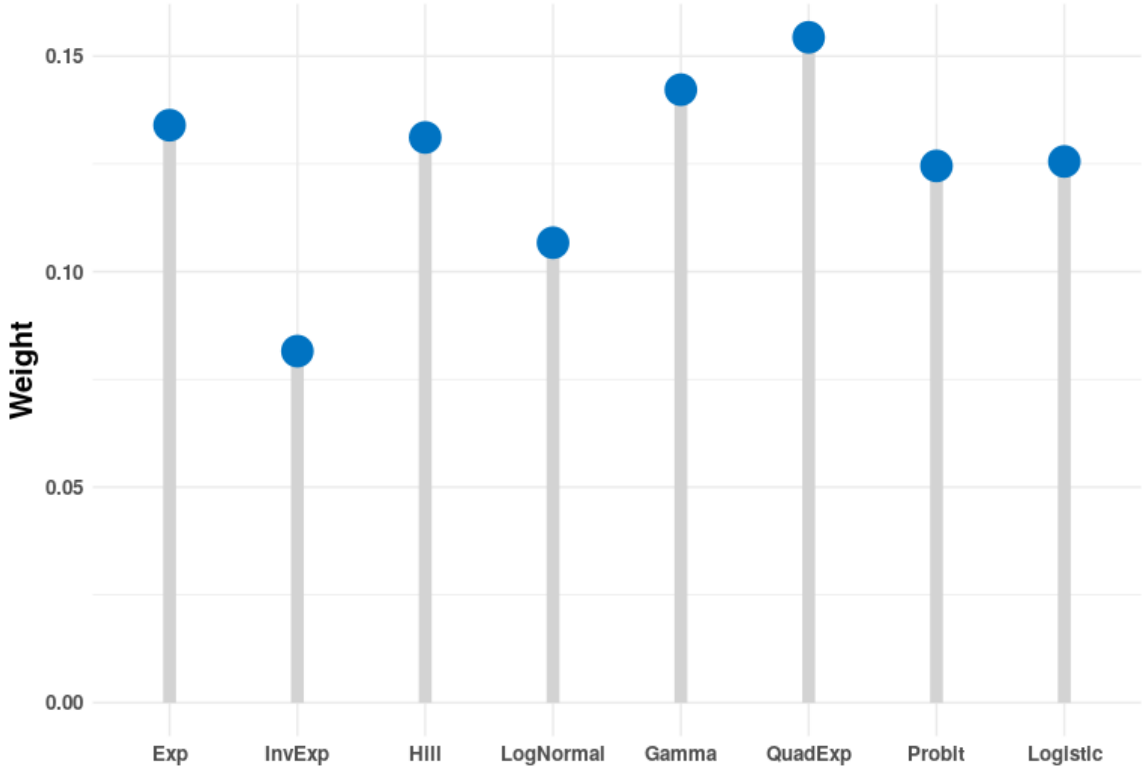
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.062	0.168	0.256

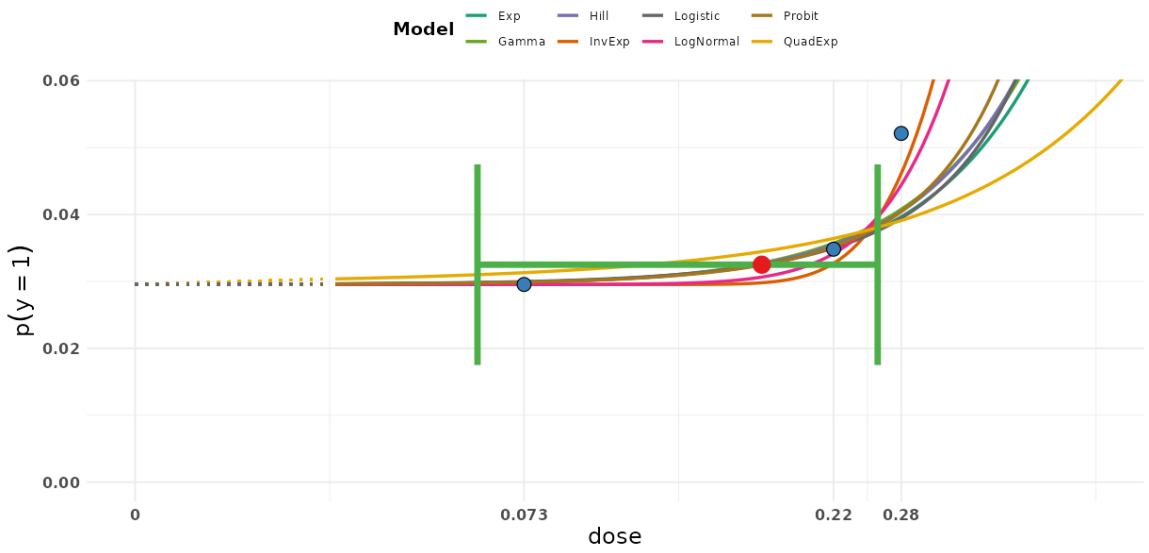
Estimated BMDs per model

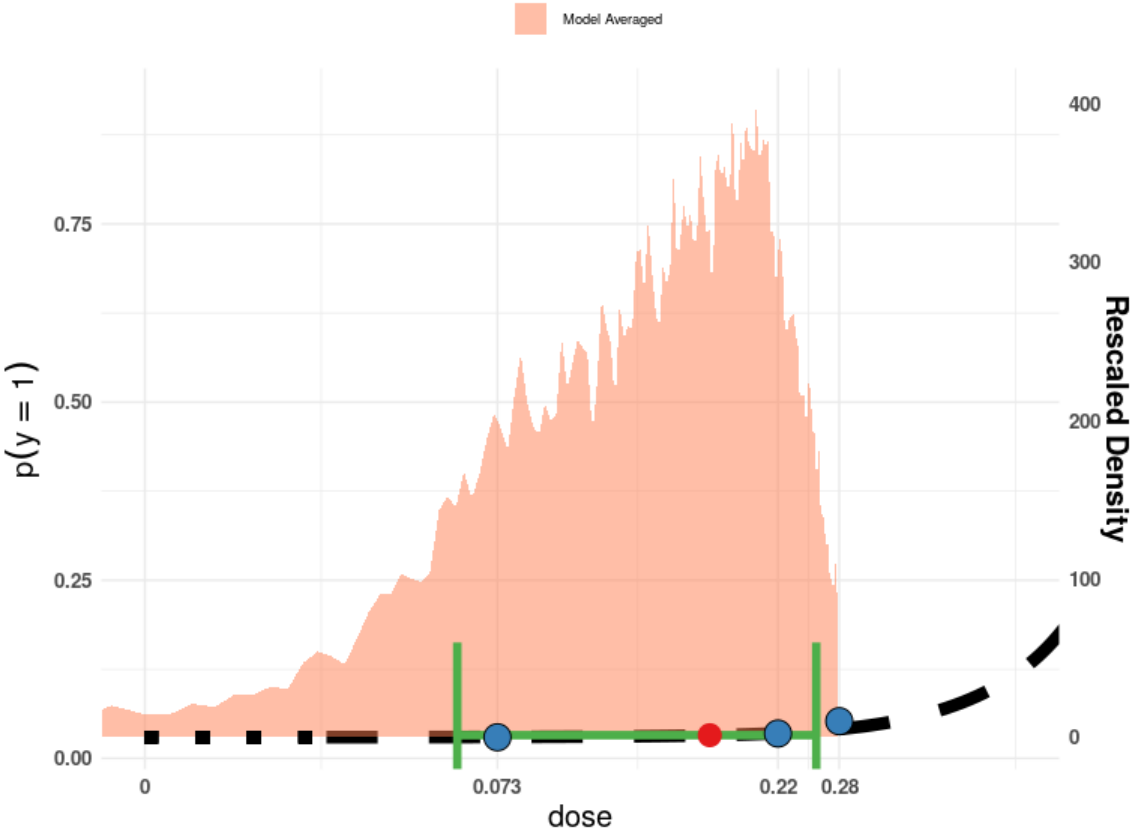
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.056	0.164	0.251	0.134	1
IE4_Q	0.129	0.219	0.268	0.082	1
H4_Q	0.061	0.167	0.250	0.131	0
LN4_Q	0.104	0.202	0.261	0.107	1
G4_Q	0.065	0.163	0.250	0.142	1
QE4_Q	0.051	0.109	0.245	0.154	1
P4_Q	0.072	0.173	0.254	0.125	1
L4_Q	0.063	0.172	0.252	0.126	1

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
0.06
0.04
0.02
0.00
p(y = 1)
0
0.073
0.22
0.28
dose


Model Averaged
p(y = 1)
0.00
0.25
0.50
0.75
0
0.073
0.22
0.28
dose
Rescaled Density
0
100
200
300
400

Rahman et al. (2007) infant death, relative BMR 10%

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 0.00485457.

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 2.59e-04).

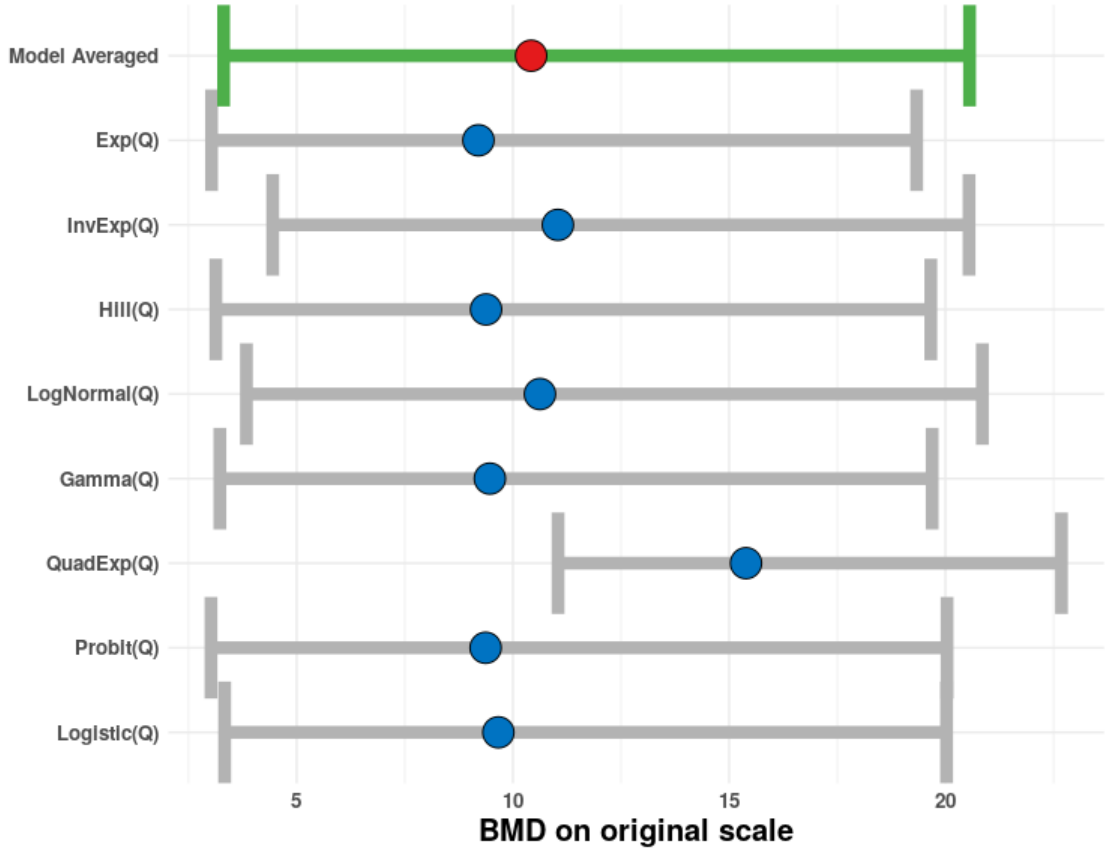
Model Averaged BMD

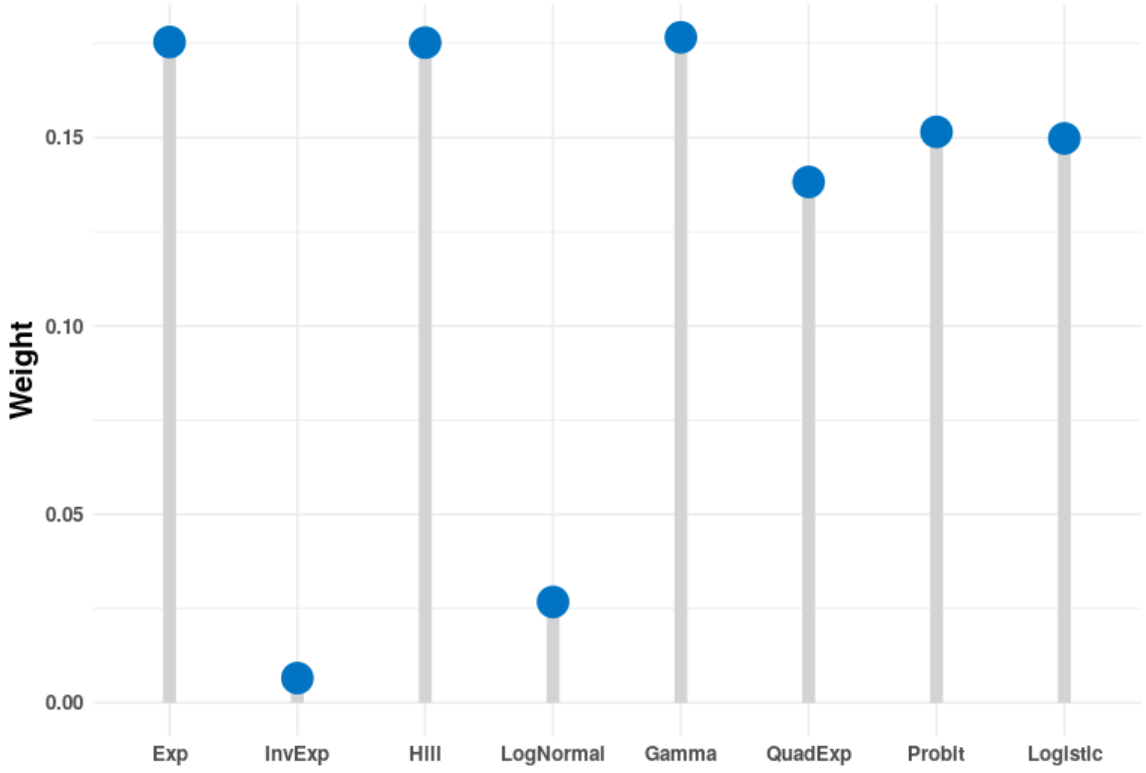
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	3.311	10.421	20.558

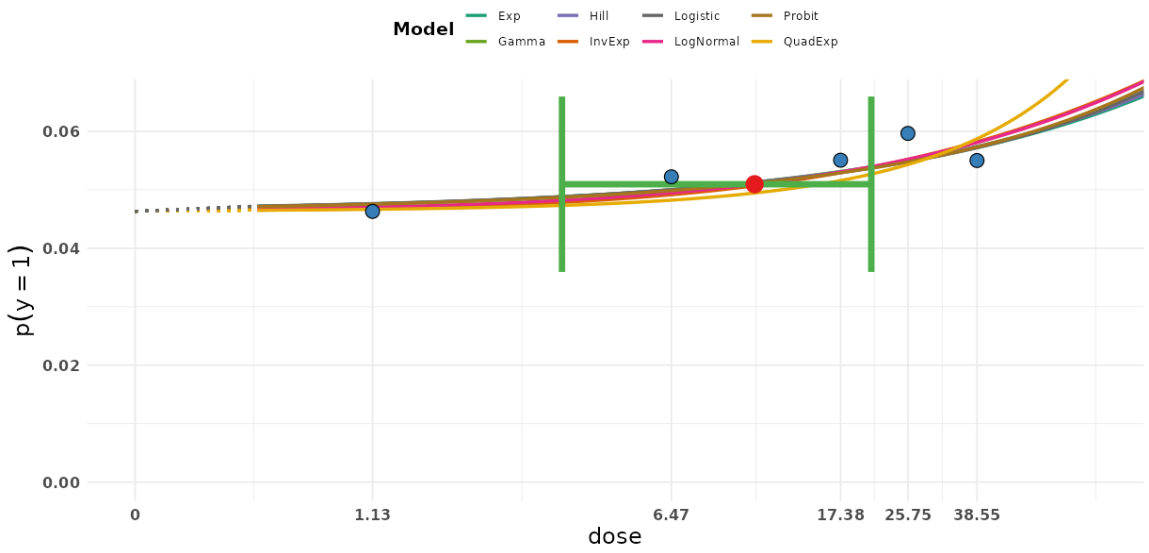
Estimated BMDs per model

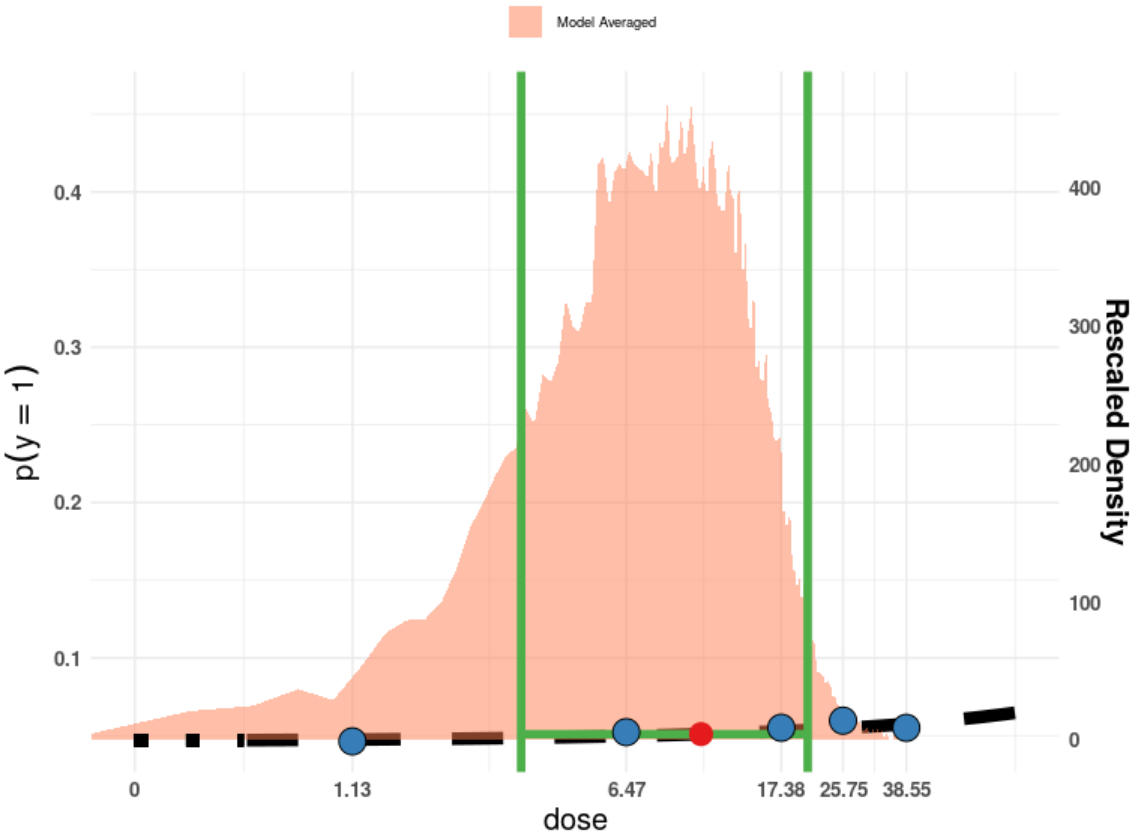
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	3.033	9.203	19.335	0.175	1
IE4_Q	4.447	11.040	20.547	0.007	1
H4_Q	3.132	9.379	19.662	0.175	1
LN4_Q	3.840	10.625	20.854	0.027	1
G4_Q	3.225	9.468	19.693	0.177	1
QE4_Q	11.044	15.389	22.683	0.138	1
P4_Q	3.020	9.369	20.037	0.152	1
L4_Q	3.336	9.664	20.026	0.150	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)
0.06
0.04
0.02
0.00
0
1.13
6.47
17.38
25.75
38.55
dose


Model Averaged
p(y = 1)
0.4
0.3
0.2
0.1
Rescaled Density
400
300
200
100
0
0
1.13
6.47
17.38
25.75
38.55
dose

Steinmaus et al. (2013) bladder cancer, relative BMR 10%

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 2.394e-05.

Extended dose range is applied.

Informative background prior: min: 0.00023699; the most likely: 0.00023938; max: 0.00024178. 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 2.33e-03).

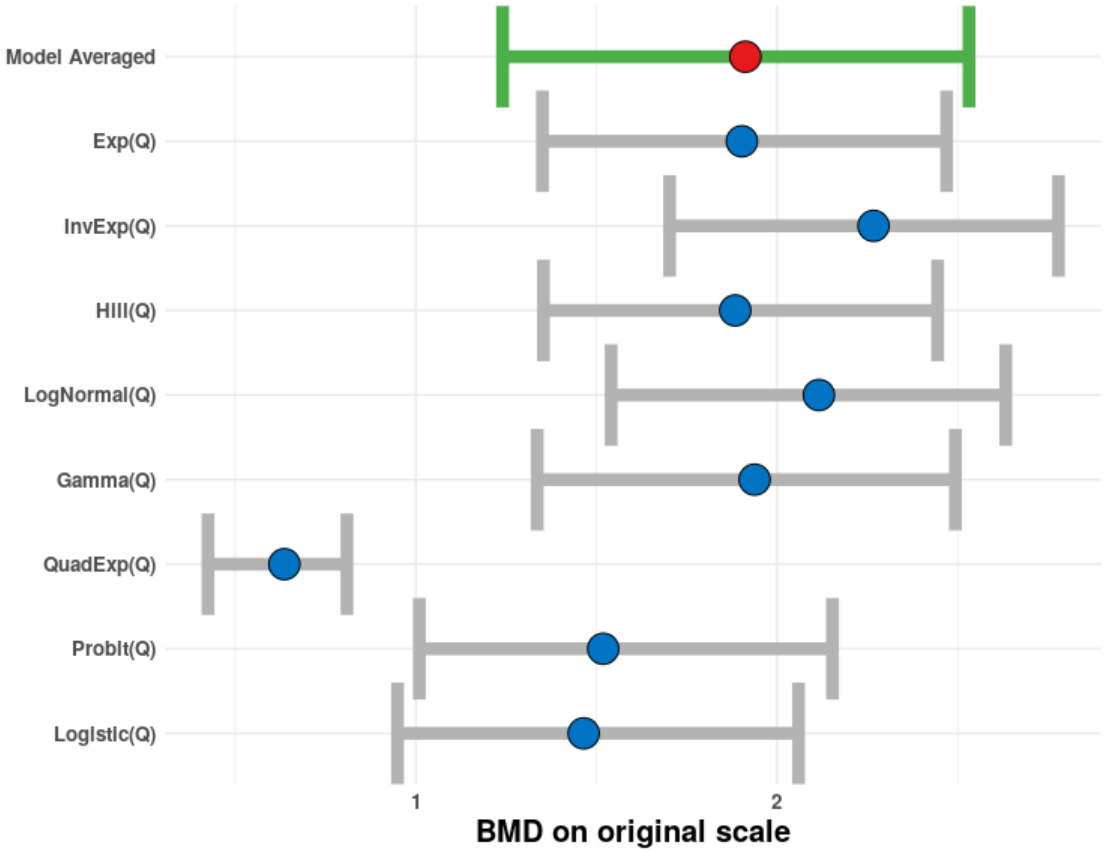
Model Averaged BMD

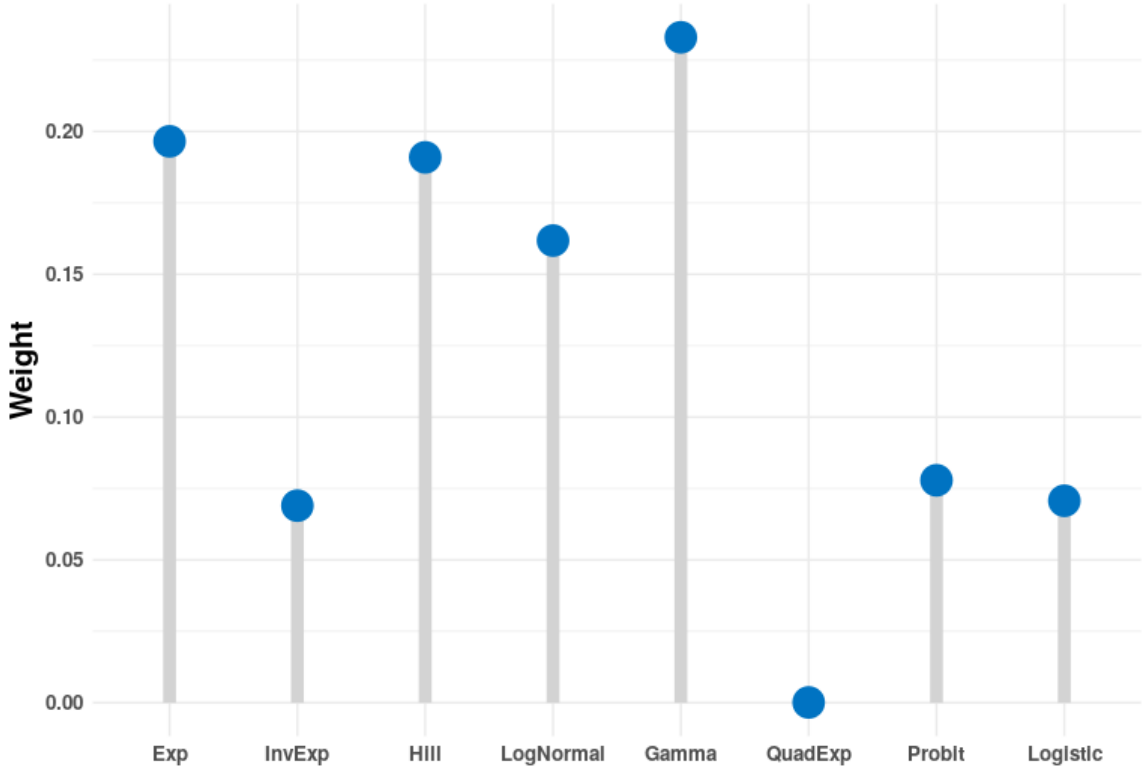
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	1.24	1.912	2.532

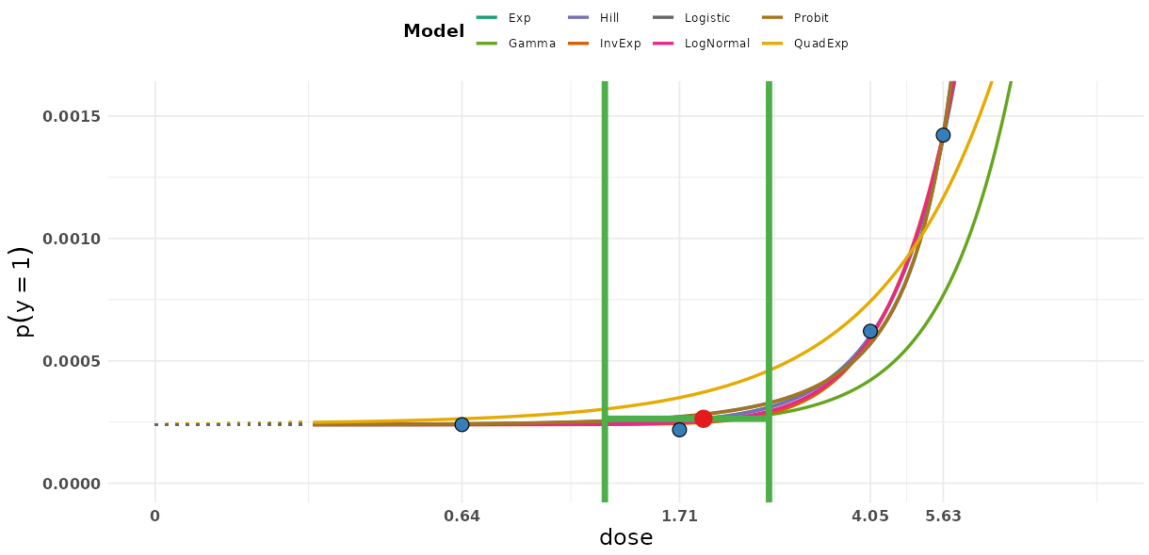
Estimated BMDs per model

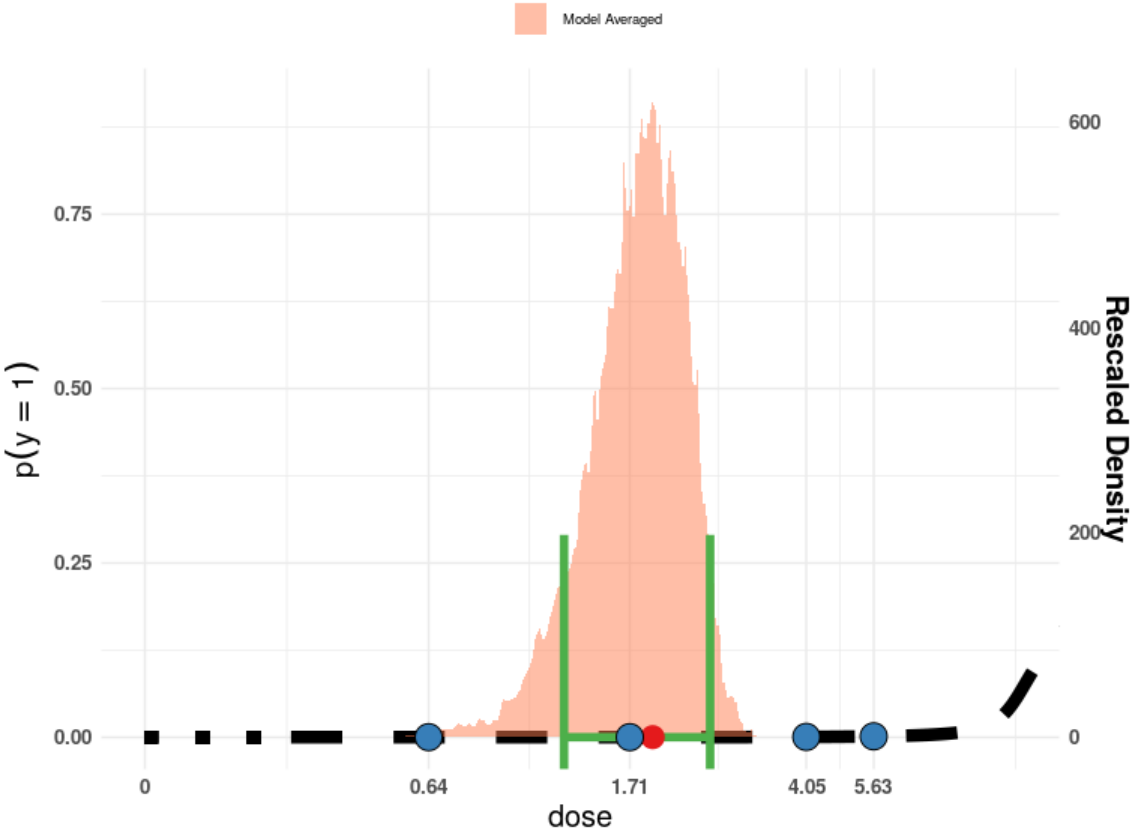
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	1.350	1.903	2.470	0.197	1
IE4_Q	1.702	2.267	2.779	0.069	1
H4_Q	1.353	1.884	2.445	0.191	1
LN4_Q	1.541	2.116	2.633	0.162	1
G4_Q	1.336	1.938	2.494	0.233	1
QE4_Q	0.424	0.636	0.809	0.000	1
P4_Q	1.010	1.519	2.154	0.078	1
L4_Q	0.949	1.465	2.059	0.071	1

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
p(y = 1)
0.00
0.25
0.50
0.75
Rescaled Density
0
200
400
600
0
0.64
1.71
4.05
5.63
dose

Steinmaus et al. (2013) bladder cancer, relative BMR 10%

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 2.311e-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 1.72e-03).

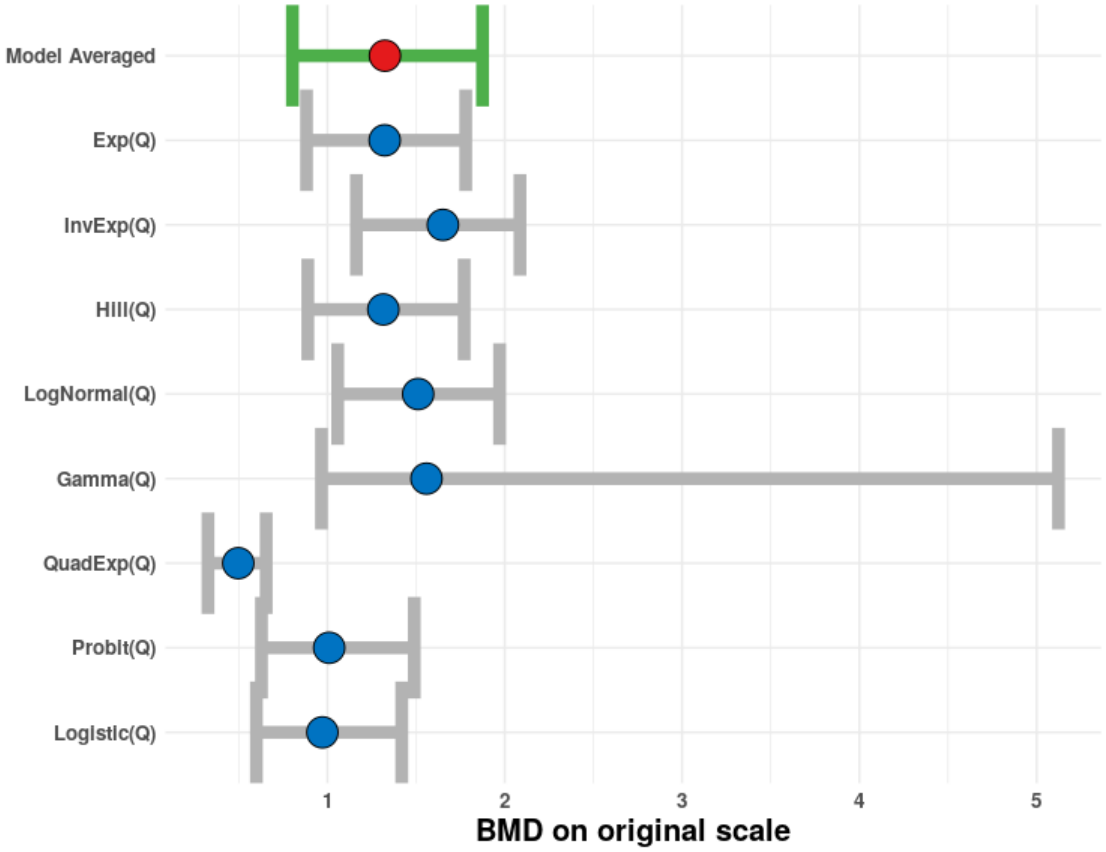
Model Averaged BMD

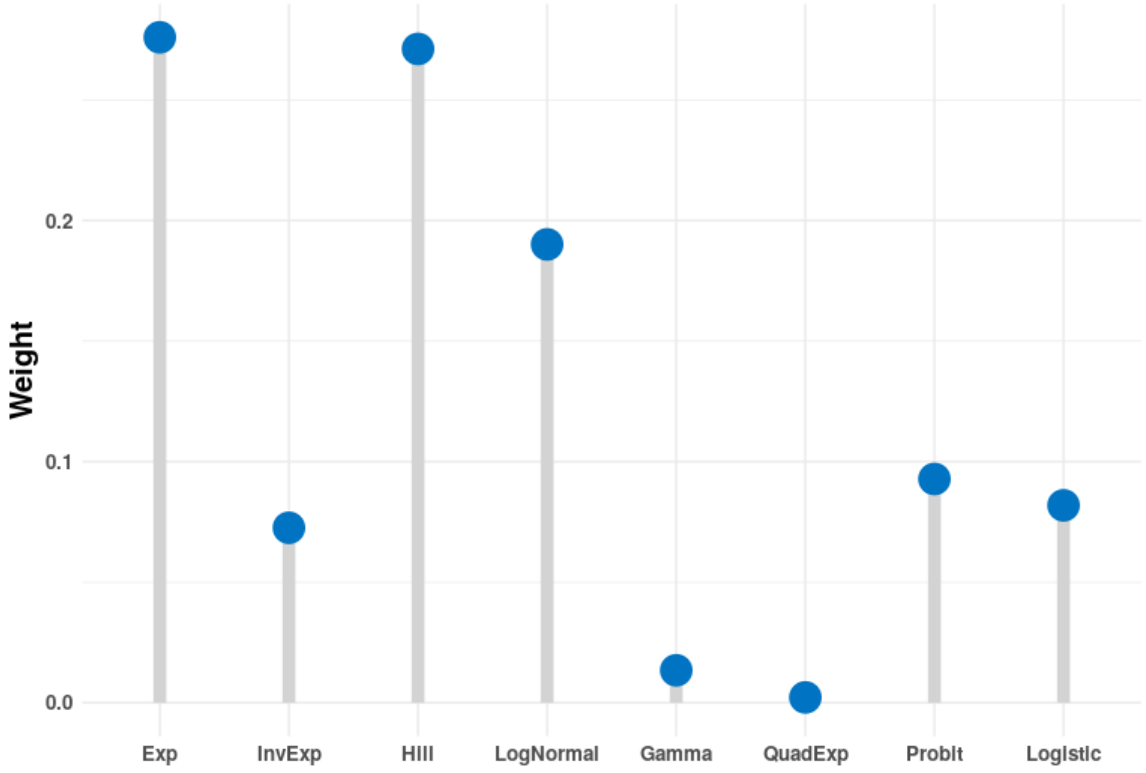
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.802	1.324	1.875

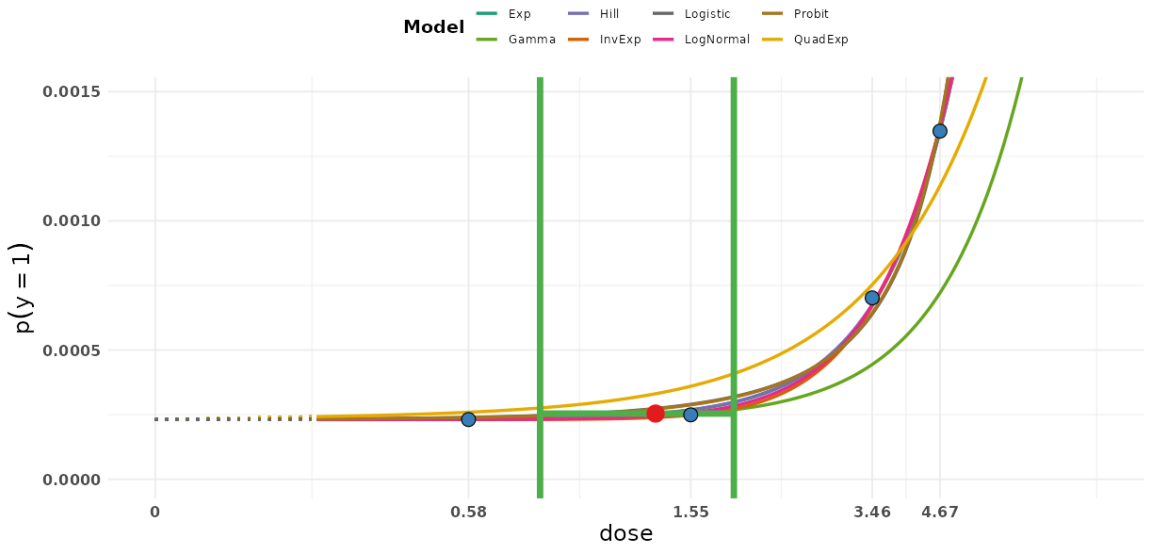
Estimated BMDs per model

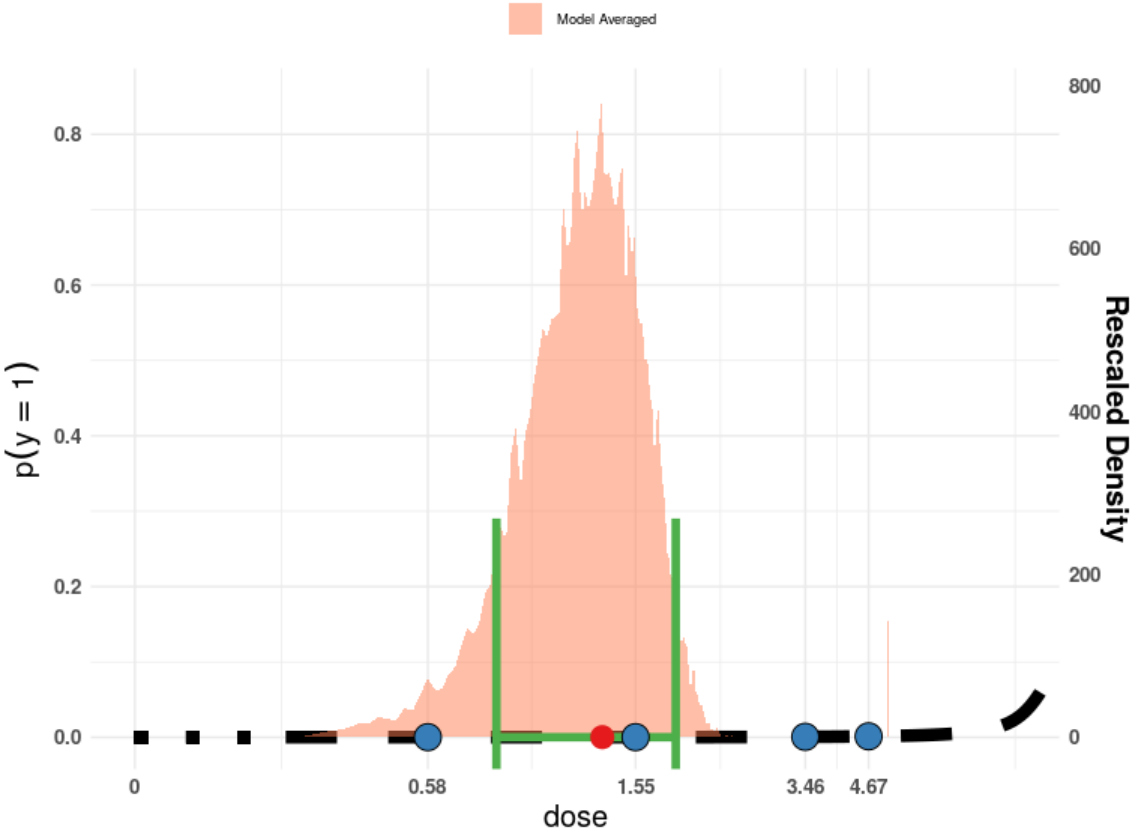
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.882	1.323	1.780	0.276	1
IE4_Q	1.163	1.651	2.086	0.073	1
H4_Q	0.889	1.315	1.771	0.271	1
LN4_Q	1.058	1.512	1.971	0.190	1
G4_Q	0.966	1.559	5.123	0.013	0
QE4_Q	0.326	0.497	0.655	0.002	1
P4_Q	0.628	1.010	1.490	0.093	1
L4_Q	0.599	0.972	1.419	0.082	1

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
p(y = 1)
0.0
0.2
0.4
0.6
0.8
Rescaled Density
0
200
400
600
800
0
0.58
1.55
3.46
4.67
dose

Steinmaus et al. (2013) bladder cancer, relative BMR 10%

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 1.918e-05.

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 1.96e-03).

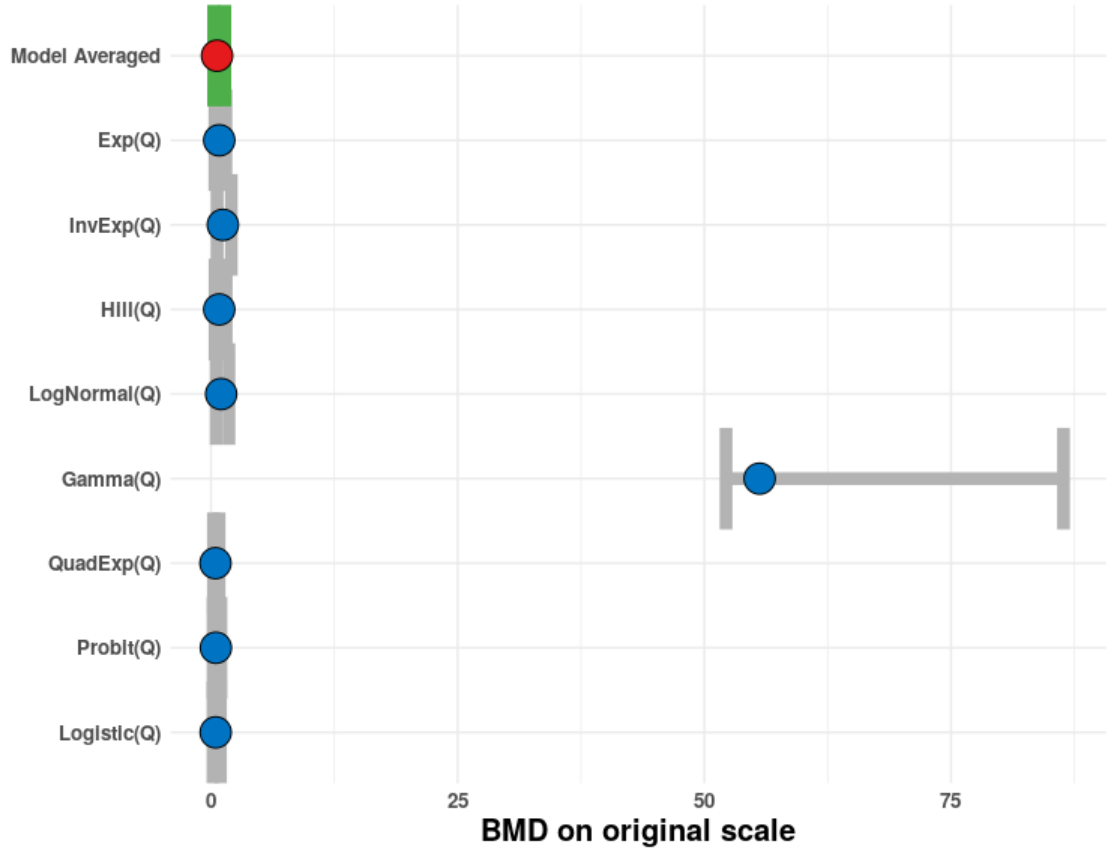
Model Averaged BMD

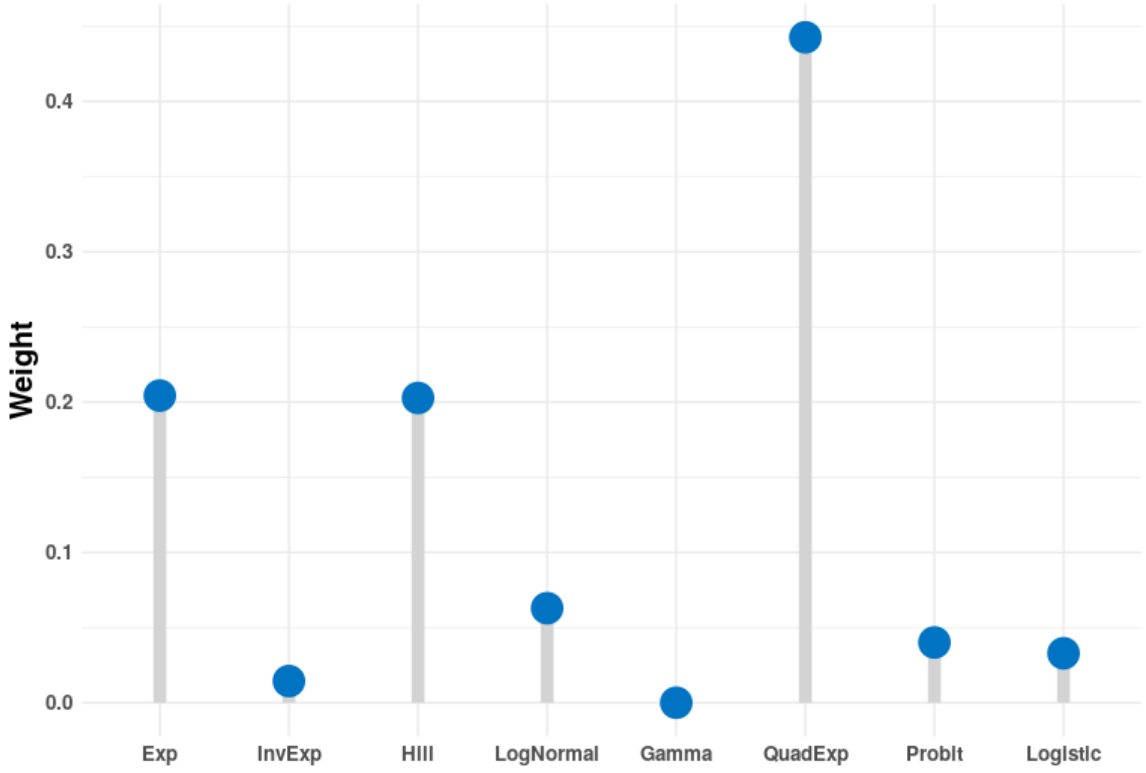
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.268	0.61	1.4

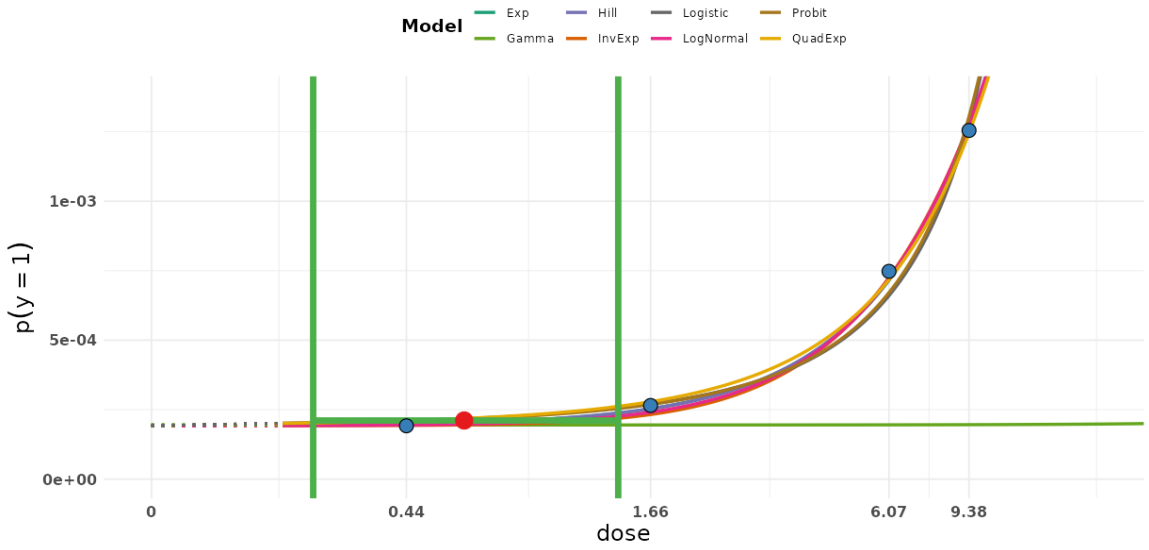
Estimated BMDs per model

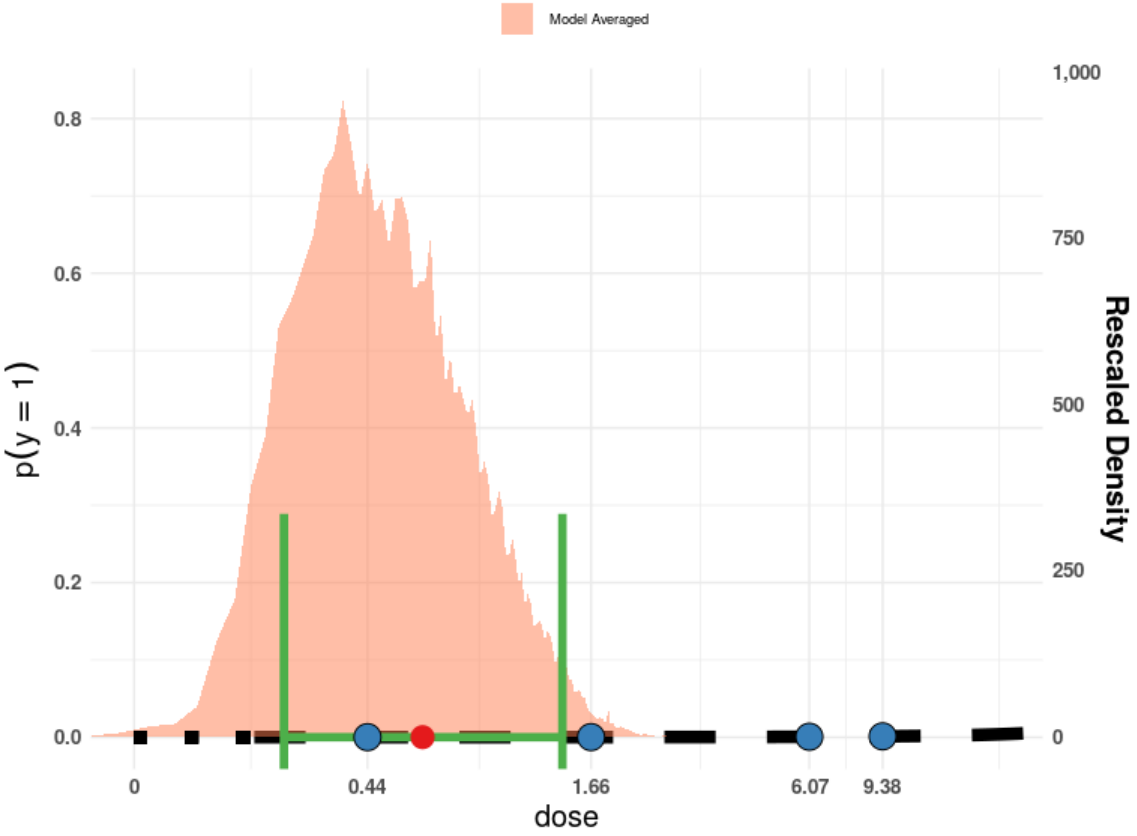
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.390	0.833	1.507	0.204	1
IE4_Q	0.619	1.200	2.049	0.014	1
H4_Q	0.404	0.833	1.534	0.203	1
LN4_Q	0.520	1.025	1.812	0.063	1
G4_Q	52.200	55.603	86.402	0.000	0
QE4_Q	0.245	0.447	0.814	0.443	1
P4_Q	0.208	0.491	0.998	0.040	1
L4_Q	0.199	0.471	0.955	0.033	1

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
p(y = 1)
0.8
0.6
0.4
0.2
0.0
1,000
750
500
250
0
Rescaled Density
0
0.44
1.66
6.07
9.38
dose

Steinmaus et al. (2013) bladder cancer, relative BMR 10%

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 2.131e-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 1.41e-03).

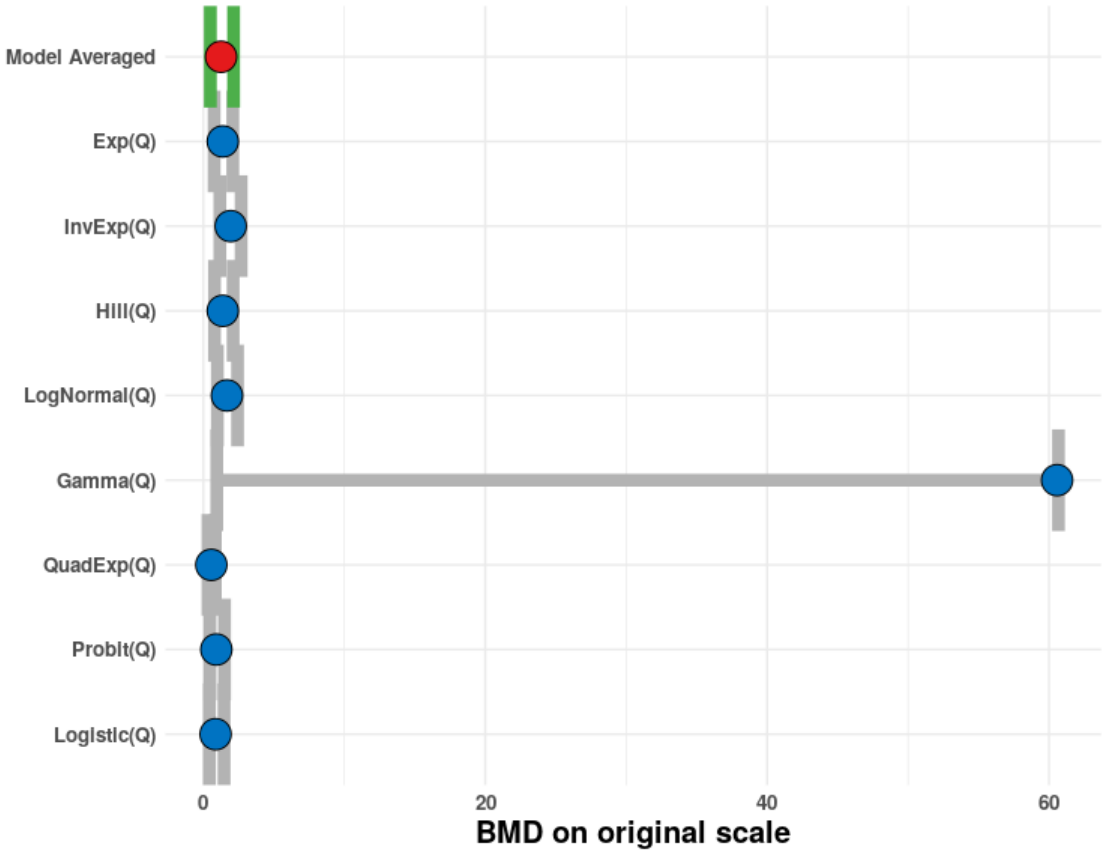
Model Averaged BMD

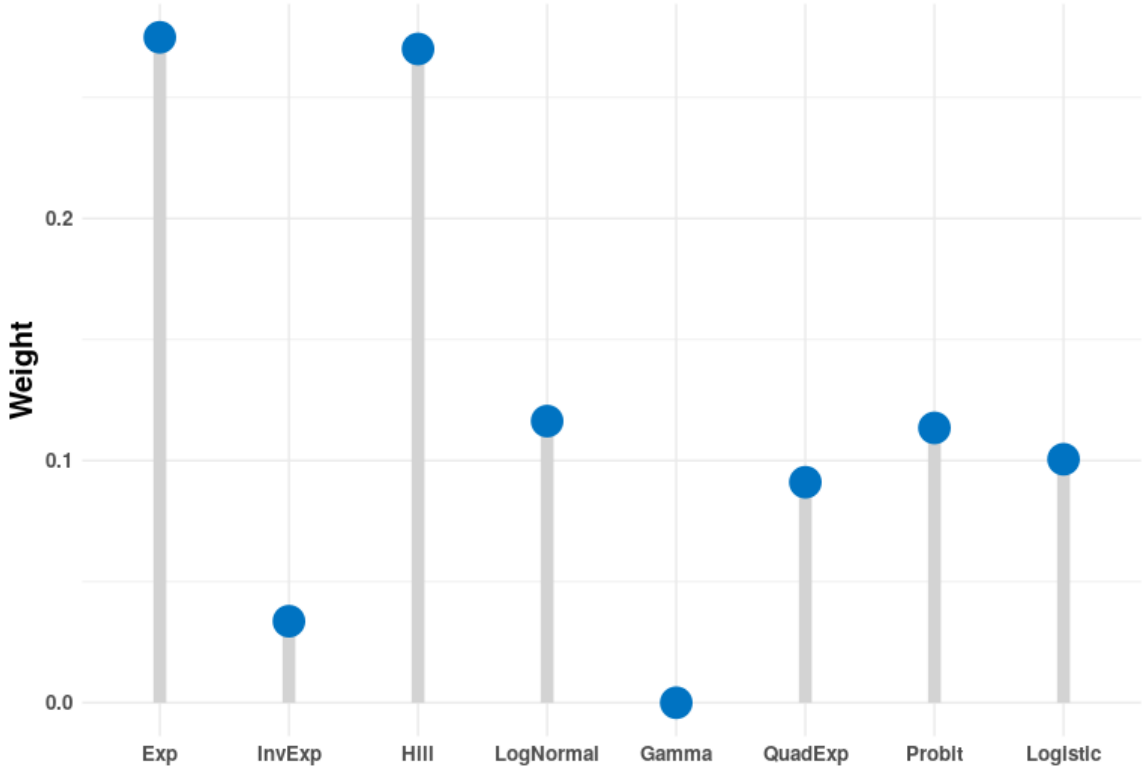
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.497	1.255	2.145

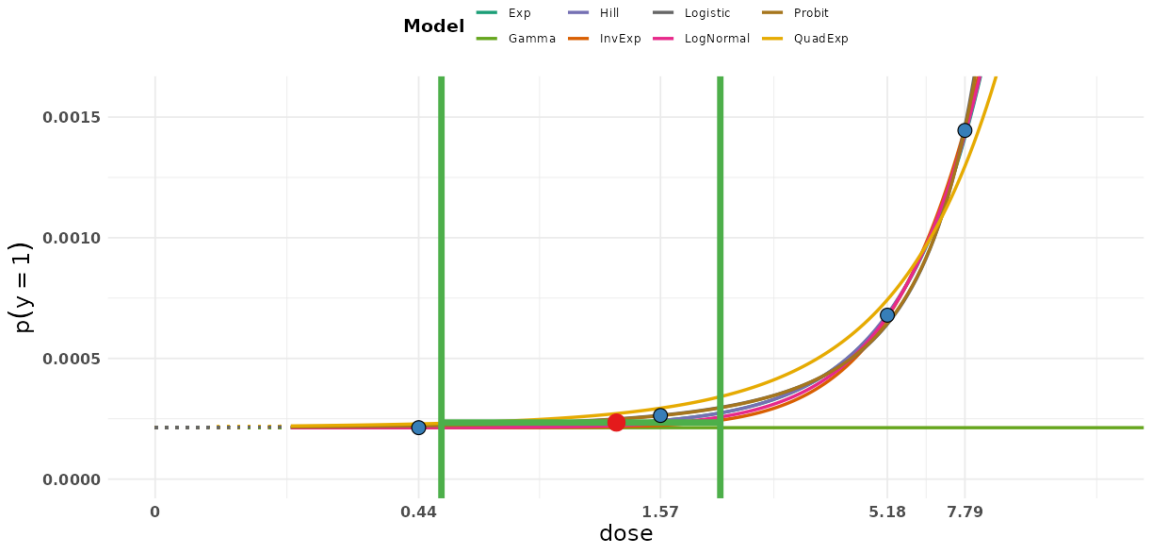
Estimated BMDs per model

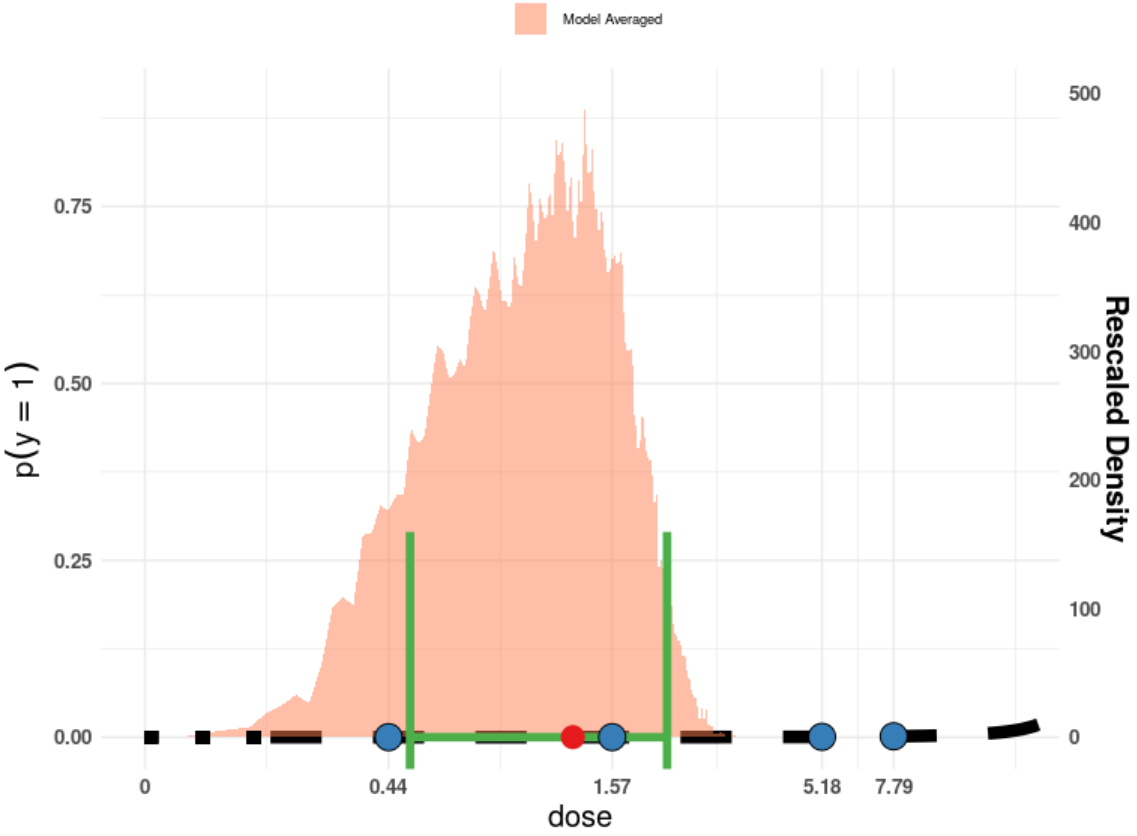
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.765	1.380	2.090	0.275	1
IE4_Q	1.172	1.940	2.682	0.034	1
H4_Q	0.789	1.378	2.111	0.270	1
LN4_Q	0.993	1.675	2.426	0.116	1
G4_Q	0.952	60.574	60.673	0.000	0
QE4_Q	0.329	0.566	0.848	0.091	1
P4_Q	0.470	0.920	1.502	0.114	1
L4_Q	0.436	0.867	1.471	0.101	1

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
0.44
1.57
5.18
7.79
dose


Model Averaged
p(y = 1)
0.00
0.25
0.50
0.75
Rescaled Density
0
100
200
300
400
500
0
0.44
1.57
5.18
7.79
dose

Steinmaus et al. (2013) lung cancer, relative BMR 10%

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 4.508e-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 1.71e-03).

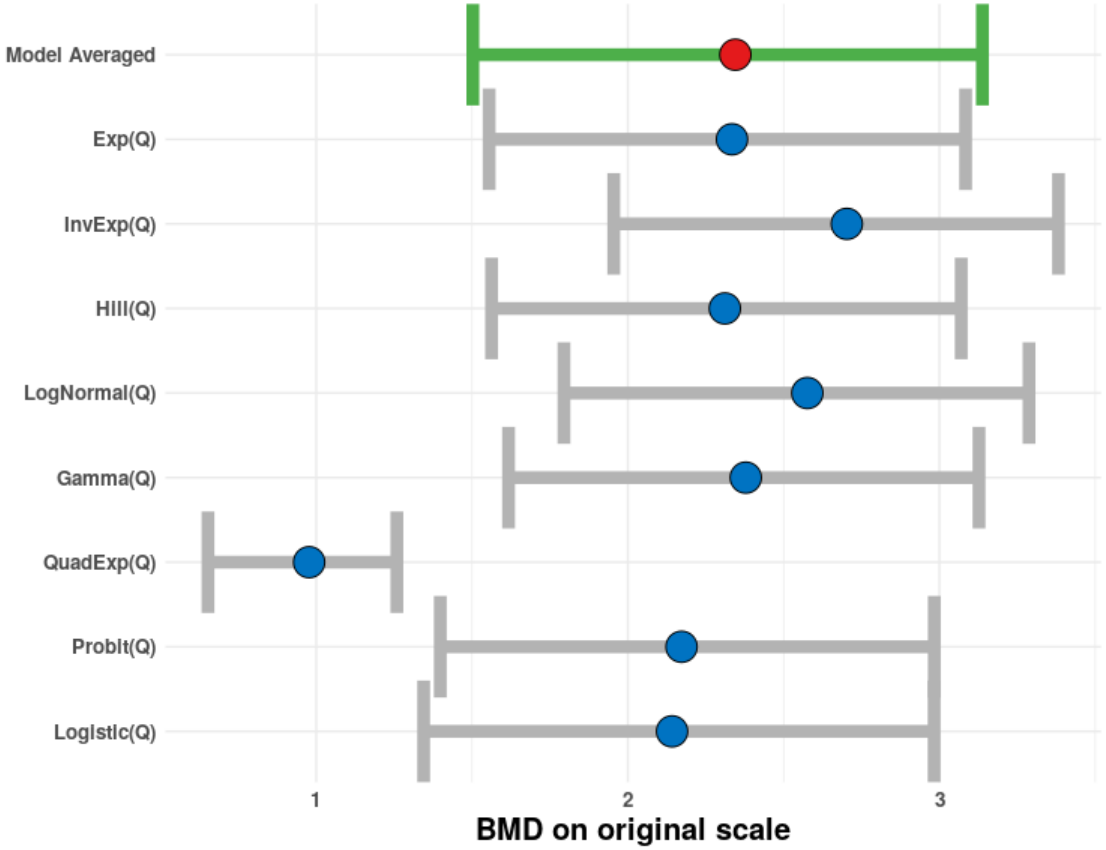
Model Averaged BMD

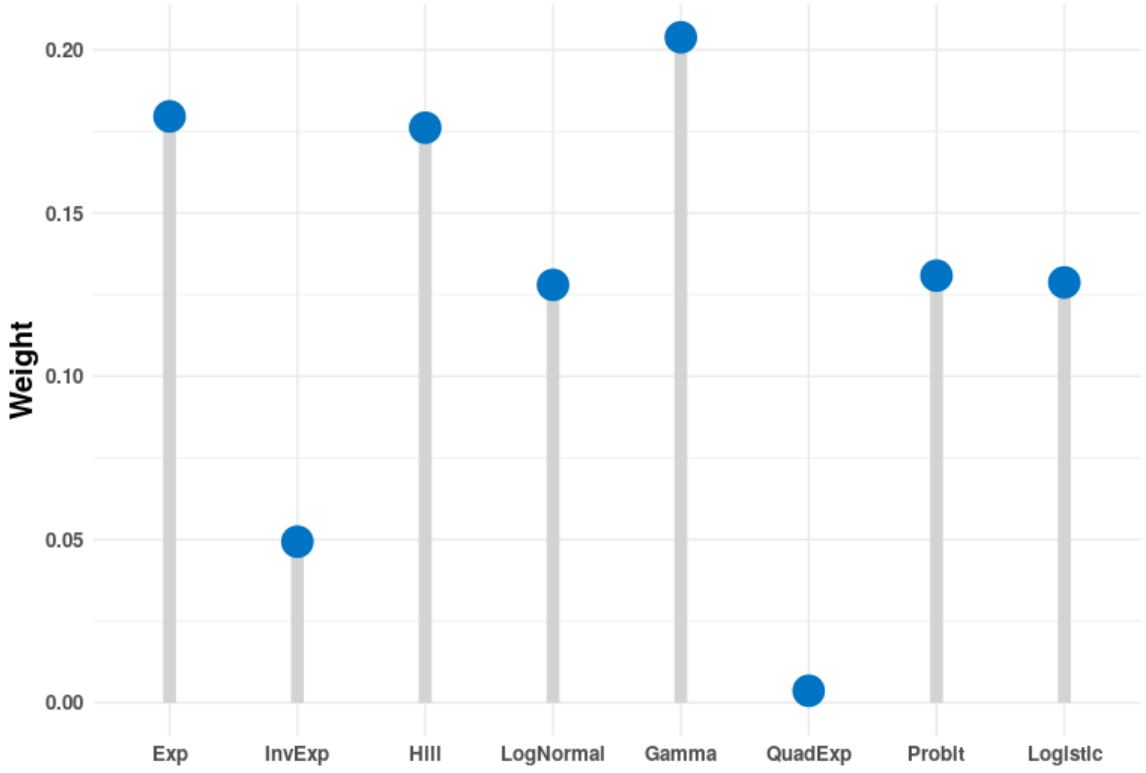
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	1.502	2.345	3.138

Estimated BMDs per model

Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	1.555	2.334	3.084	0.180	1
IE4_Q	1.955	2.703	3.382	0.049	1
H4_Q	1.563	2.311	3.070	0.176	1
LN4_Q	1.795	2.576	3.288	0.128	1
G4_Q	1.617	2.378	3.127	0.204	1
QE4_Q	0.652	0.977	1.259	0.004	1
P4_Q	1.398	2.172	2.984	0.131	1
L4_Q	1.345	2.142	2.983	0.129	1

Plots of Fitted Models




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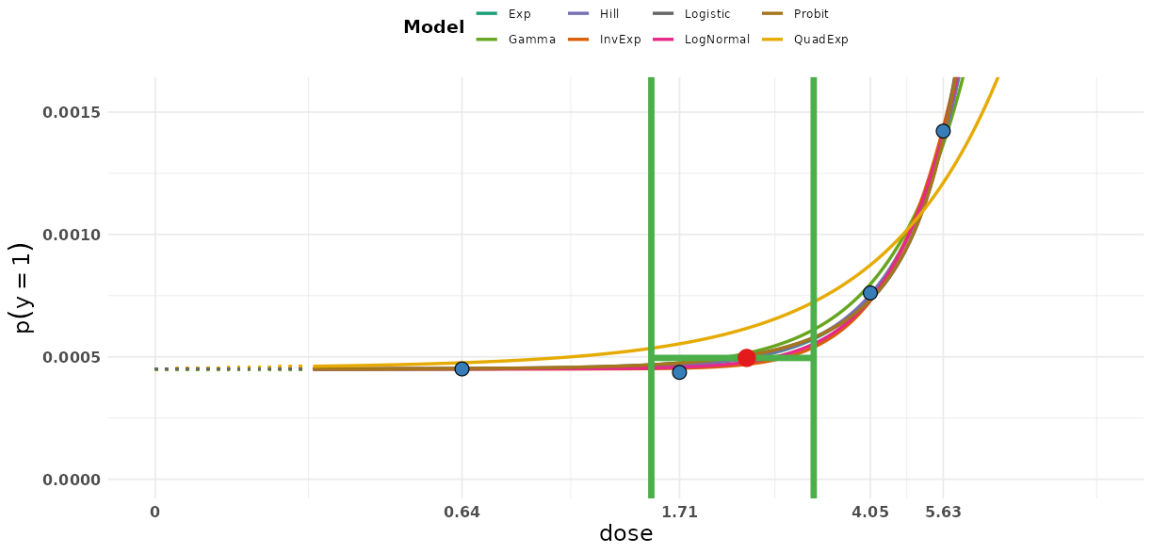
0.10
0.05
0.00
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


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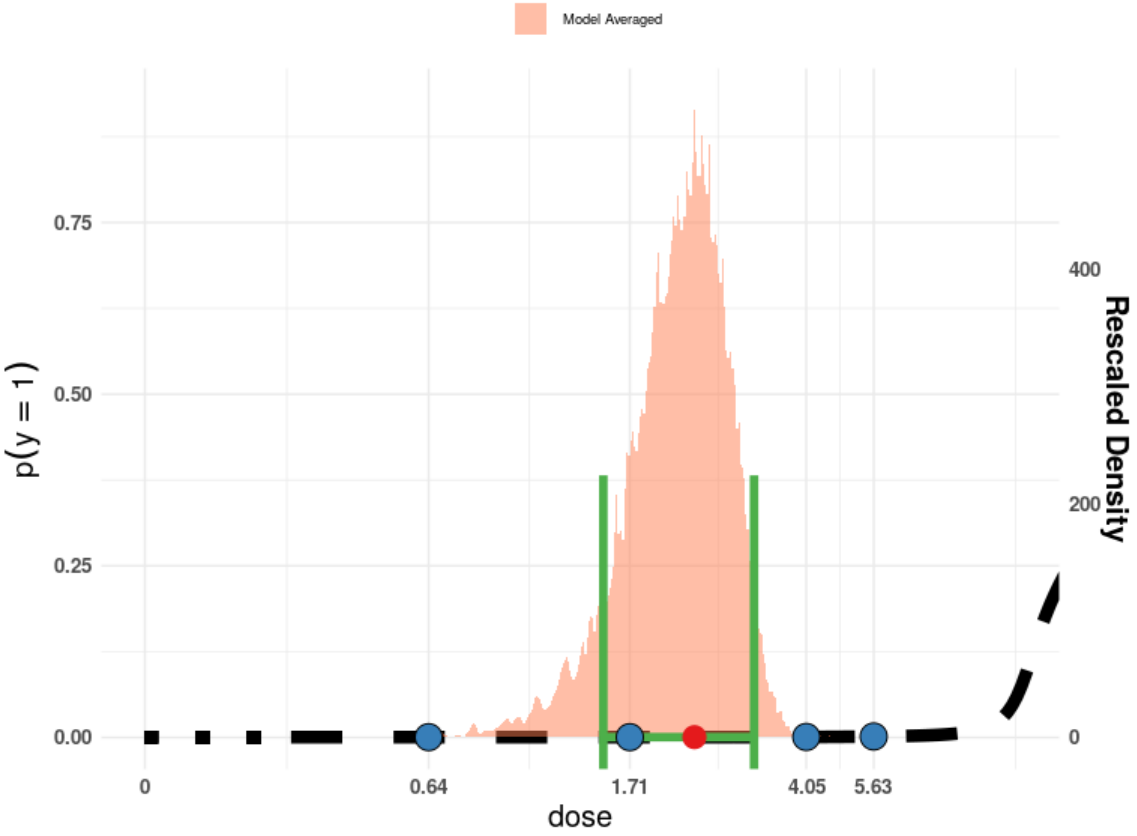
0.0010
0.0005
0.0000
0
0.64
1.71
4.05
5.63
dose


Model Averaged
0.75
0.50
0.25
0.00
p(y = 1)
400
200
0
Rescaled Density
0
0.64
1.71
4.05
5.63
dose

Steinmaus et al. (2013) lung cancer, relative BMR 10%

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 5.056e-05.

Extended dose range is applied.

Informative background prior: min: 0.00050030; the most likely: 0.00050536; max: 0.00051041. 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 3.08e-03).

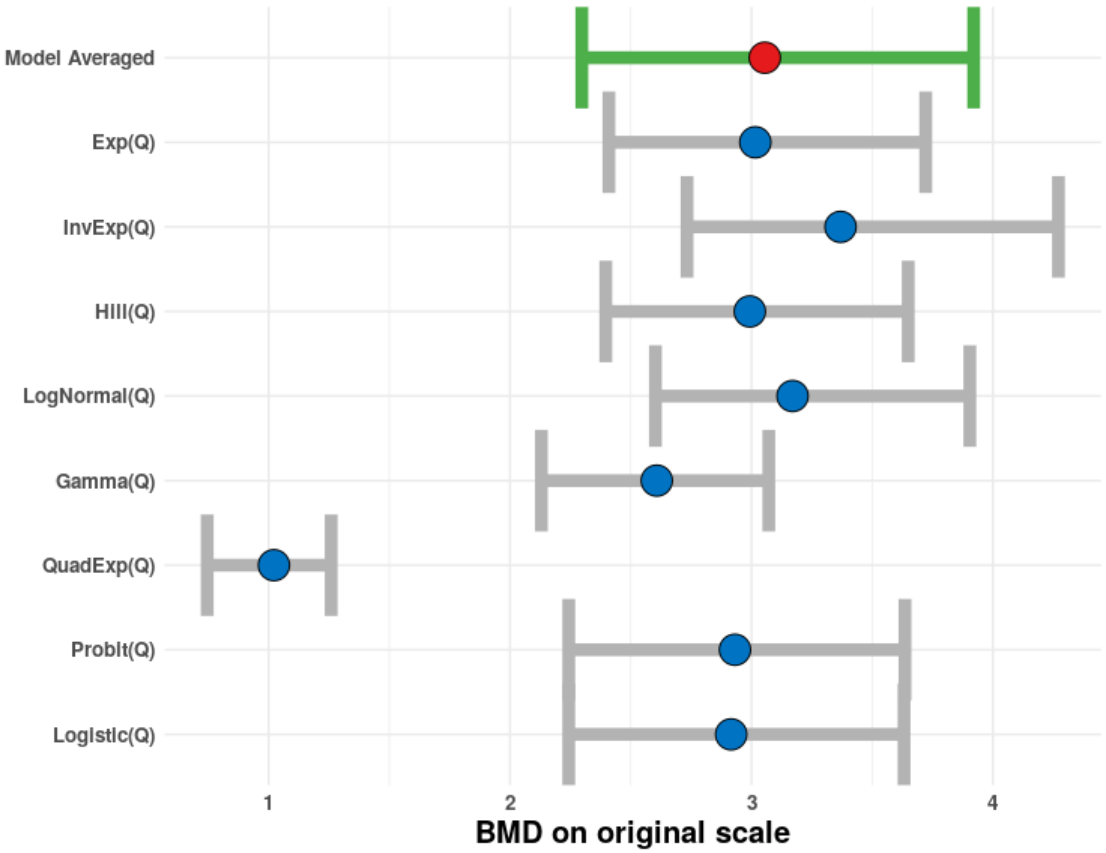
Model Averaged BMD

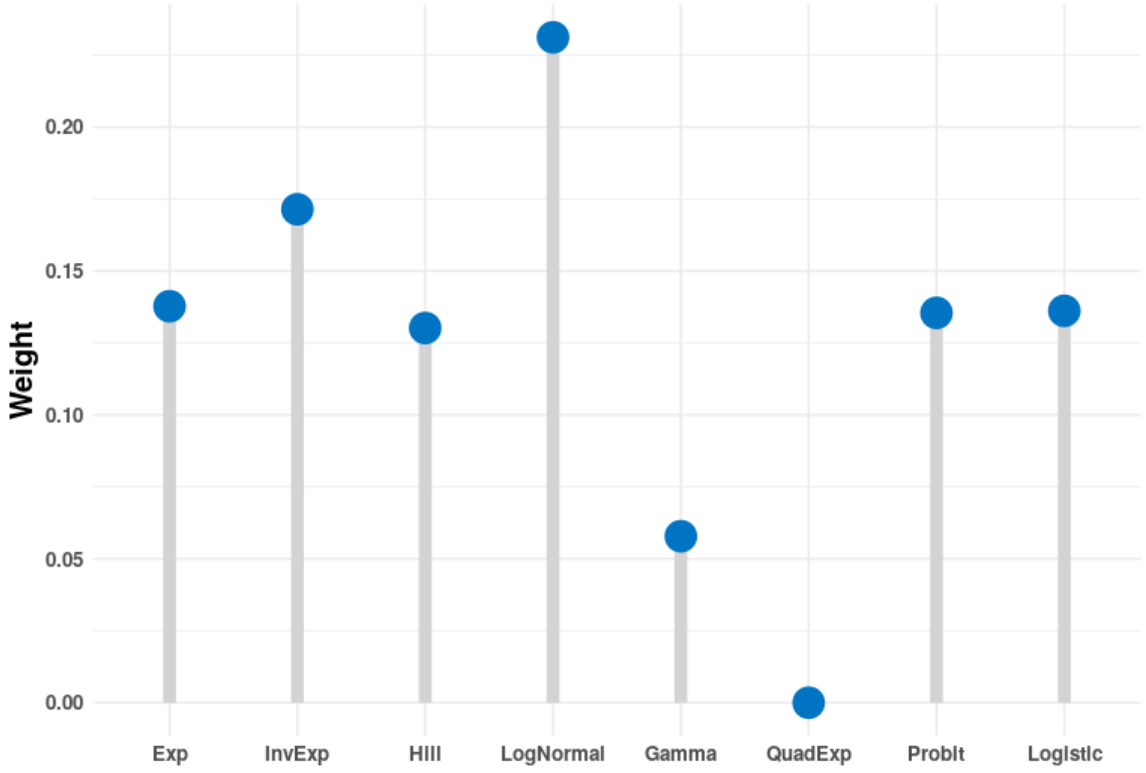
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	2.297	3.055	3.921

Estimated BMDs per model

Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	2.410	3.016	3.722	0.138	1
IE4_Q	2.733	3.369	4.272	0.171	1
H4_Q	2.397	2.993	3.649	0.130	1
LN4_Q	2.602	3.170	3.905	0.231	1
G4_Q	2.130	2.608	3.072	0.058	0
QE4_Q	0.746	1.022	1.259	0.000	1
P4_Q	2.243	2.932	3.636	0.135	1
L4_Q	2.243	2.916	3.632	0.136	1

Plots of Fitted Models




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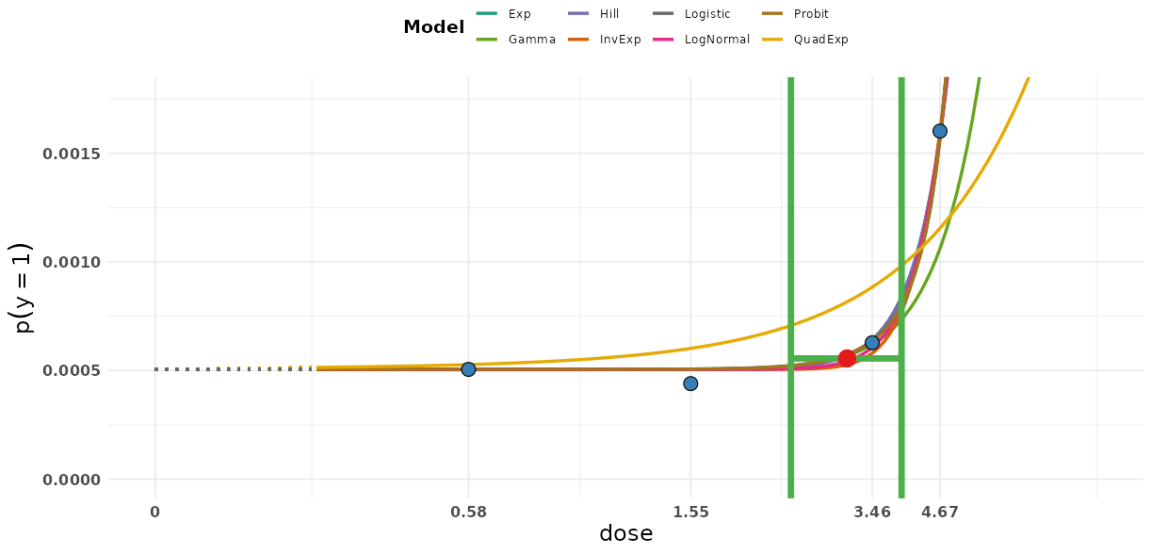
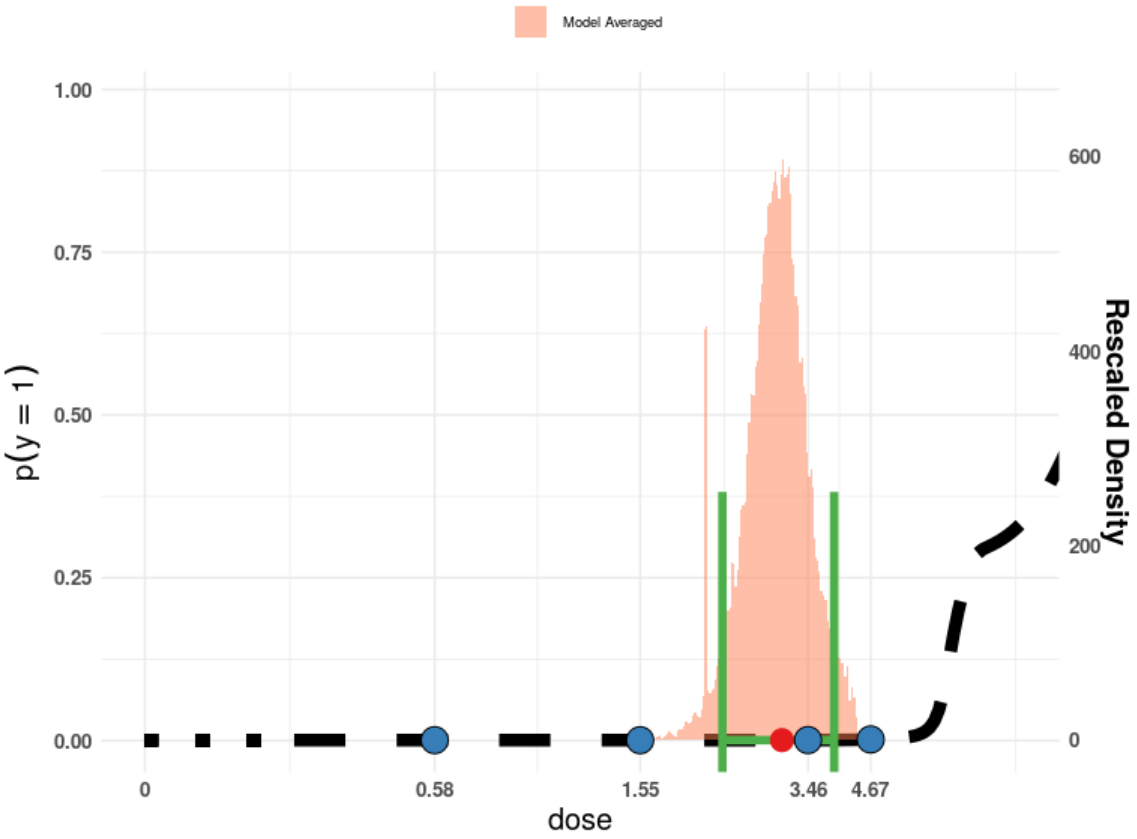
0.15
0.10
0.05
0.00
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
p(y = 1)
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)
600
400
200
0
Rescaled Density
0
0.58
1.55
3.46
4.67
dose

Steinmaus et al. (2013) lung cancer, relative BMR 10%

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 3.623e-05.

Extended dose range is applied.

Informative background prior: min: 0.00035859; the most likely: 0.00036221; max: 0.00036583. 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 3.40e-03).

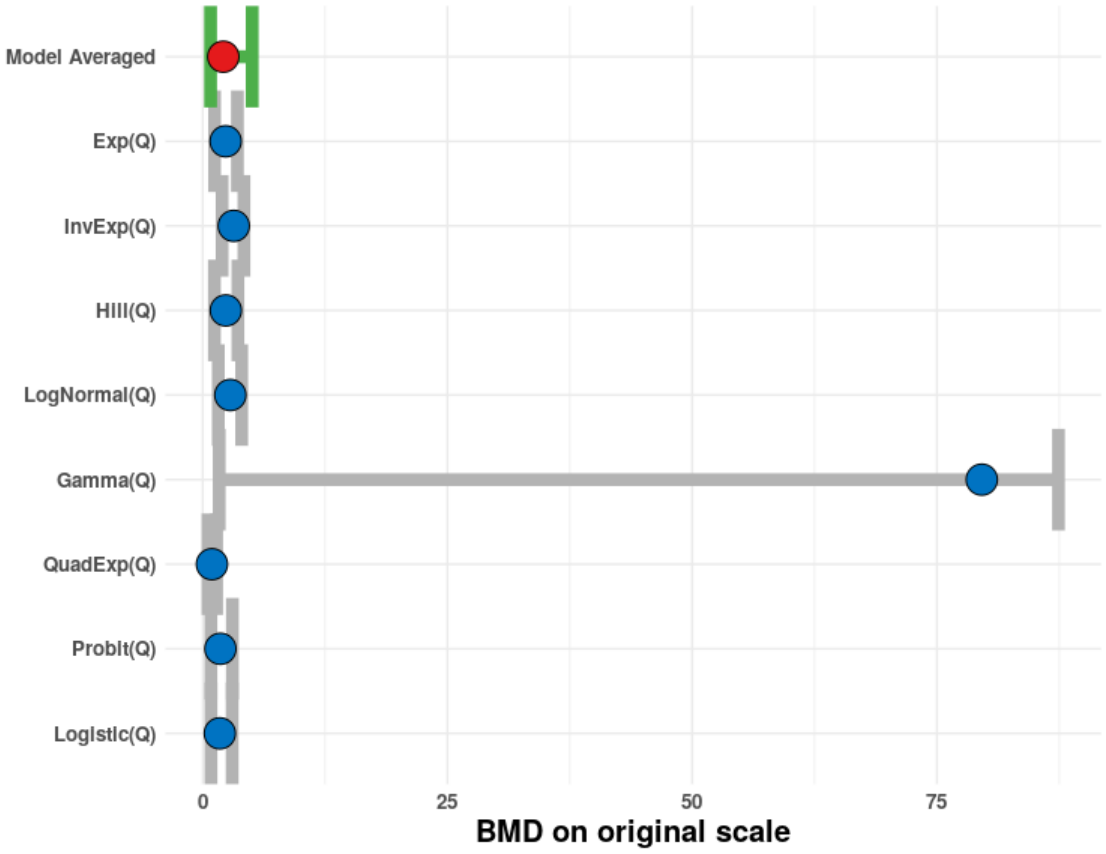
Model Averaged BMD

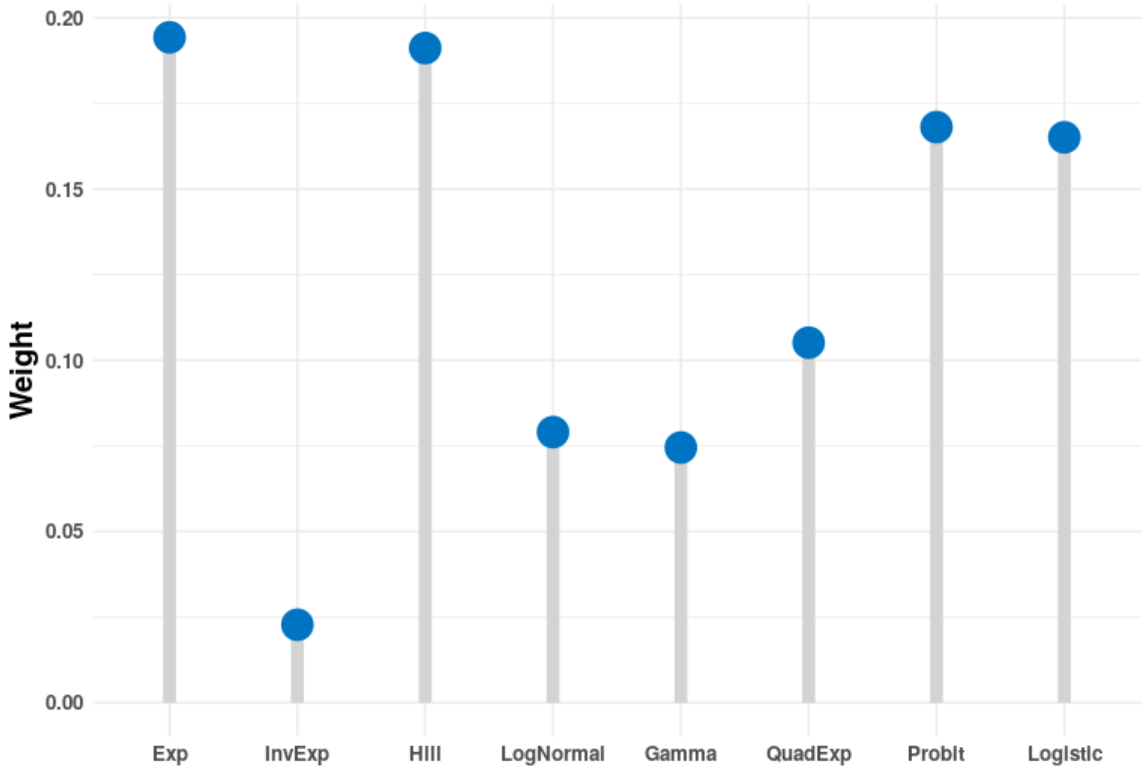
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.801	2.102	5.055

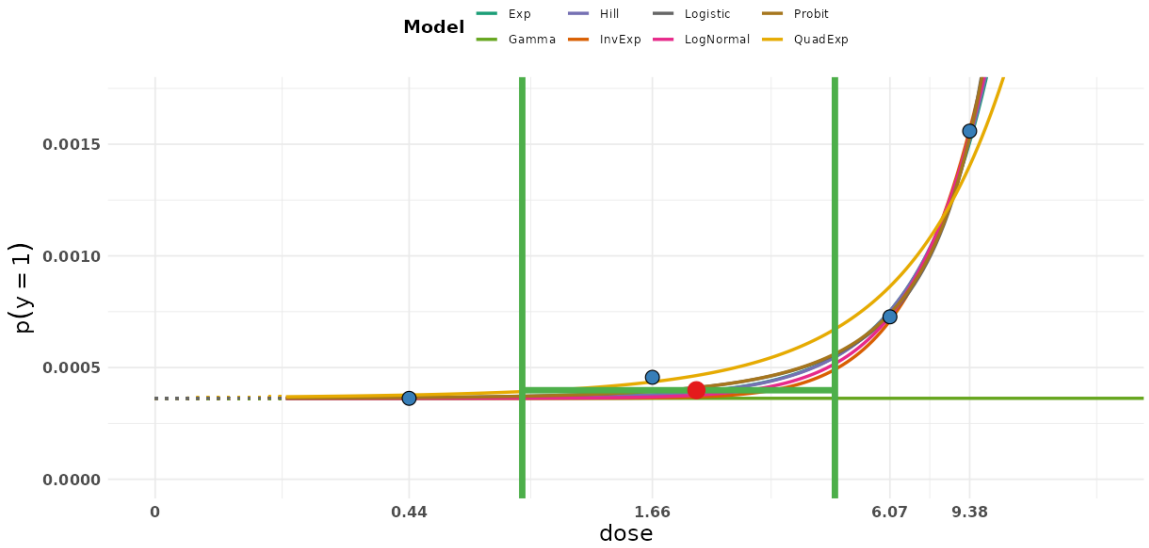
Estimated BMDs per model

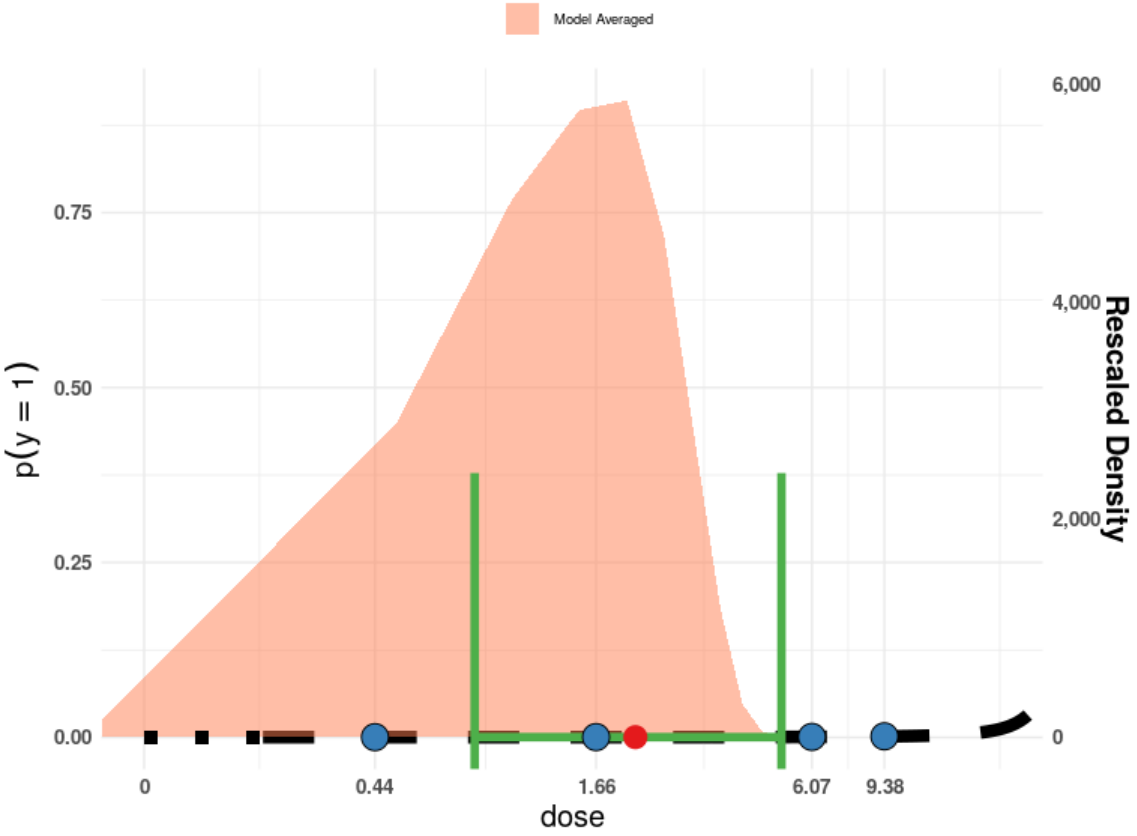
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	1.211	2.343	3.547	0.194	1
IE4_Q	1.980	3.170	4.212	0.023	1
H4_Q	1.194	2.362	3.597	0.191	1
LN4_Q	1.594	2.821	3.980	0.079	1
G4_Q	1.685	79.583	87.418	0.075	0
QE4_Q	0.539	0.944	1.420	0.105	1
P4_Q	0.836	1.809	3.031	0.168	1
L4_Q	0.843	1.747	3.009	0.165	1

Plots of Fitted Models




0.20
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
0.0015
0.0010
0.0005
0.0000
p(y = 1)
0
0.44
1.66
6.07
9.38
dose


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

Steinmaus et al. (2013) lung cancer, relative BMR 10%

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 3.837e-05.

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 2.55e-03).

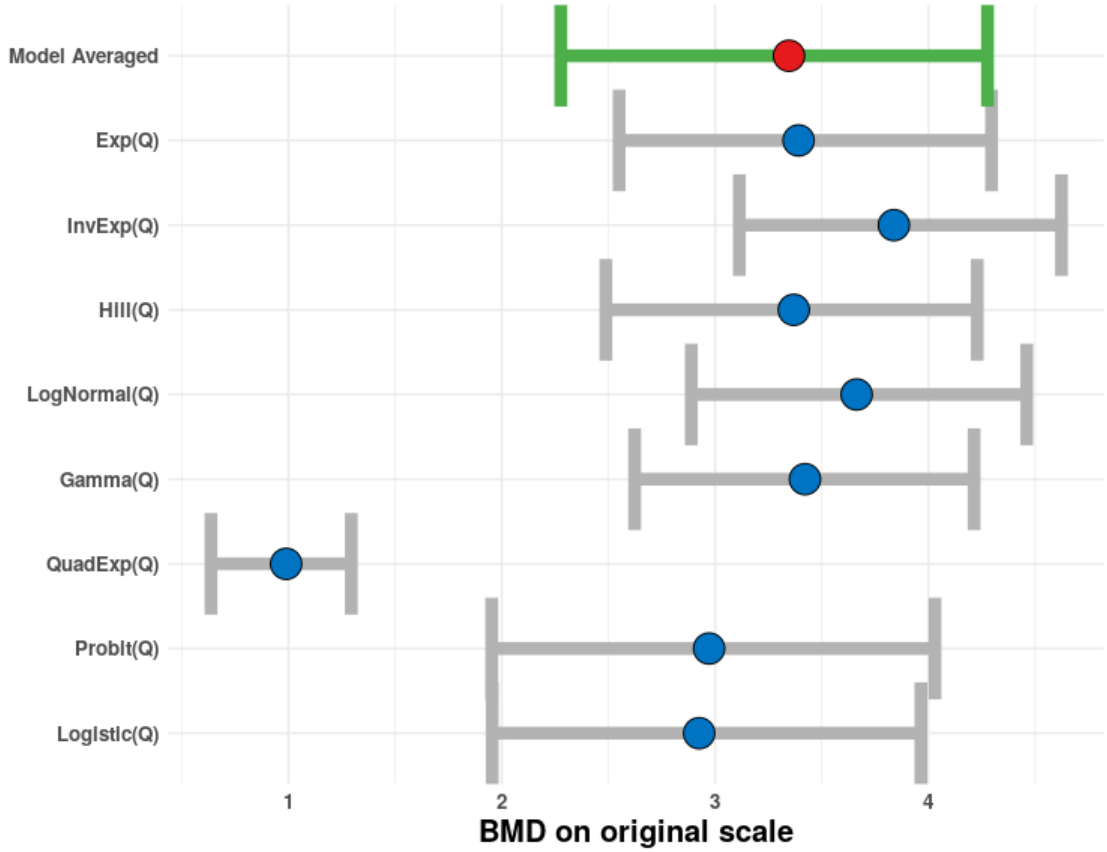
Model Averaged BMD

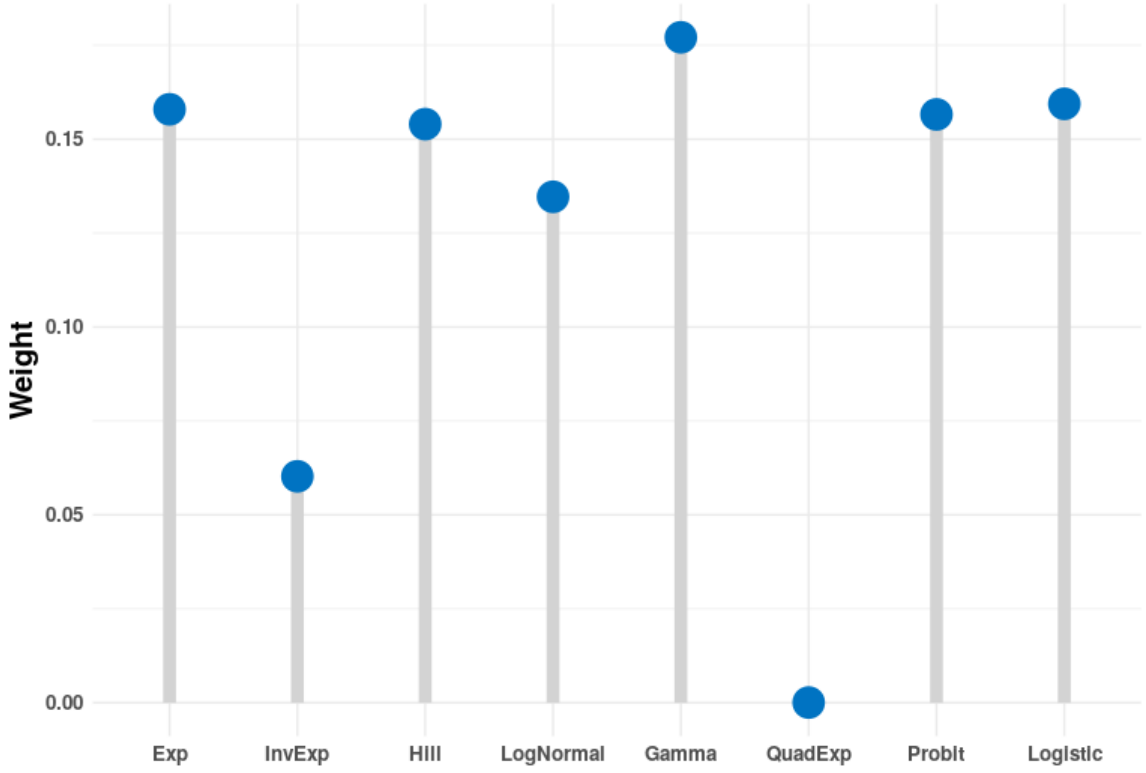
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	2.277	3.346	4.276

Estimated BMDs per model

Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	2.550	3.391	4.295	0.158	1
IE4_Q	3.113	3.838	4.623	0.060	1
H4_Q	2.488	3.368	4.228	0.154	1
LN4_Q	2.888	3.663	4.460	0.135	1
G4_Q	2.623	3.421	4.214	0.177	1
QE4_Q	0.637	0.989	1.295	0.000	1
P4_Q	1.953	2.971	4.030	0.157	1
L4_Q	1.955	2.925	3.964	0.159	1

Plots of Fitted Models




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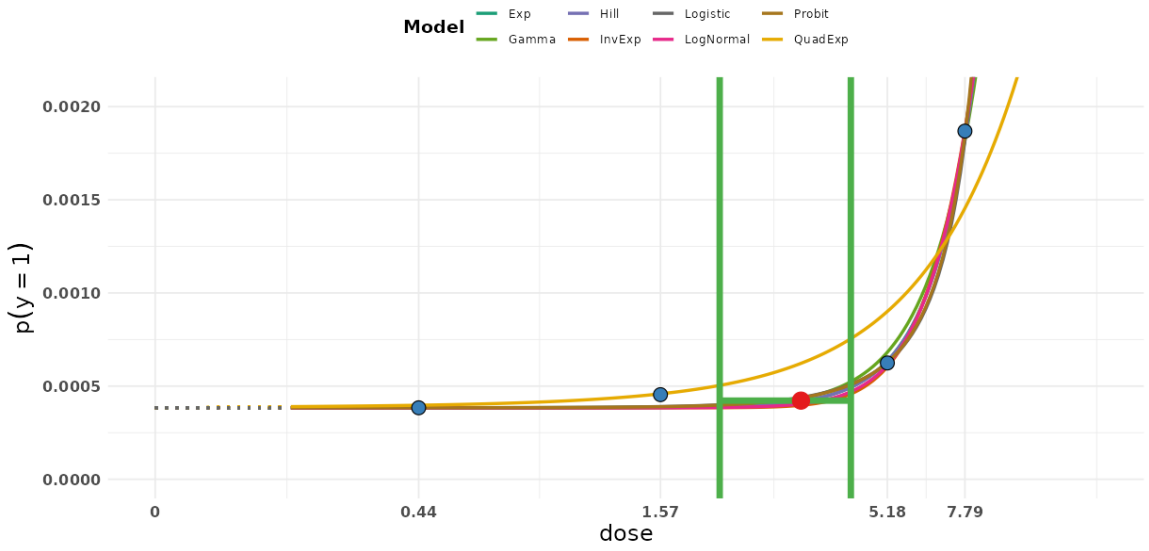
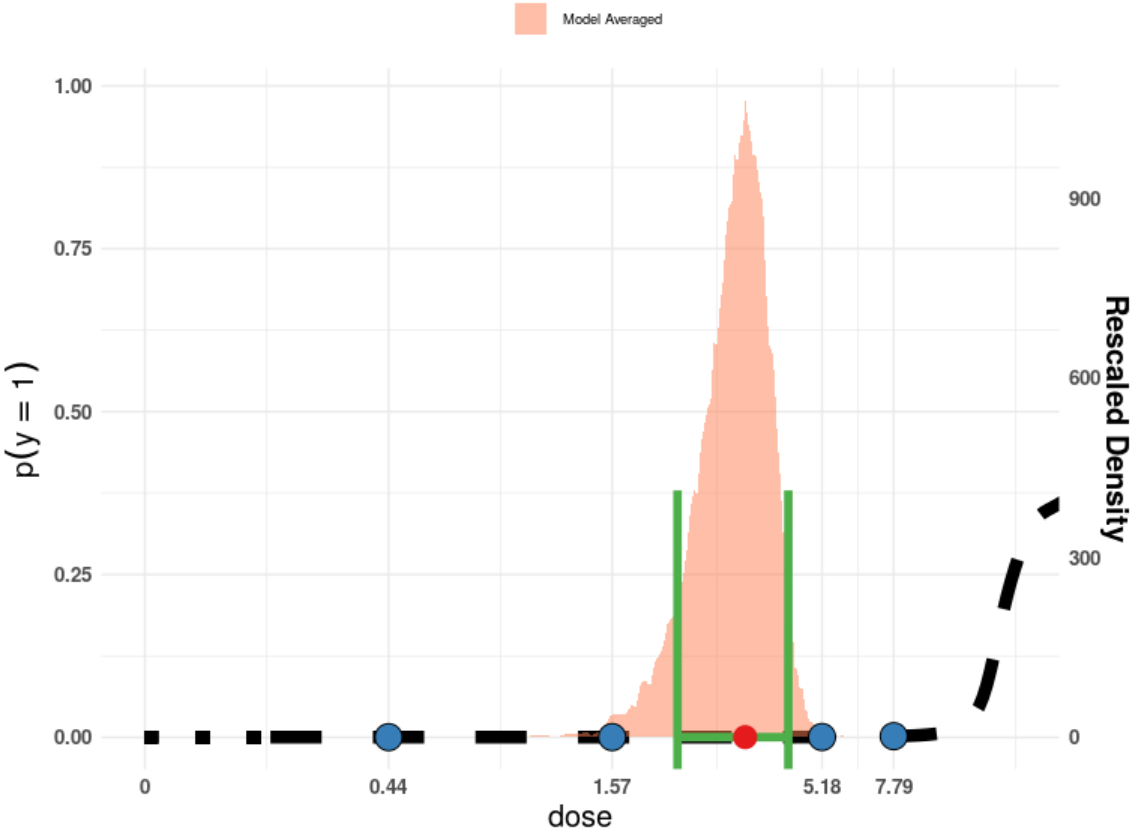
0.10
0.05
0.00
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Model
Exp
Hill
Logistic
Probit
Gamma
InvExp
LogNormal
QuadExp
p(y = 1)
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)
900
600
300
0
Rescaled Density
0
0.44
1.57
5.18
7.79
dose

Steinmaus et al. (2014a) lung cancer, relative BMR 10%

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 3.356e-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 1.40e+00).

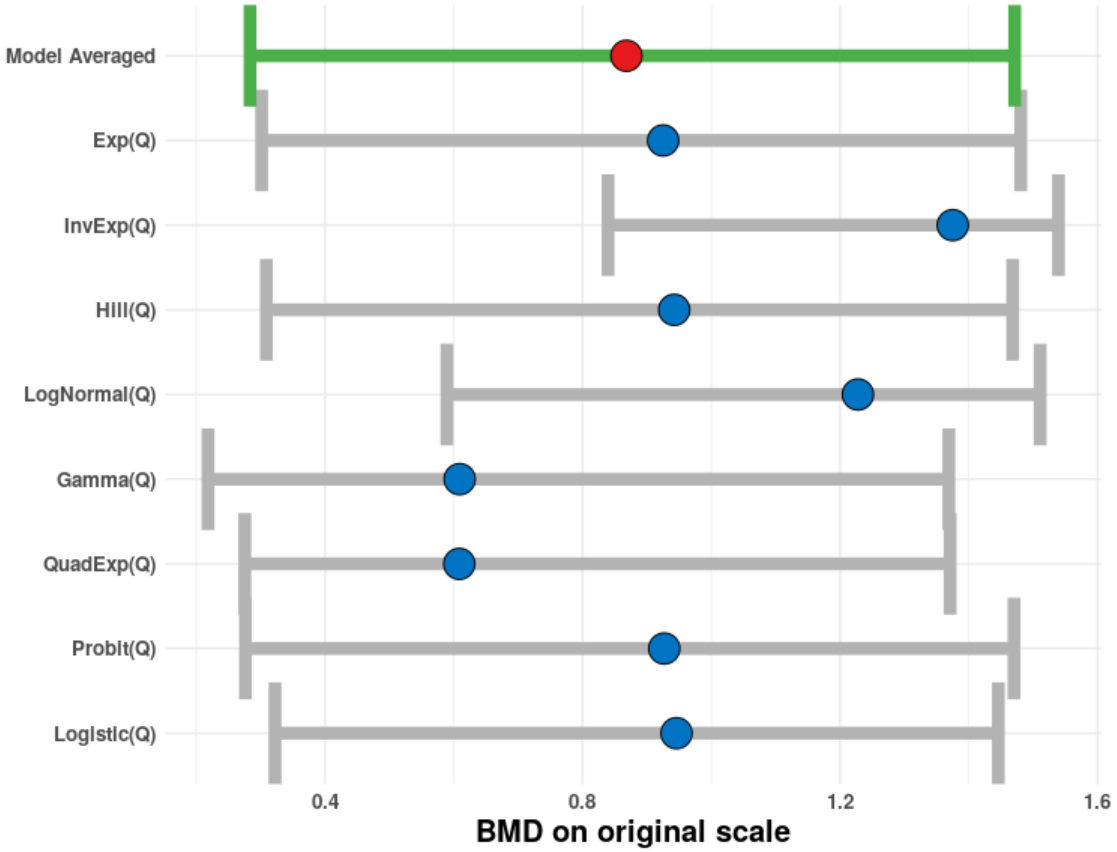
Model Averaged BMD

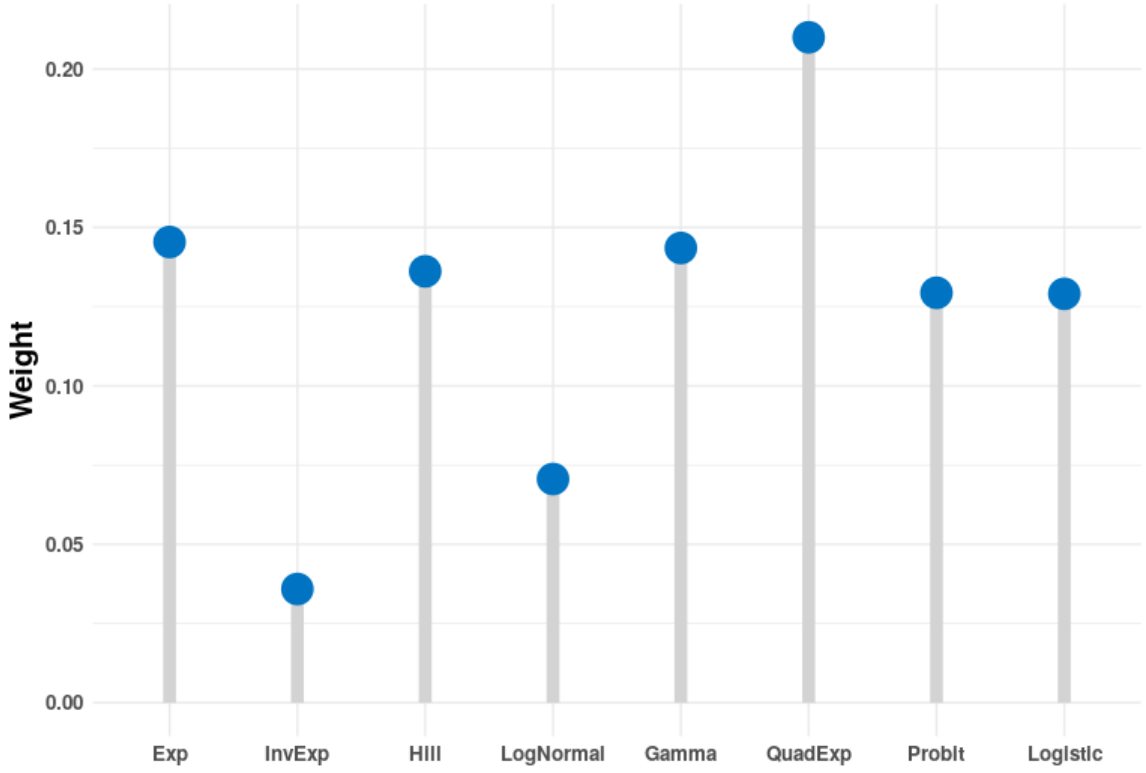
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.284	0.868	1.471

Estimated BMDs per model

Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.302	0.925	1.481	0.145	1
IE4_Q	0.840	1.375	1.539	0.036	1
H4_Q	0.309	0.942	1.468	0.136	1
LN4_Q	0.589	1.228	1.511	0.071	1
G4_Q	0.218	0.609	1.369	0.144	0
QE4_Q	0.275	0.609	1.371	0.210	1
P4_Q	0.277	0.927	1.470	0.129	1
L4_Q	0.322	0.946	1.446	0.129	1

Plots of Fitted Models




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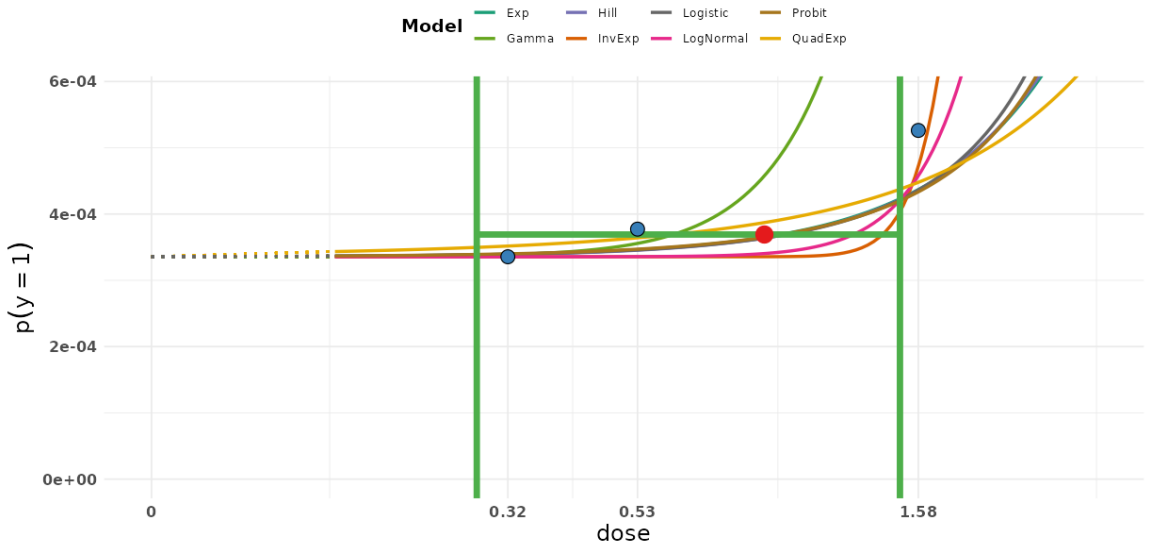
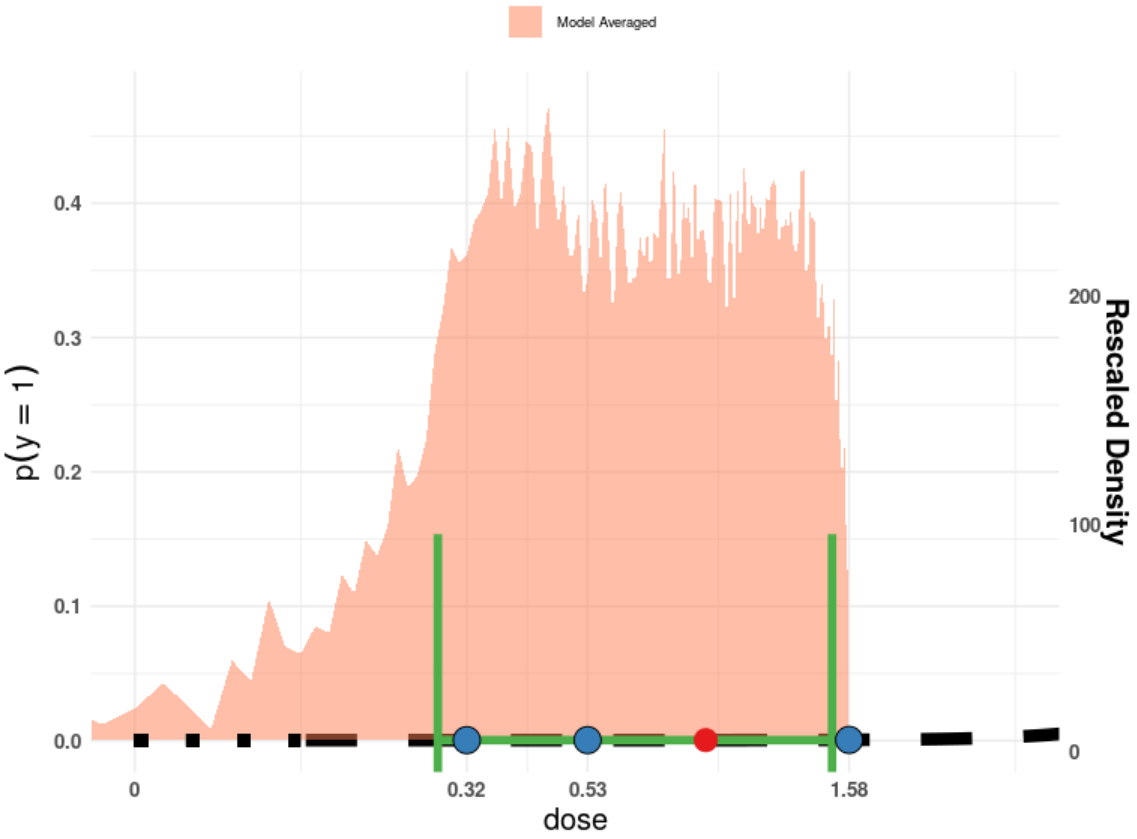
0.15
0.10
0.05
0.00
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


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


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

Steinmaus et al. (2014a) lung cancer, relative BMR 10%

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 3.138e-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 1.37e+00).

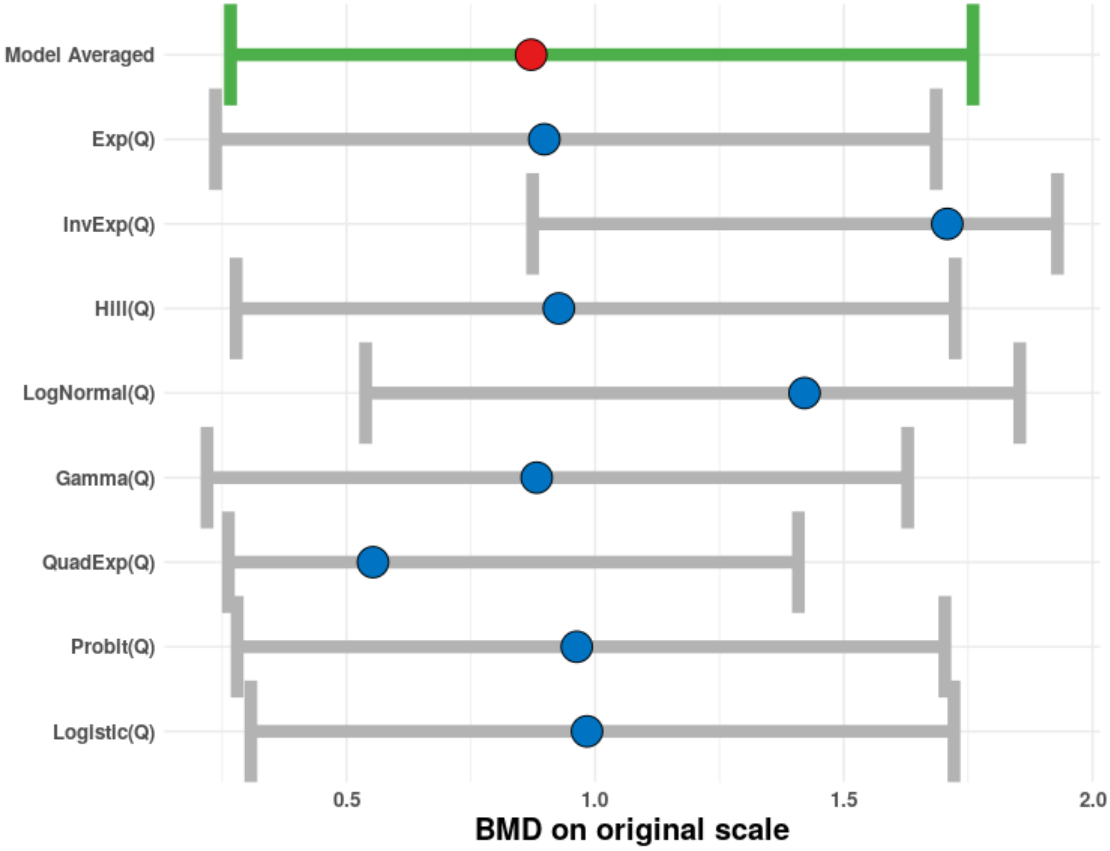
Model Averaged BMD

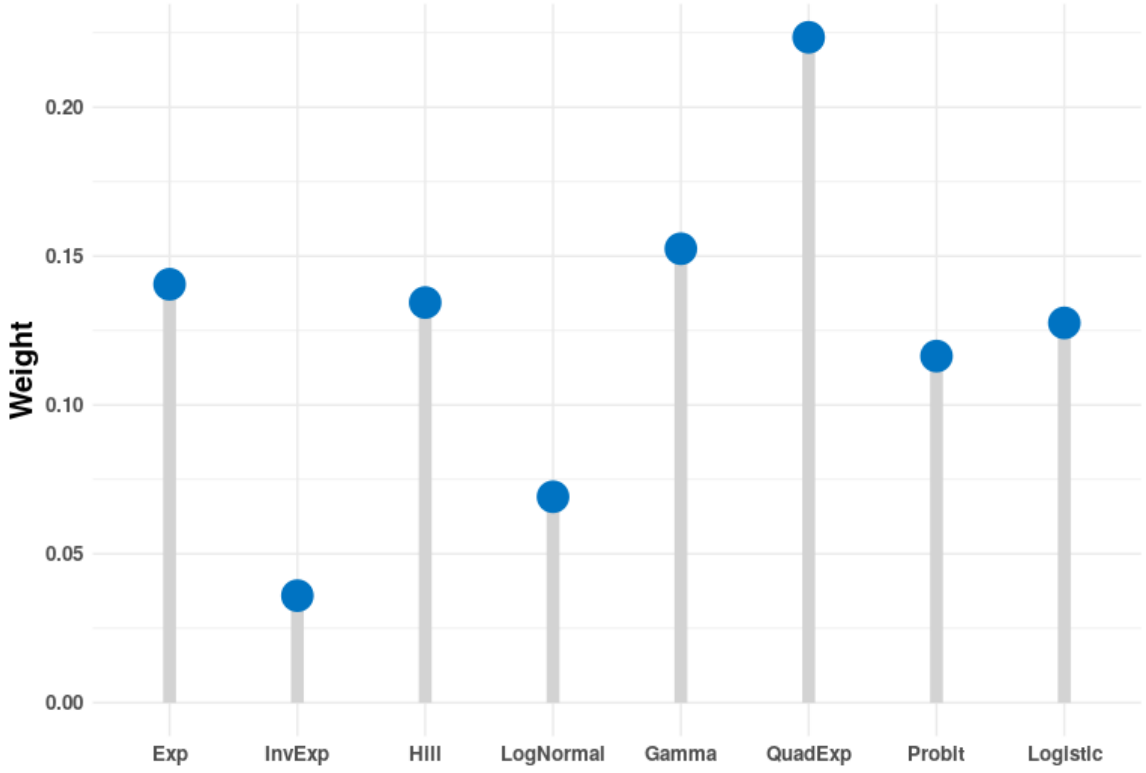
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.267	0.871	1.76

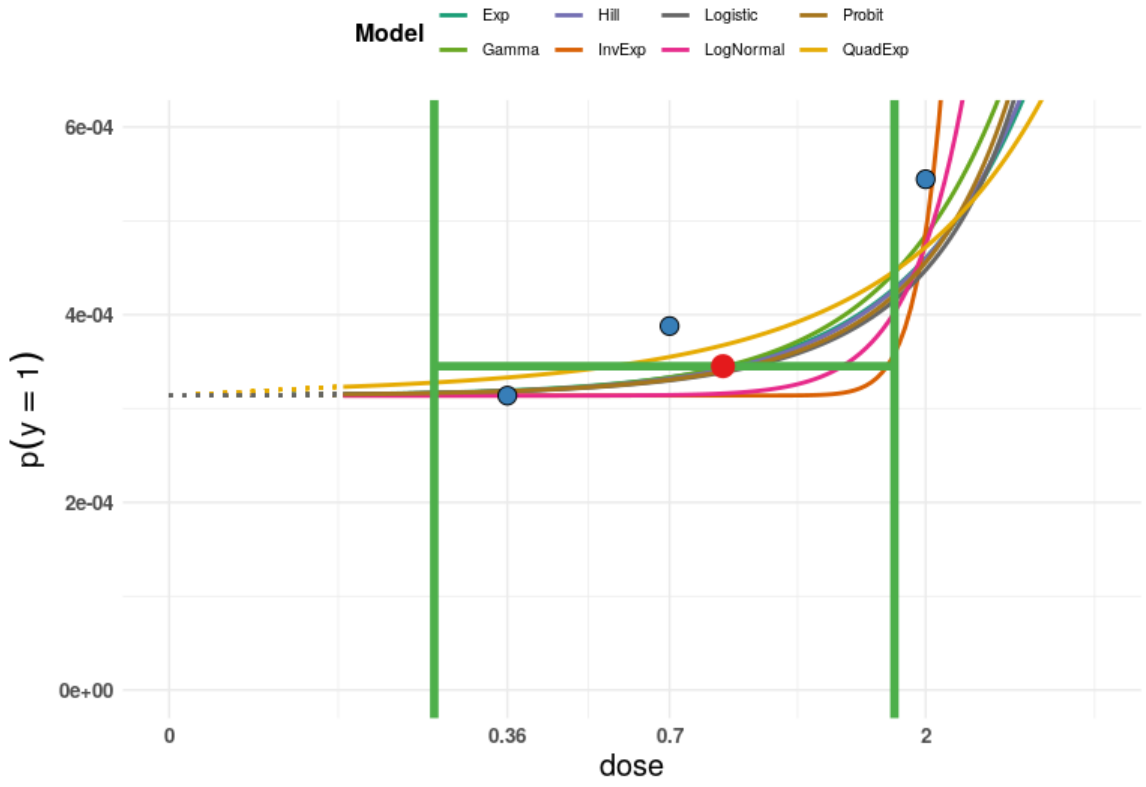
Estimated BMDs per model

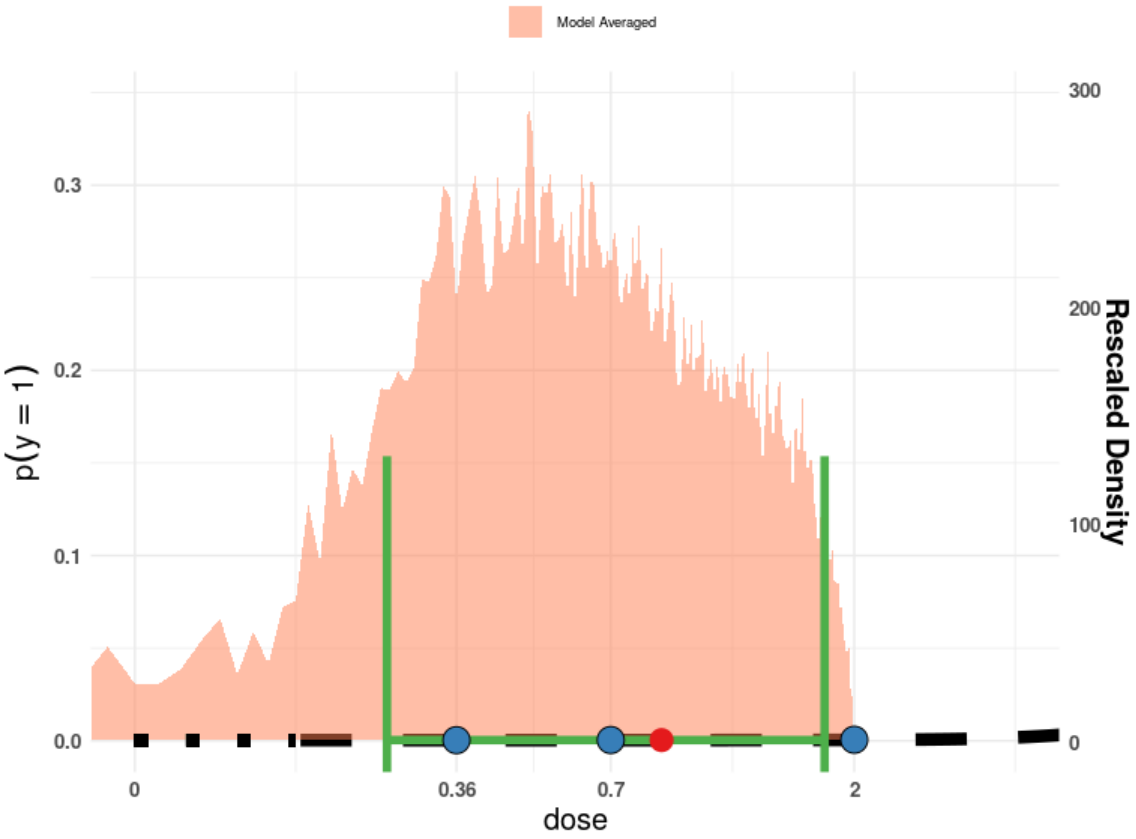
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.237	0.898	1.686	0.141	1
IE4_Q	0.874	1.708	1.930	0.036	1
H4_Q	0.278	0.927	1.724	0.134	1
LN4_Q	0.539	1.421	1.854	0.069	1
G4_Q	0.219	0.882	1.629	0.152	1
QE4_Q	0.262	0.553	1.409	0.223	1
P4_Q	0.280	0.963	1.703	0.116	1
L4_Q	0.308	0.984	1.722	0.128	1

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)
6e-04
4e-04
2e-04
0e+00
0
0.36
0.7
2
dose


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

Steinmaus et al. (2014a) lung cancer, relative BMR 10%

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 2.859e-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 1.89e+00).

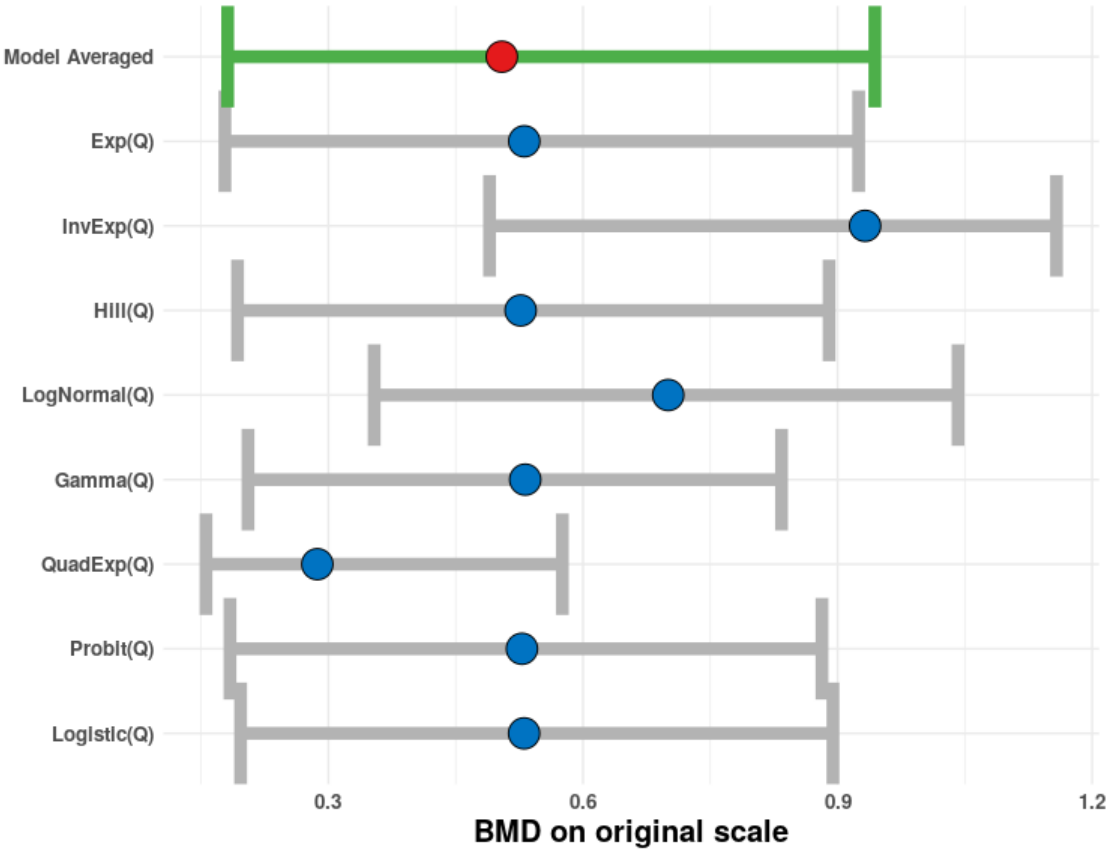
Model Averaged BMD

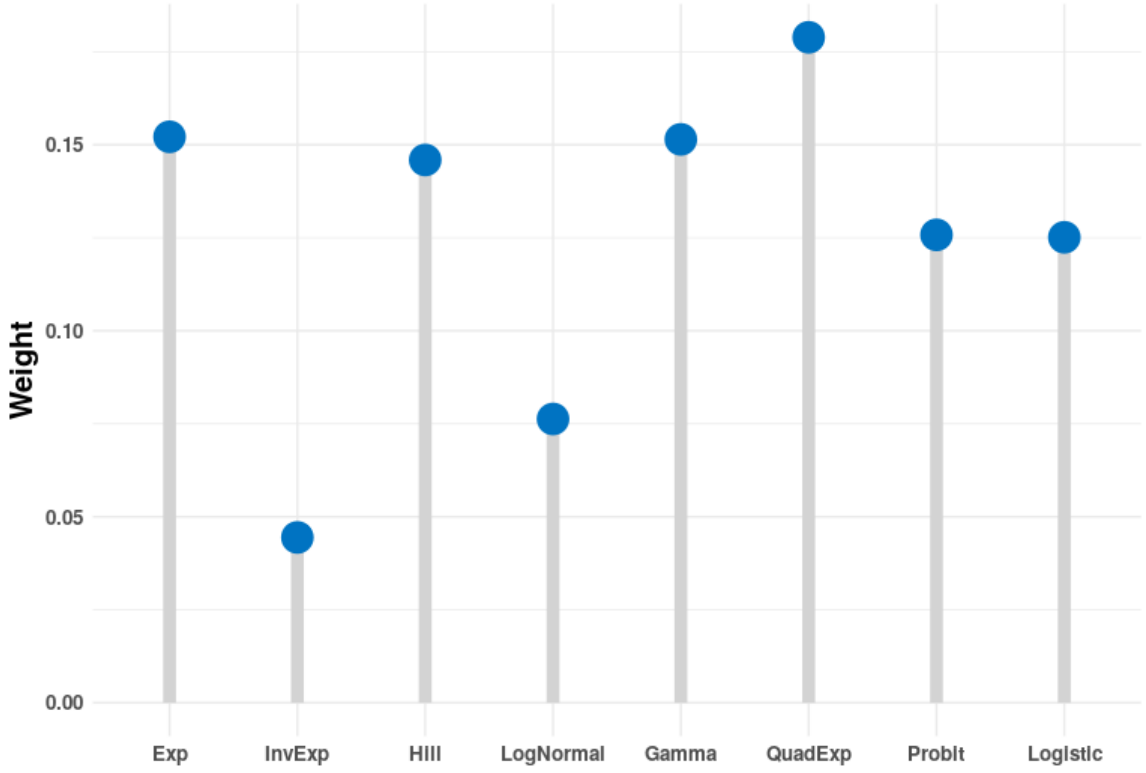
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.181	0.504	0.944

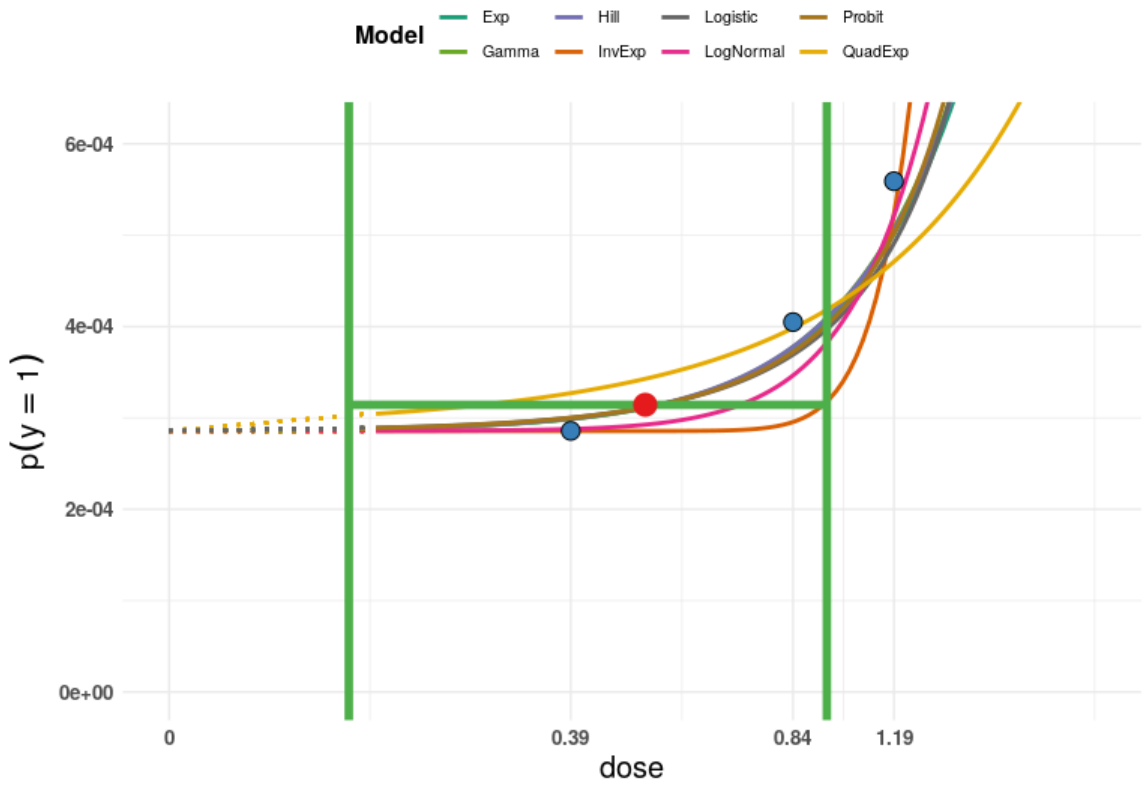
Estimated BMDs per model

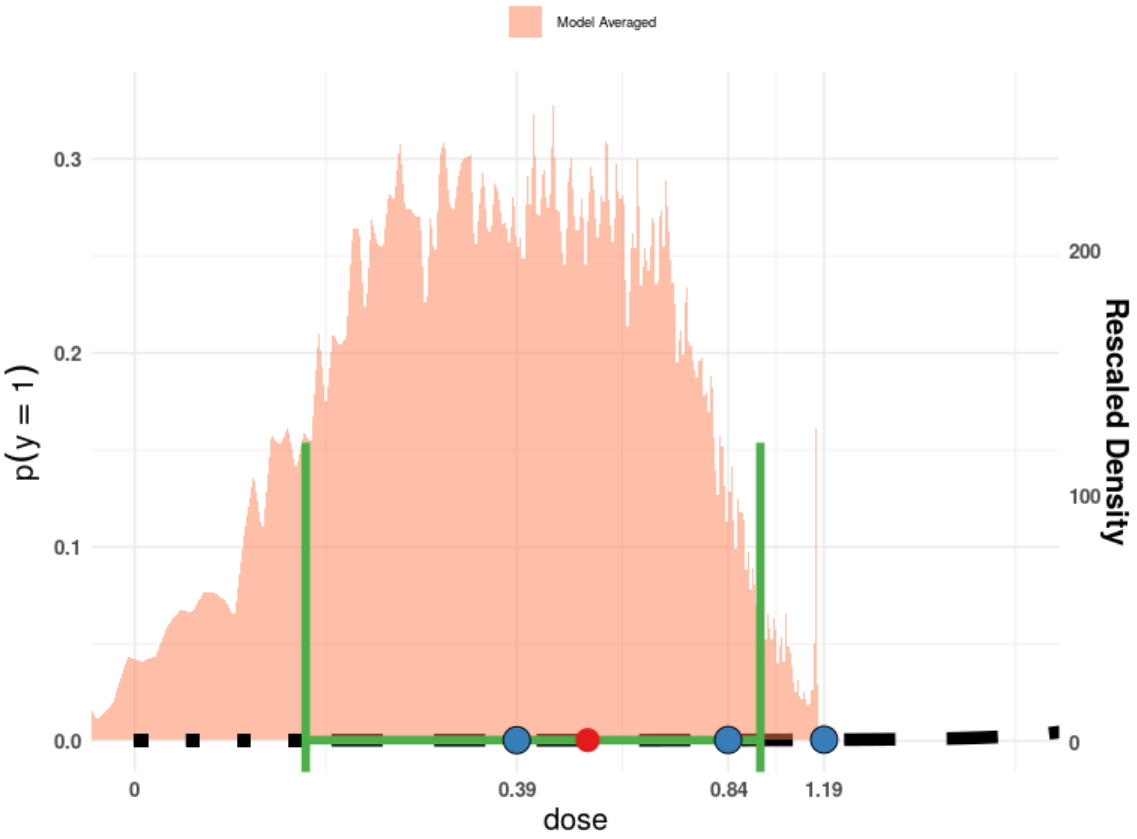
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.178	0.531	0.925	0.152	0
IE4_Q	0.490	0.932	1.158	0.044	1
H4_Q	0.193	0.527	0.890	0.146	1
LN4_Q	0.354	0.700	1.042	0.076	1
G4_Q	0.205	0.532	0.834	0.151	1
QE4_Q	0.156	0.287	0.576	0.179	1
P4_Q	0.184	0.528	0.882	0.126	1
L4_Q	0.197	0.531	0.895	0.125	1

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
0.39
0.84
1.19
dose


Model Averaged
0.3
0.2
0.1
0.0
p(y = 1)
200
100
0
Rescaled Density
0
0.39
0.84
1.19
dose

Vahter et al. (2020) full developmental score, mothers u-tiAs at GW 8, BMR 10%

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 0.1.

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 1.83e+00).

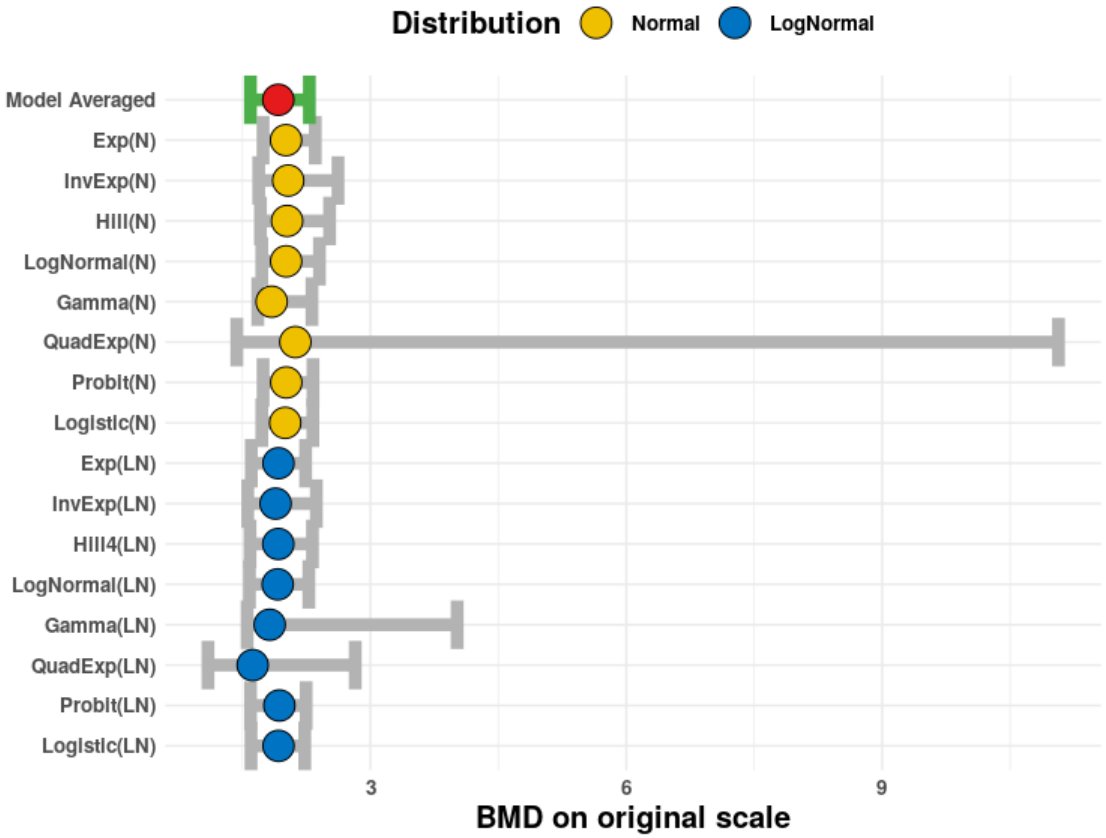
Model Averaged BMD

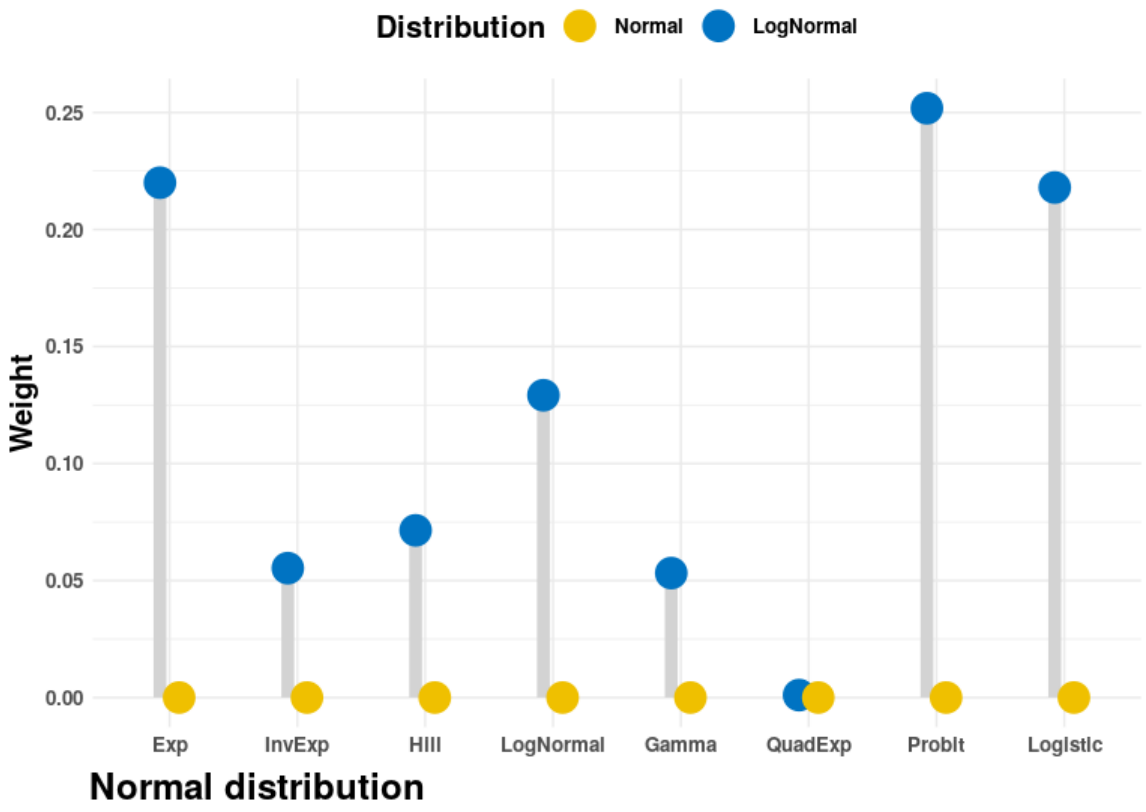
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	1.594	1.92	2.285

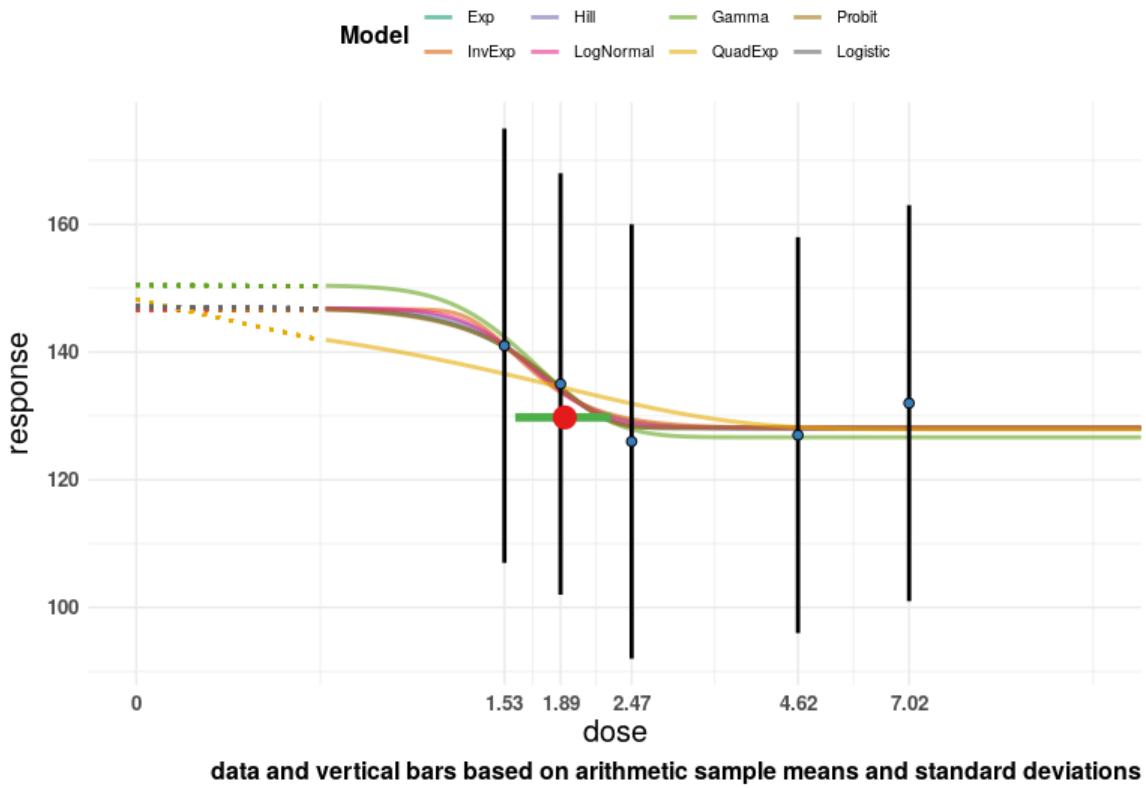
Estimated BMDs per model

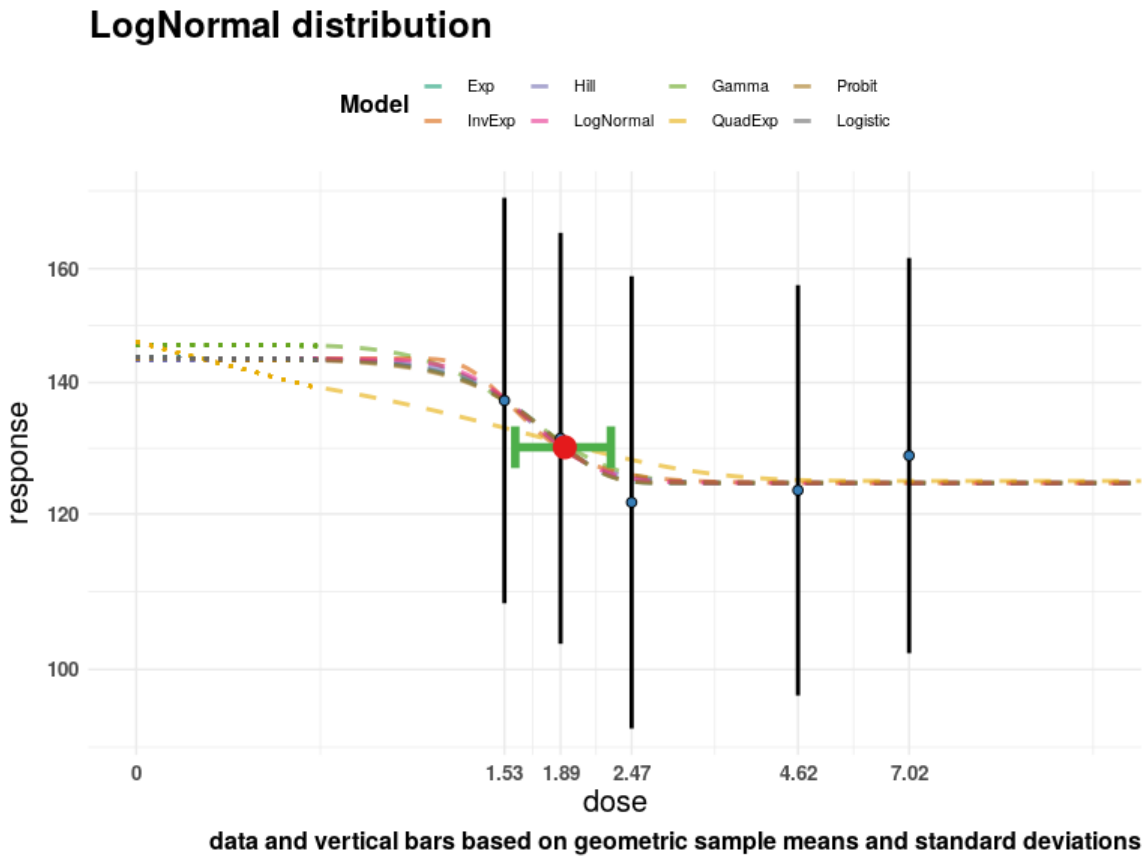
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_N	1.742	2.011	2.354	0.000	1
IE4_N	1.691	2.037	2.621	0.000	1
H4_N	1.711	2.024	2.522	0.000	1
LN4_N	1.727	2.012	2.403	0.000	1
G4_N	1.680	1.843	2.315	0.000	0
QE4_N	1.434	2.121	11.067	0.000	1
P4_N	1.742	2.014	2.327	0.000	1
L4_N	1.727	2.001	2.326	0.000	1
E4_LN	1.604	1.922	2.241	0.220	1
IE4_LN	1.562	1.888	2.366	0.055	1
H4_LN	1.589	1.920	2.321	0.071	1
LN4_LN	1.583	1.914	2.279	0.129	1
G4_LN	1.555	1.820	4.018	0.053	0
QE4_LN	1.096	1.620	2.823	0.001	1
P4_LN	1.595	1.933	2.247	0.252	1
L4_LN	1.601	1.923	2.231	0.218	1

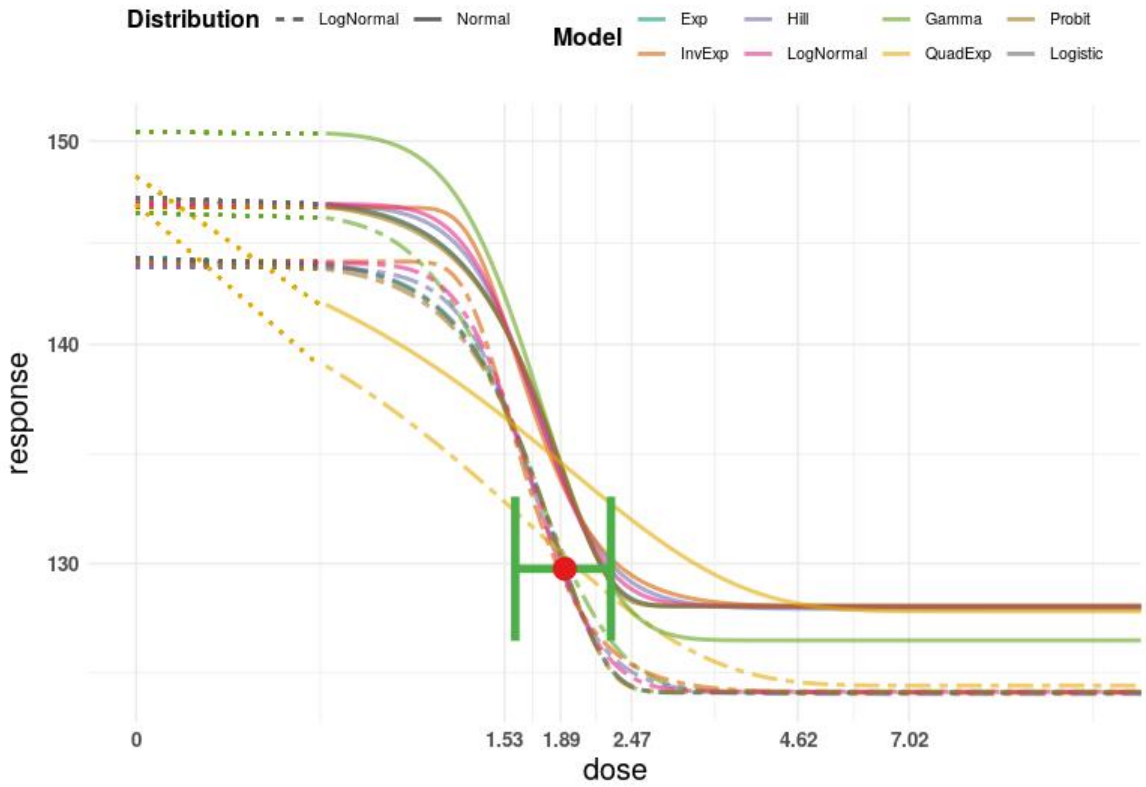
Plots of Fitted Models

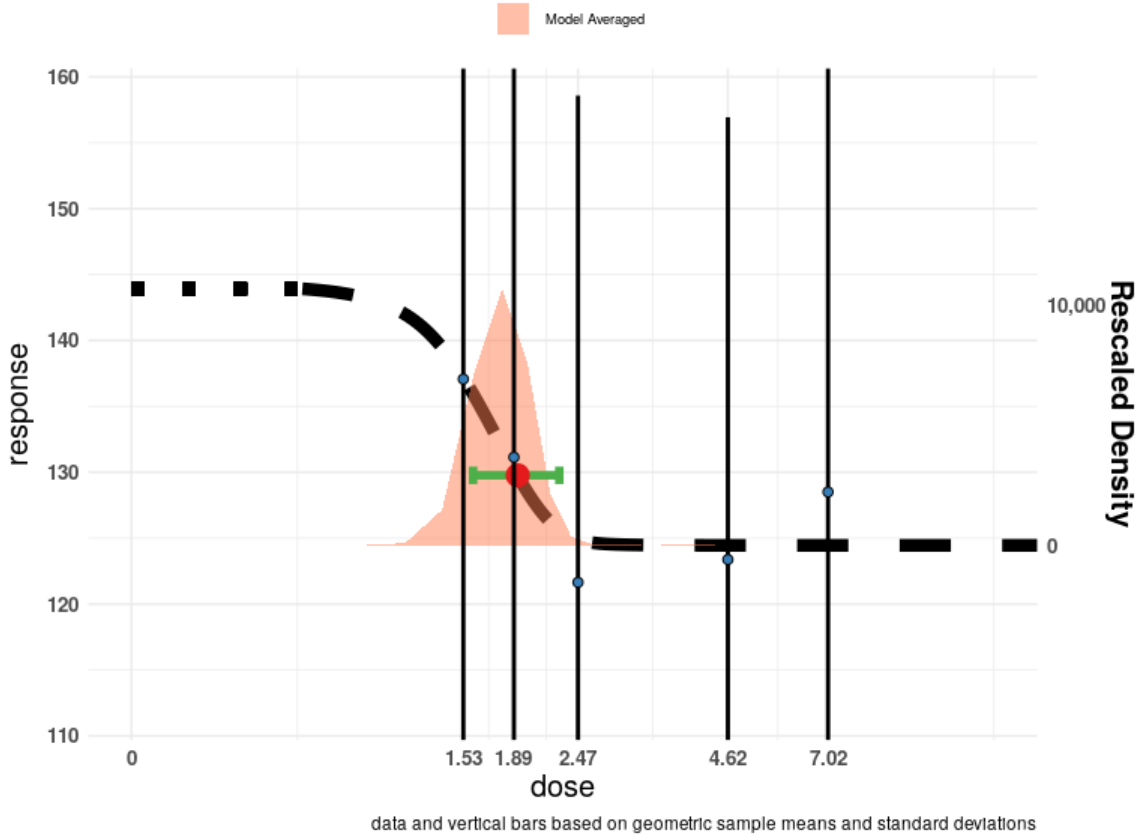



Distribution
Normal
LogNormal
Weight
0.25
0.20
0.15
0.10
0.05
0.00
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic
Normal distribution


Model
Exp
Hill
Gamma
Probit
InvExp
LogNormal
QuadExp
Logistic
response
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
150
140
130
0
1.53
1.89
2.47
4.62
7.02
dose


Model Averaged
160
150
140
130
120
110
response
0
1.53
1.89
2.47
4.62
7.02
dose
10,000
0
Rescaled Density
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 10%

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 0.1.

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 2.50e+00).

Model Averaged BMD

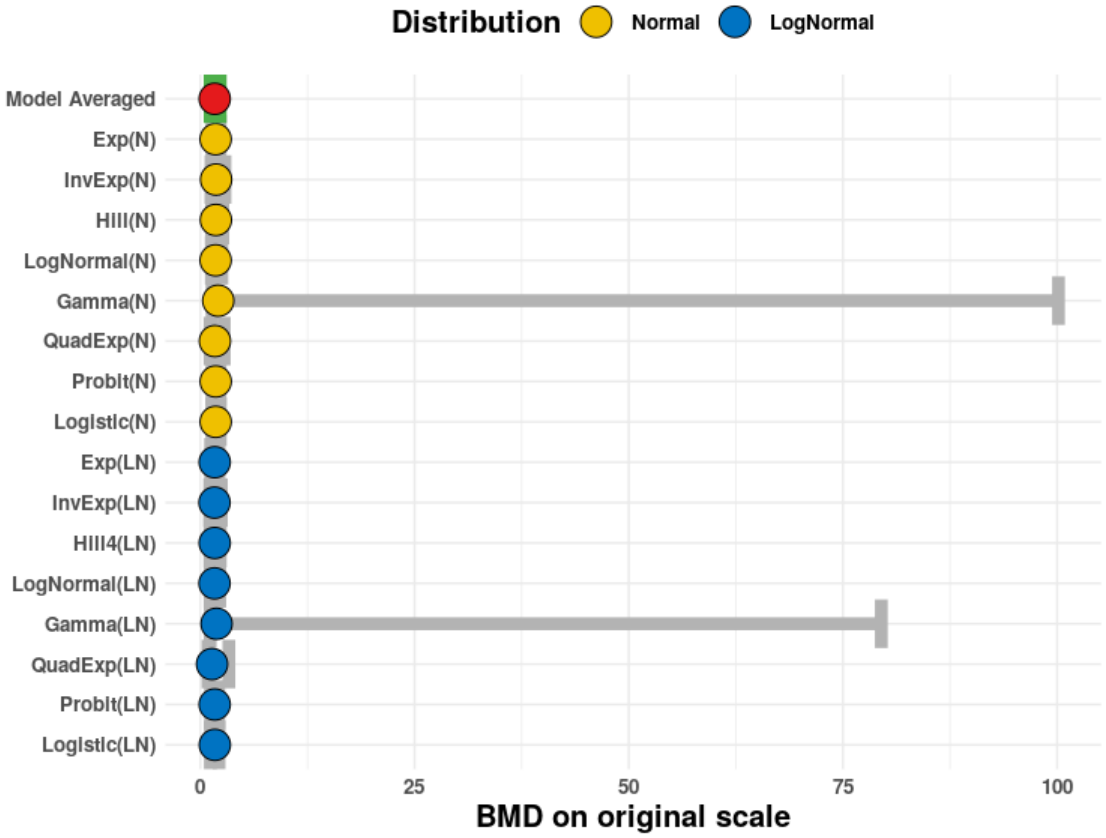
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	1.126	1.668	2.311

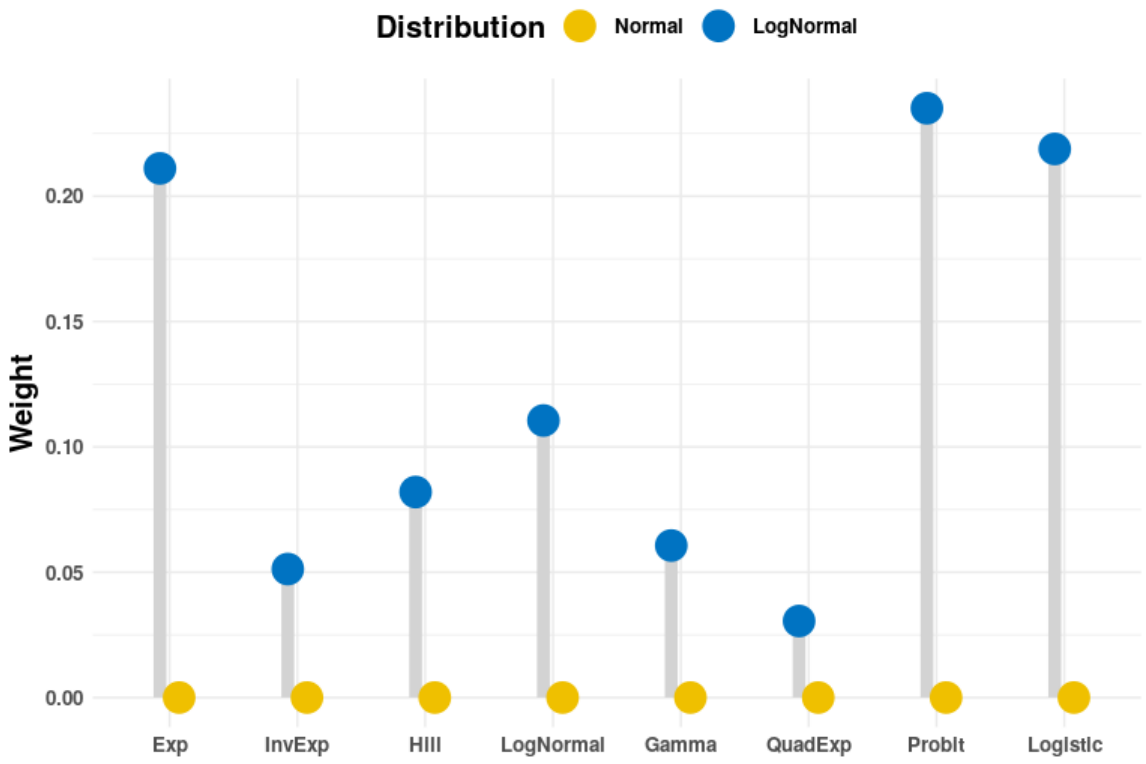
Estimated BMDs per model

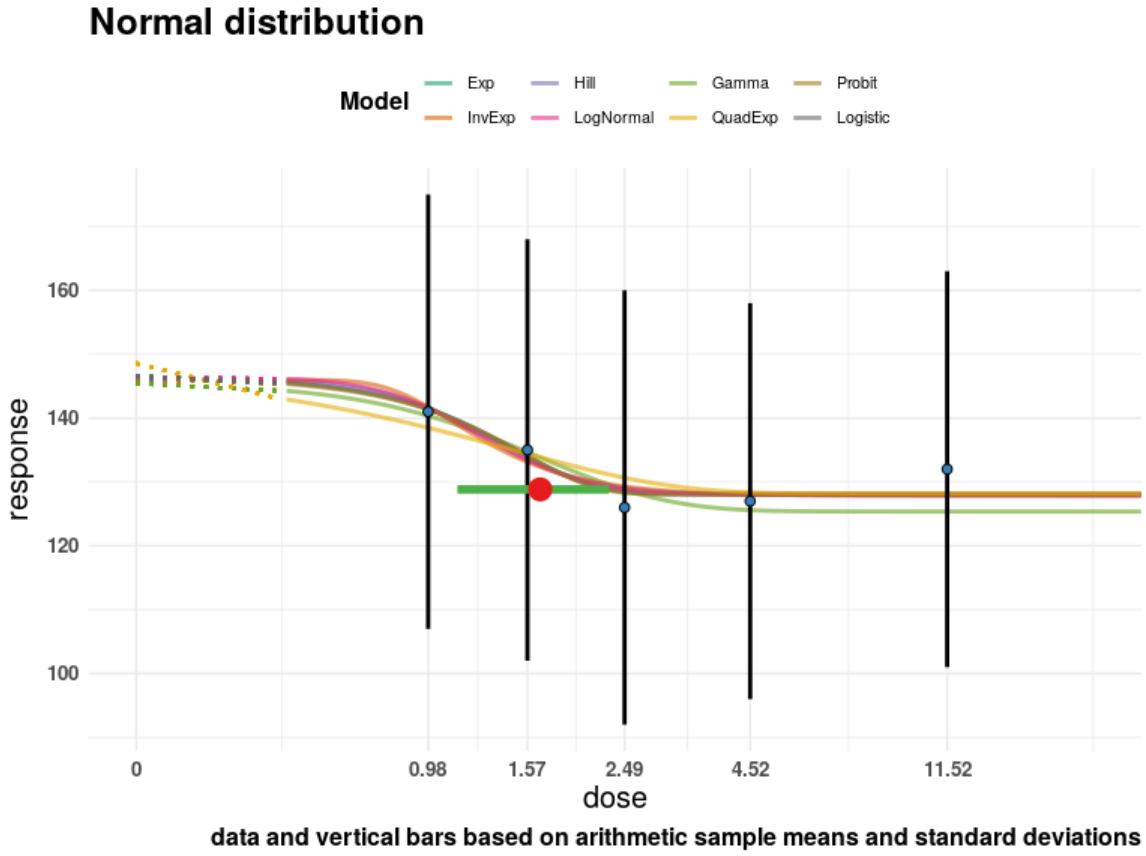
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_N	1.335	1.774	2.300	0.000	1
IE4_N	1.227	1.828	2.864	0.000	1
H4_N	1.286	1.805	2.614	0.000	1
LN4_N	1.273	1.772	2.502	0.000	1
G4_N	1.354	2.078	100.162	0.000	0
QE4_N	1.117	1.692	2.777	0.000	1

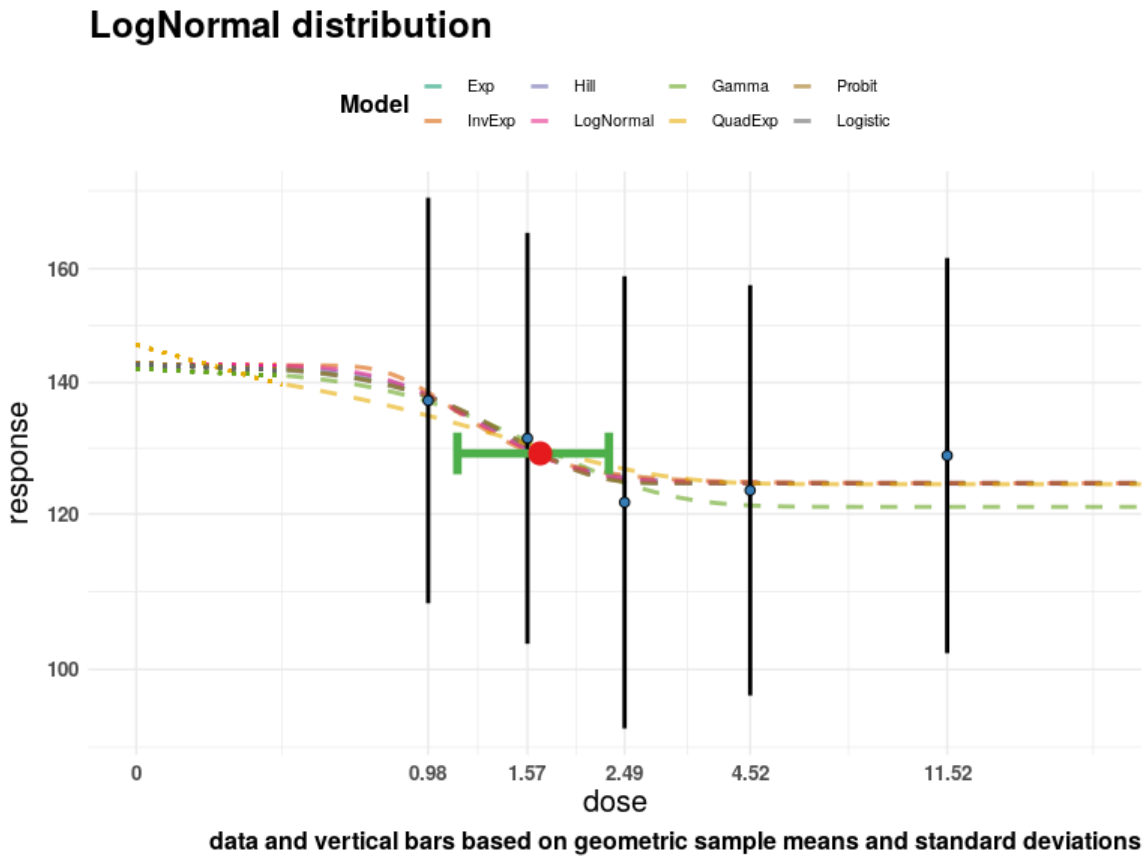
P4_N	1.344	1.783	2.290	0.000	1
L4_N	1.333	1.779	2.315	0.000	1
E4_LN	1.183	1.668	2.170	0.211	1
IE4_LN	1.081	1.647	2.443	0.051	1
H4_LN	1.104	1.670	2.313	0.082	1
LN4_LN	1.121	1.648	2.252	0.111	1
G4_LN	1.132	1.882	79.480	0.061	0
QE4_LN	0.883	1.354	3.319	0.031	0
P4_LN	1.176	1.666	2.137	0.235	1
L4_LN	1.153	1.684	2.172	0.219	1

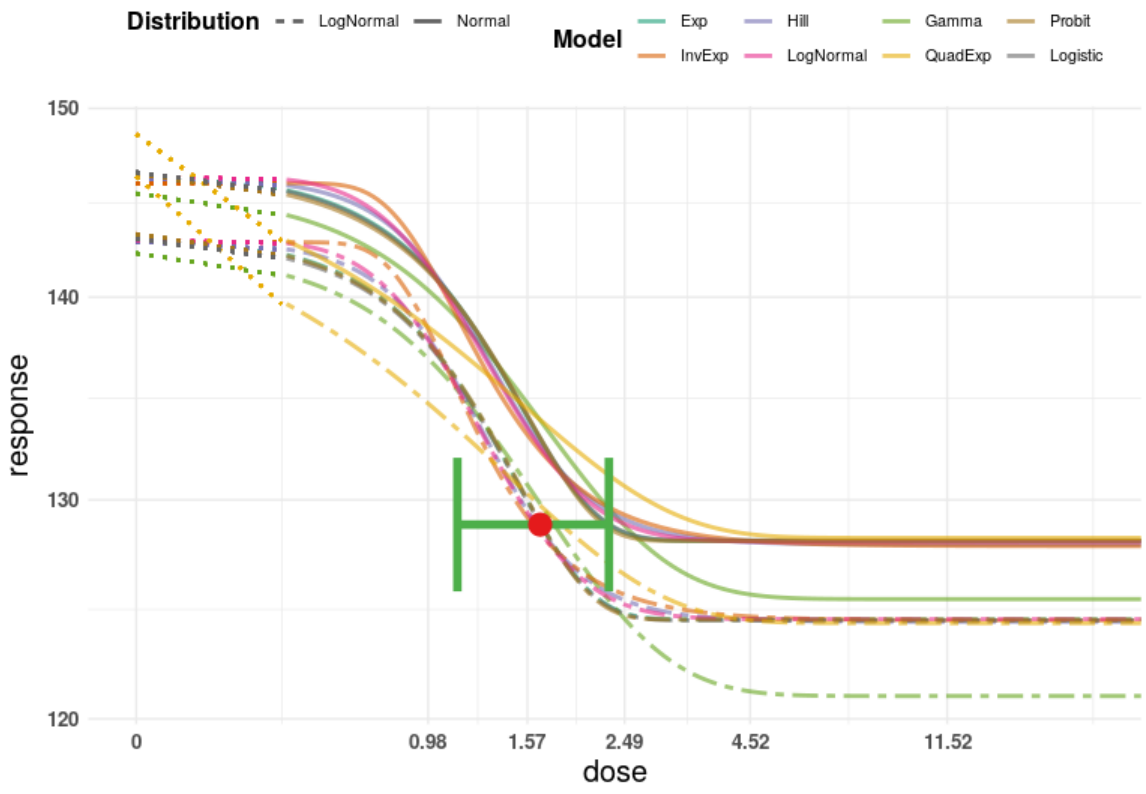
Plots of Fitted Models

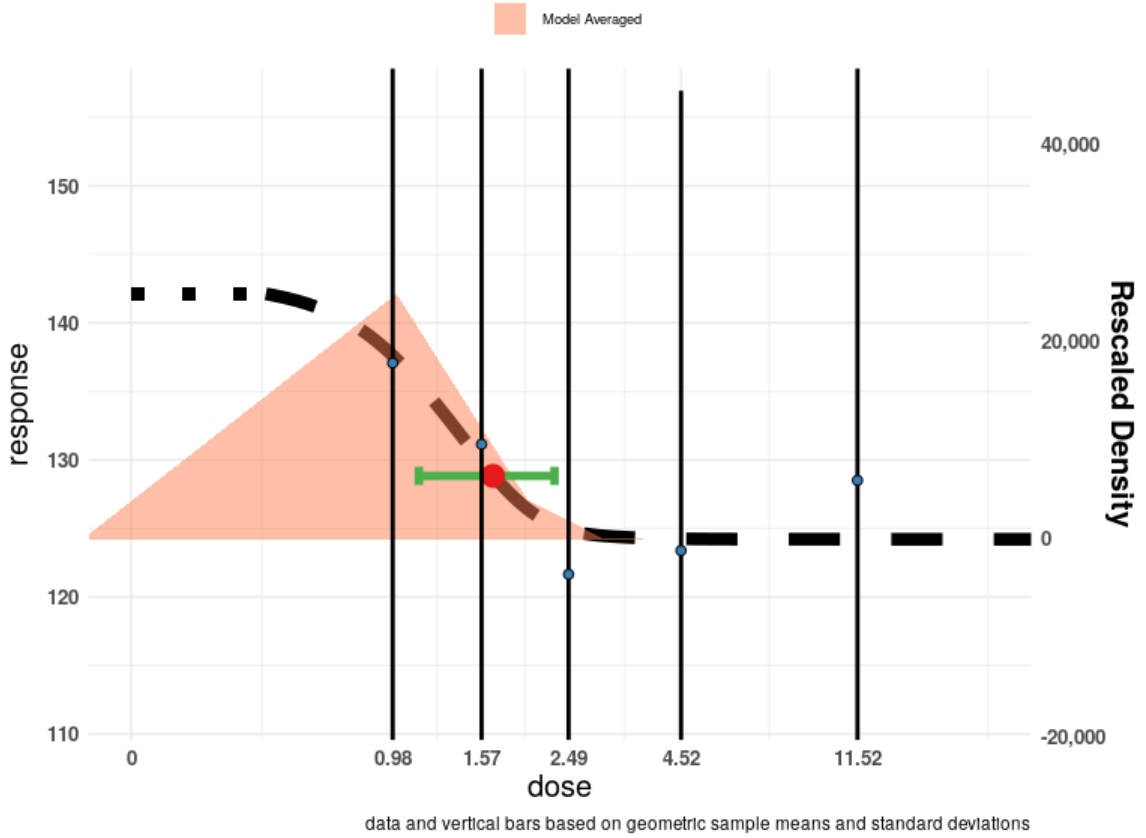



Distribution
Normal
LogNormal
Weight
0.20
0.15
0.10
0.05
0.00
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic


Normal distribution
Model
Exp
InvExp
Hill
LogNormal
Gamma
QuadExp
Probit
Logistic
response
160
140
120
100
0
0.98
1.57
2.49
4.52
11.52
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
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
120
0
0.98
1.57
2.49
4.52
11.52
dose


Model Averaged
response
150
140
130
120
110
0
0.98
1.57
2.49
4.52
11.52
dose
40,000
20,000
0
-20,000
Rescaled Density
data and vertical bars based on geometric sample means and standard deviations

Wade et al. (2015), ischemic heart disease, relative BMR 10%

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 0.00012325.

Extended dose range is applied.

Informative background prior: min: 0.00080012; the most likely: 0.00123095; max: 0.00166179. Shape parameter is applied.

The 'Sampling Method' is set to Bridge Sampling.

Goodness of Fit

Best fitting model fits sufficiently well (Bayes factor is 1.09e+00).

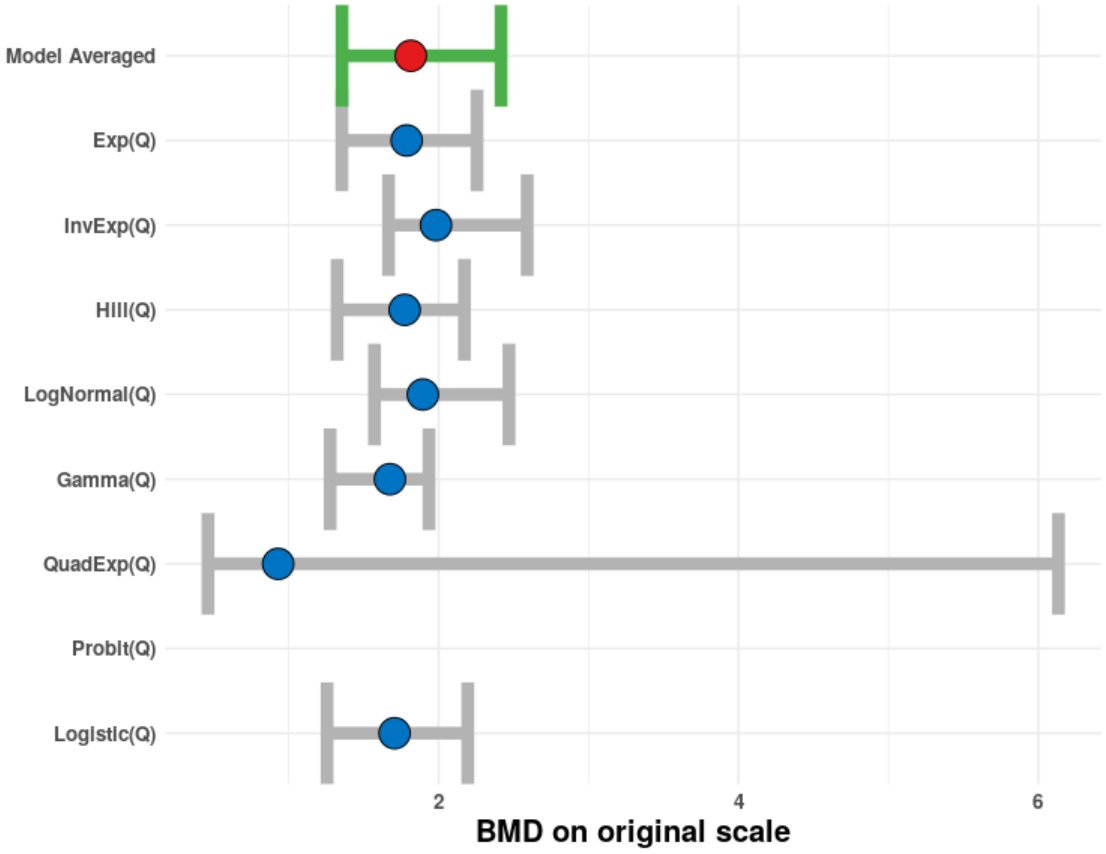
Model Averaged BMD

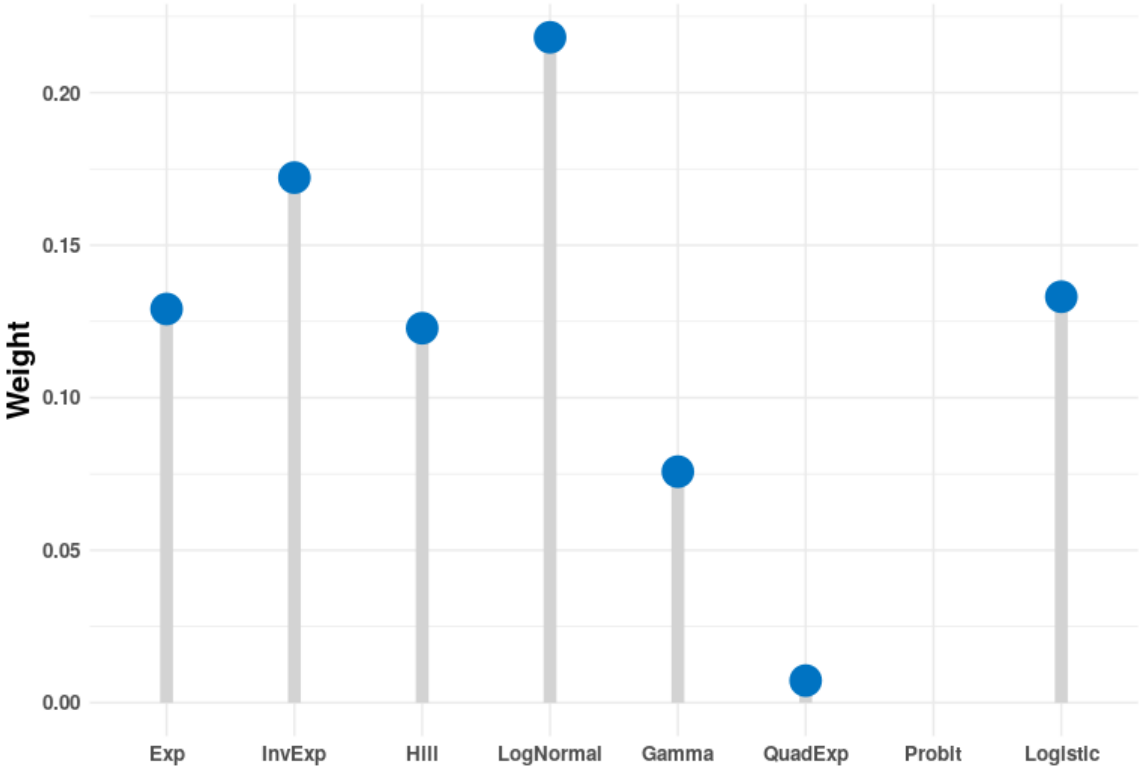
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	1.356	1.815	2.416

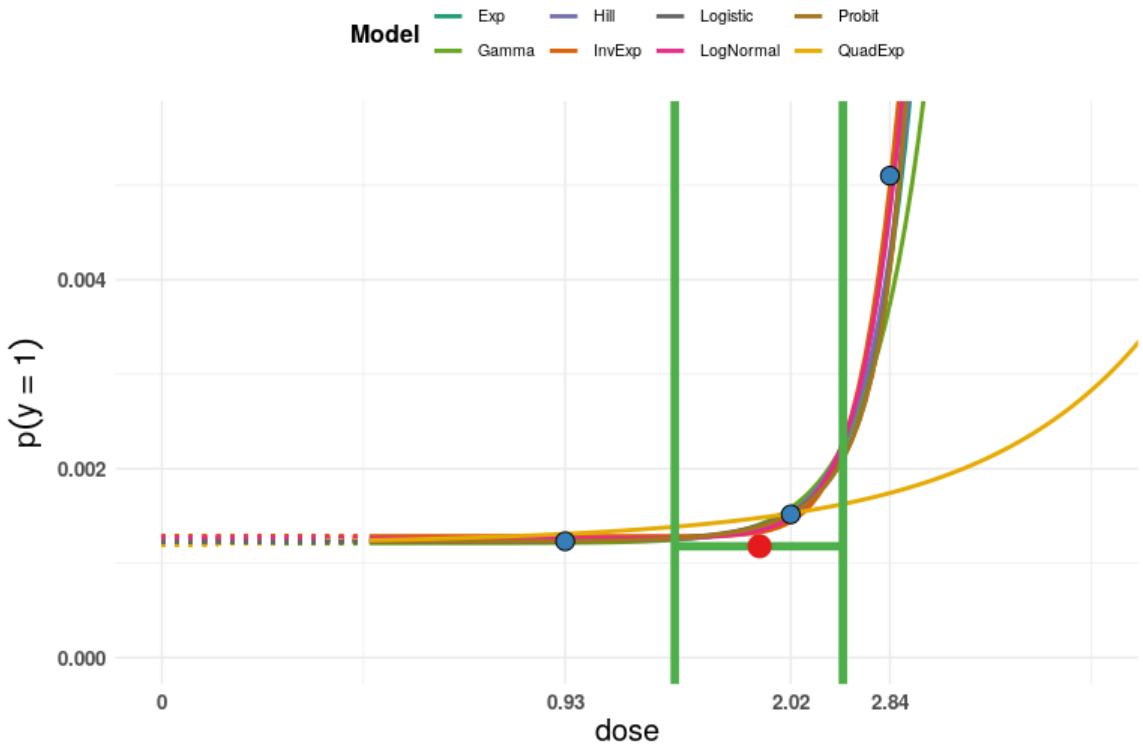
Estimated BMDs per model

Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	1.355	1.787	2.256	0.129	1
IE4_Q	1.666	1.982	2.591	0.172	1
H4_Q	1.323	1.773	2.172	0.123	1
LN4_Q	1.572	1.895	2.469	0.218	1
G4_Q	1.276	1.675	1.936	0.076	1
QE4_Q	0.462	0.930	6.134	0.007	1
L4_Q	1.256	1.706	2.194	0.133	1

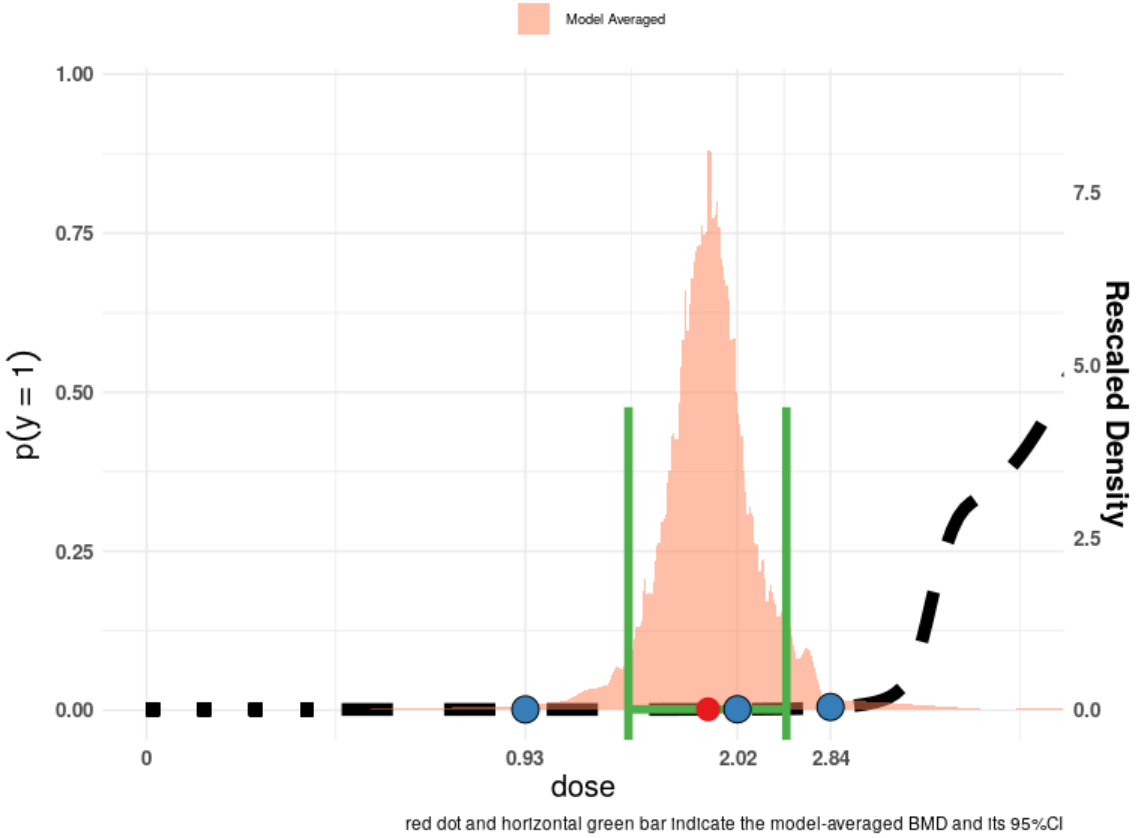
Plots of Fitted Models







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)
7.5
5.0
2.5
0.0
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 10%

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 0.01645244.

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 4.54e+00).

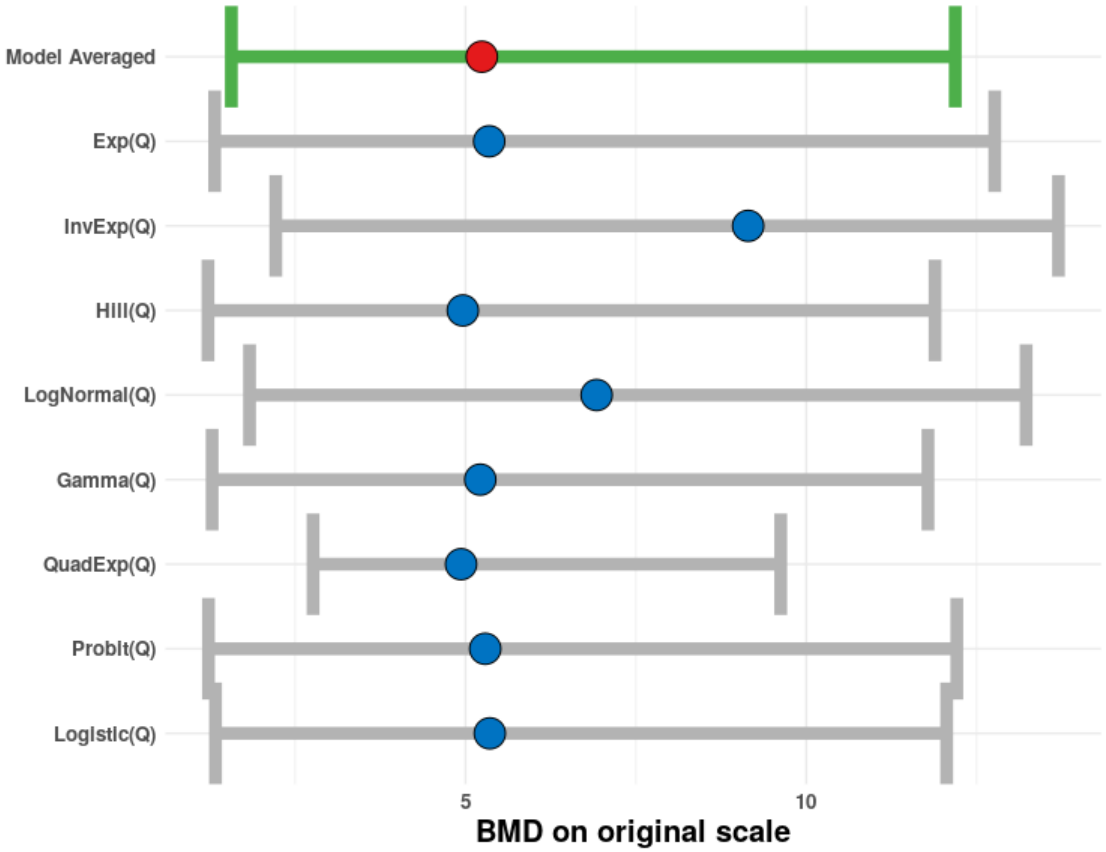
Model Averaged BMD

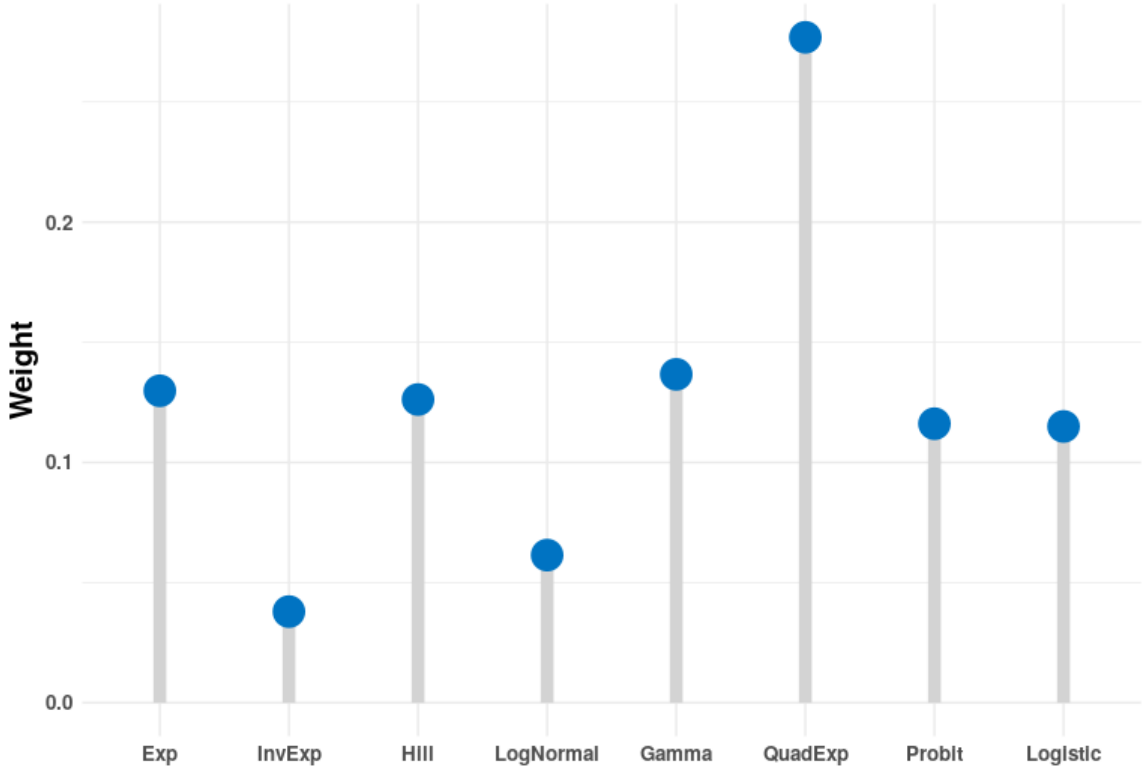
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	1.564	5.239	12.186

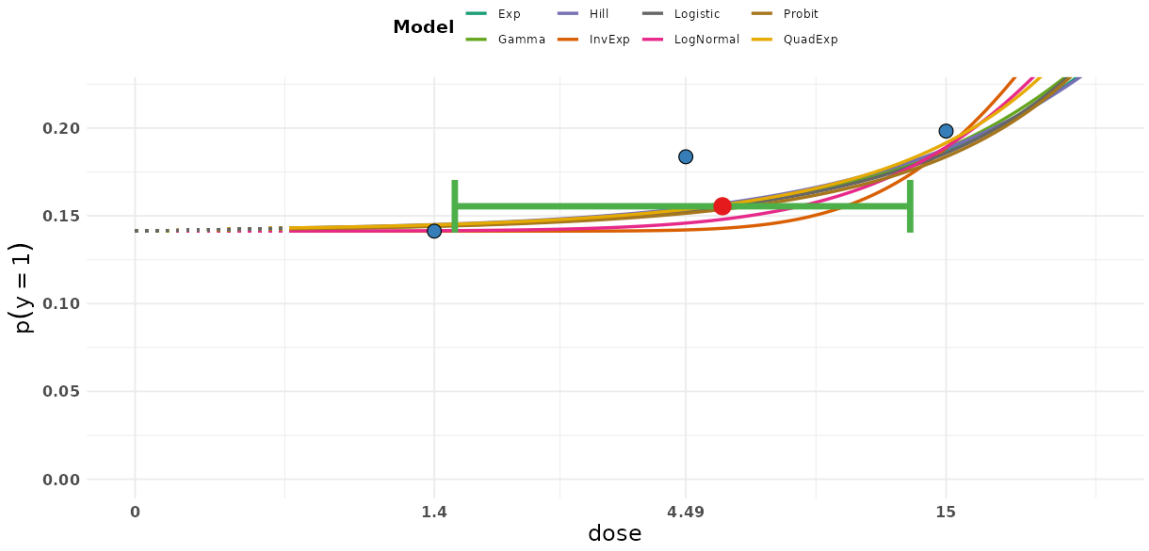
Estimated BMDs per model

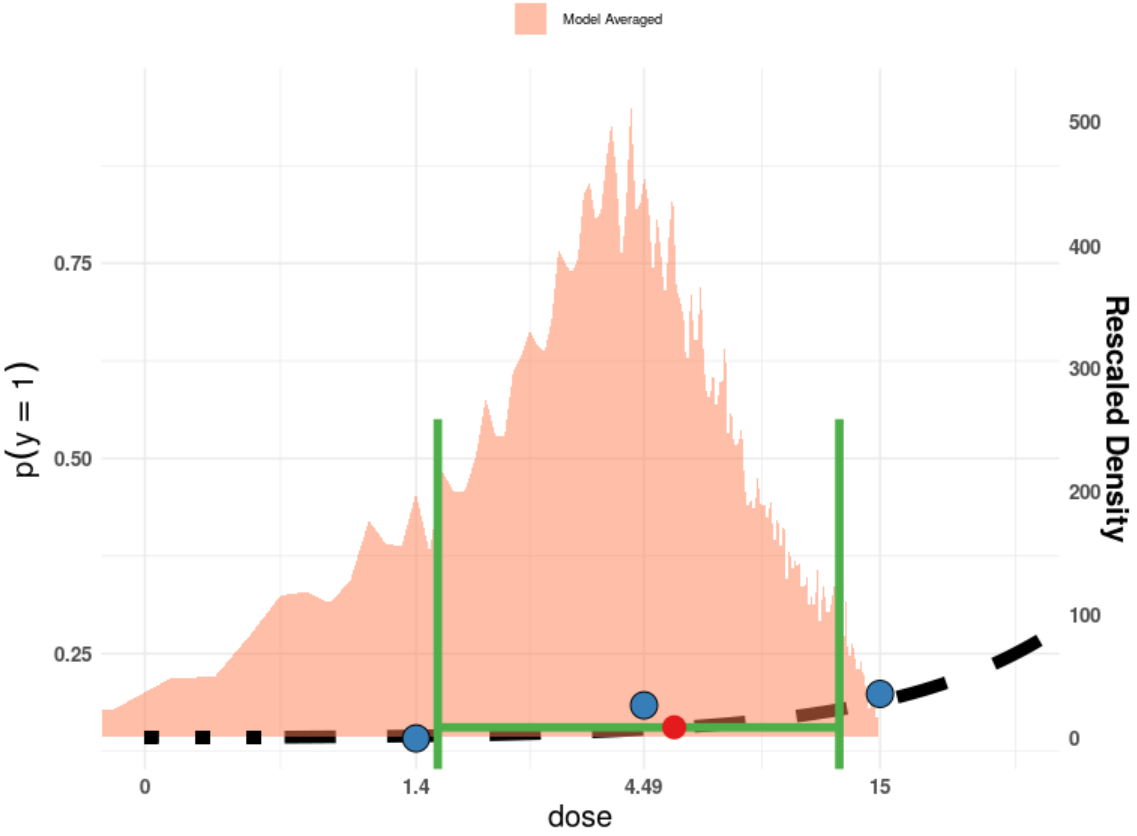
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	1.319	5.347	12.766	0.130	1
IE4_Q	2.216	9.147	13.701	0.038	1
H4_Q	1.221	4.961	11.889	0.126	1
LN4_Q	1.831	6.924	13.226	0.061	1
G4_Q	1.282	5.217	11.786	0.137	1
QE4_Q	2.763	4.935	9.625	0.277	1
P4_Q	1.229	5.289	12.209	0.116	1
L4_Q	1.332	5.357	12.060	0.115	1

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
p(y = 1)
0.75
0.50
0.25
0
1.4
4.49
15
dose
500
400
300
200
100
0
Rescaled Density

Xia et al. (2009), skin lesions, relative BMR 10%

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 0.00164401.

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 1.97e-03).

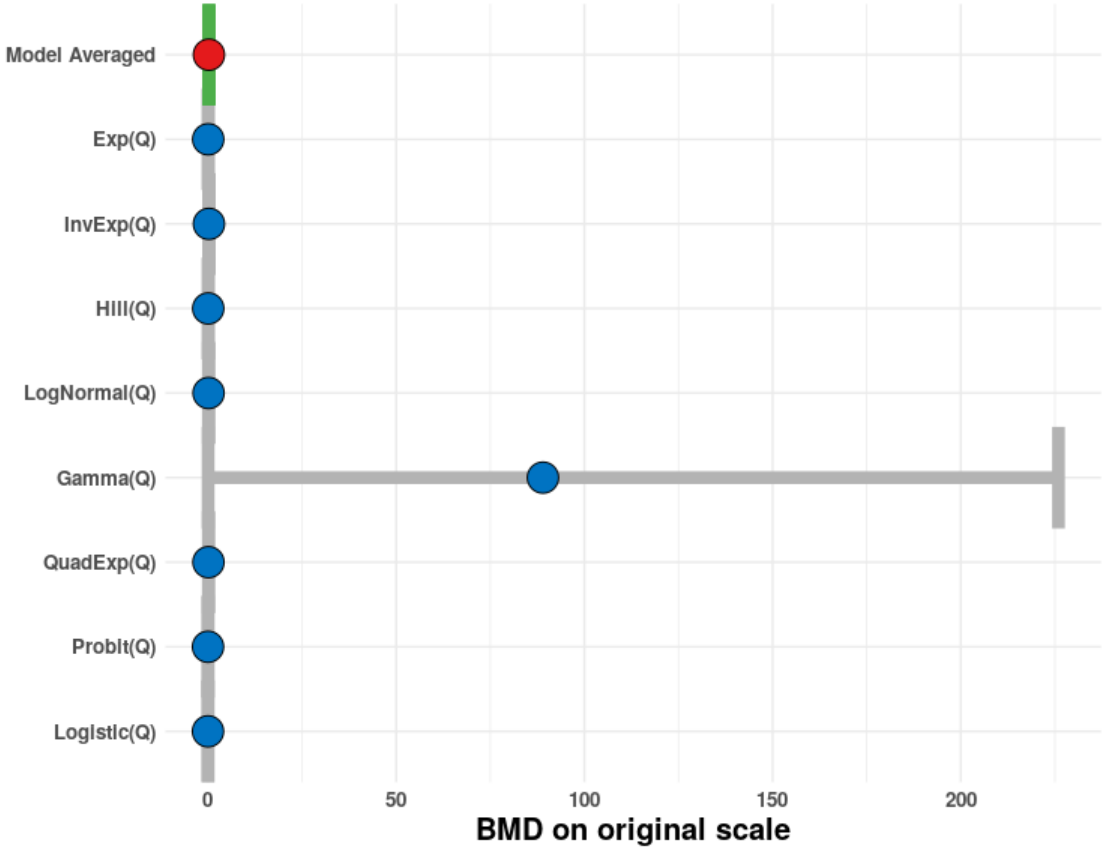
Model Averaged BMD

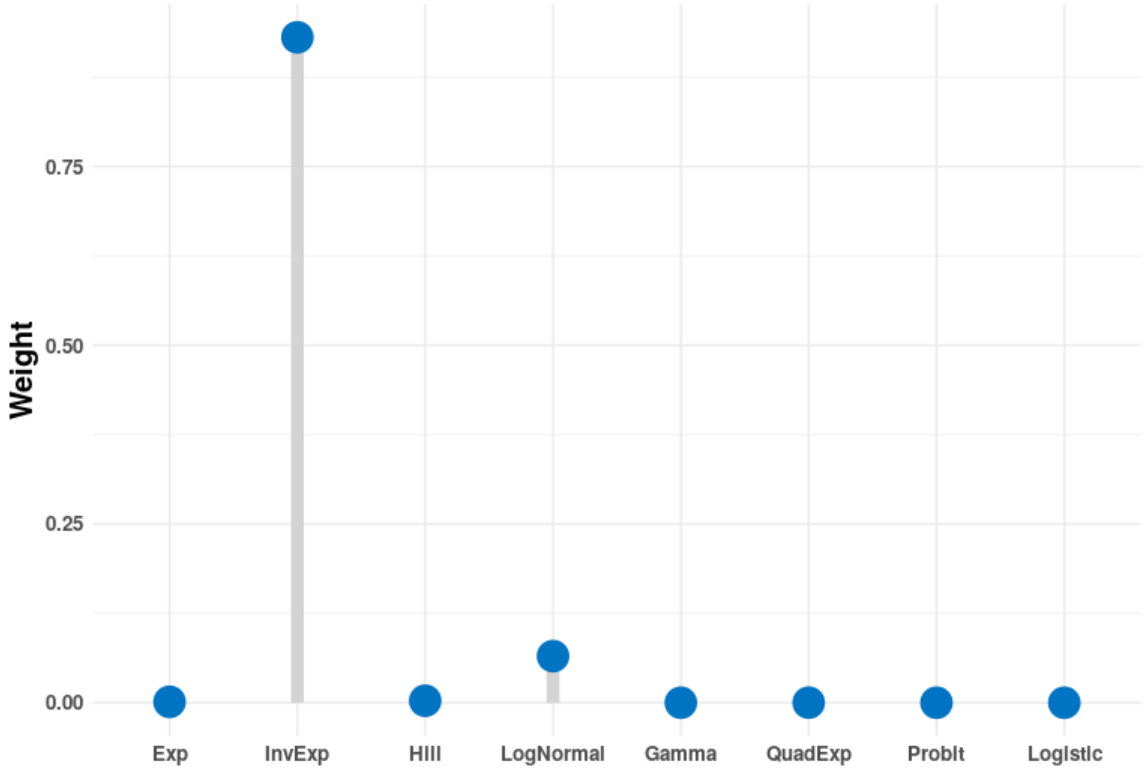
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.159	0.255	0.345

Estimated BMDs per model

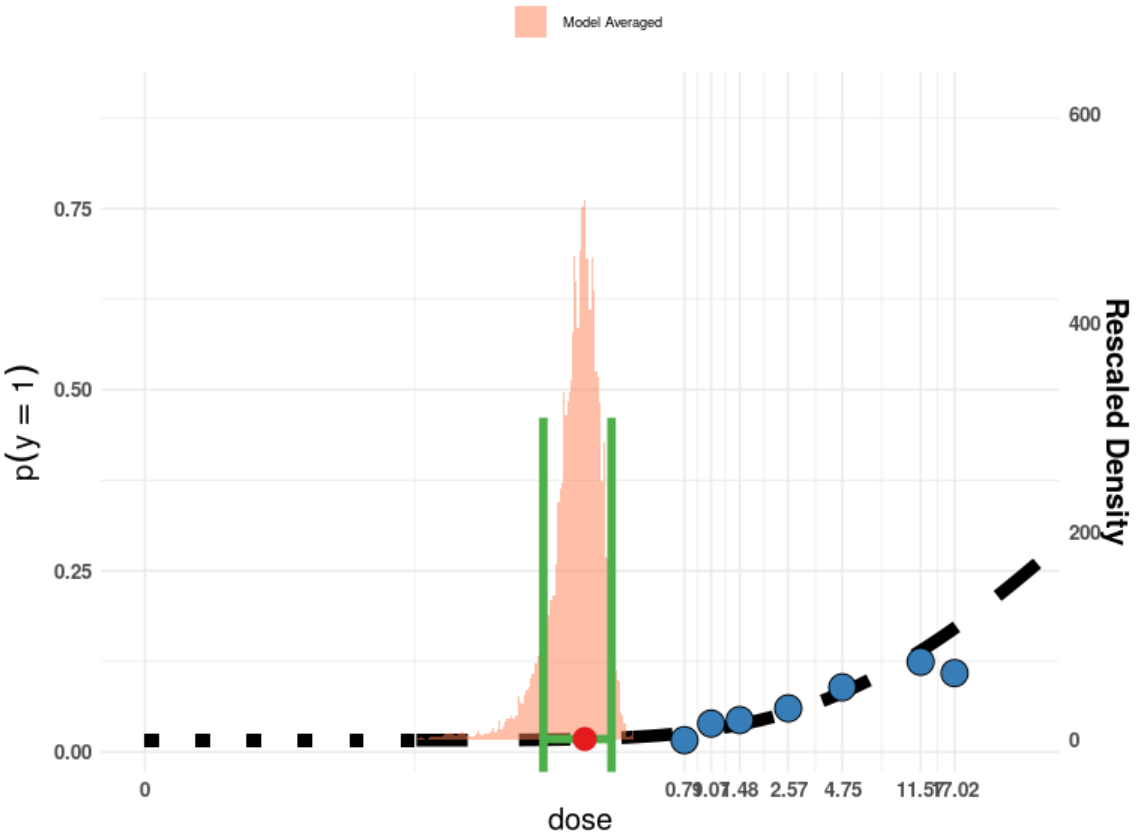
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.037	0.063	0.101	0.001	1
IE4_Q	0.185	0.258	0.347	0.931	1
H4_Q	0.041	0.070	0.110	0.003	1
LN4_Q	0.105	0.158	0.226	0.065	1
G4_Q	0.043	88.990	225.953	0.000	0
QE4_Q	0.116	0.127	0.141	0.000	1
P4_Q	0.005	0.012	0.023	0.000	1
L4_Q	0.003	0.008	0.016	0.000	1

Plots of Fitted Models




Weight
0.75
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
11.51
17.02
dose


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

Zheng et al. (2015), chronic kidney disease, relative BMR 10%

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
0.310	164	782

The 'Value for CES' is set to 0.01505216

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 2.45e-02).

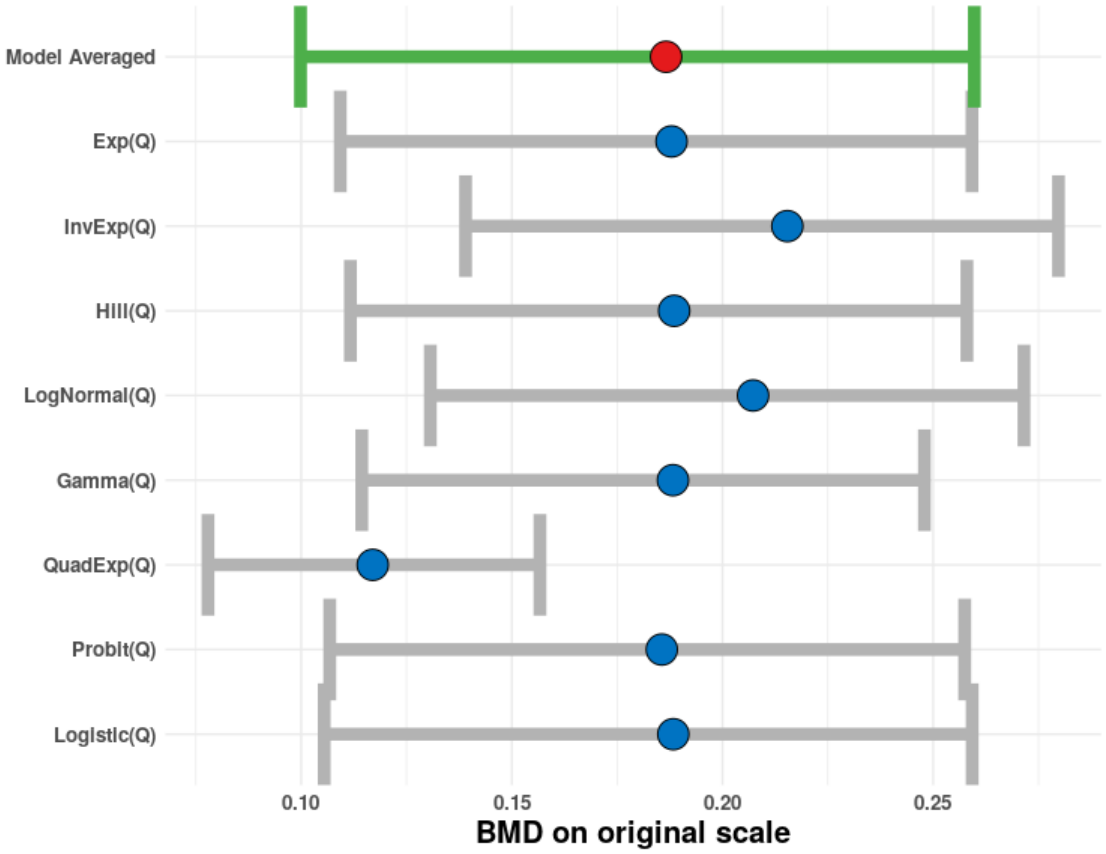
Model Averaged BMD

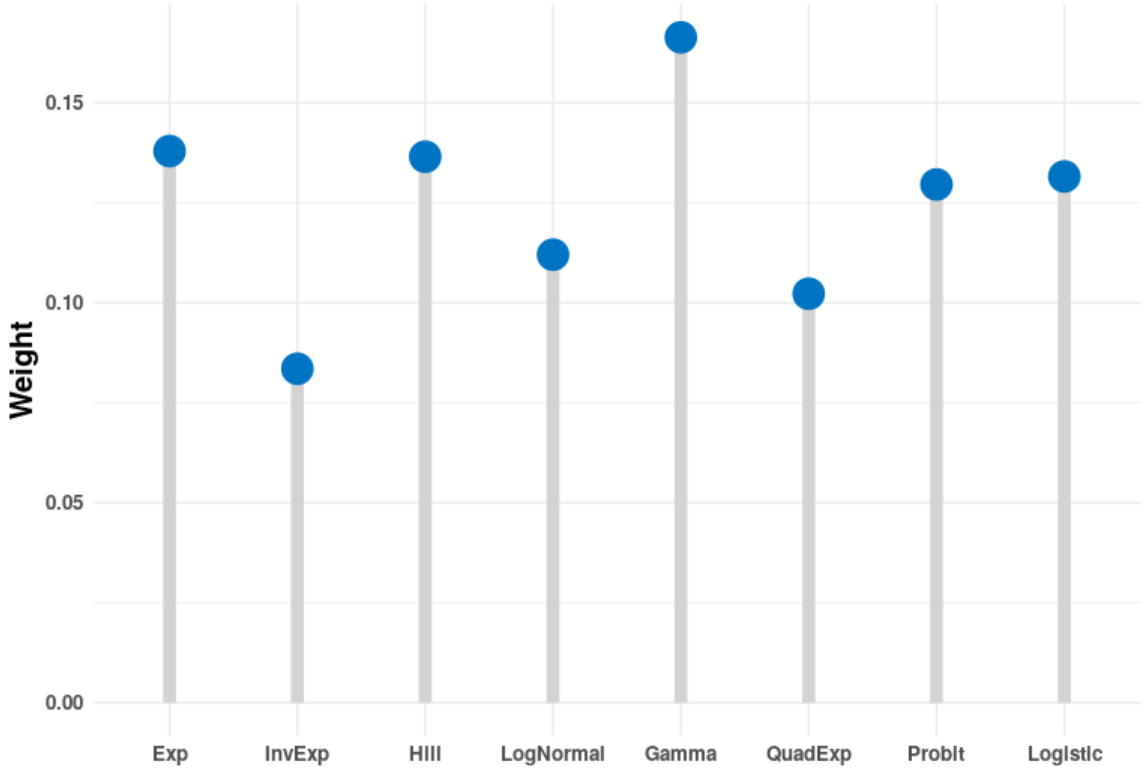
Model	Type	BMDL	BMD	BMDU
Model Averaged	BS	0.1	0.187	0.26

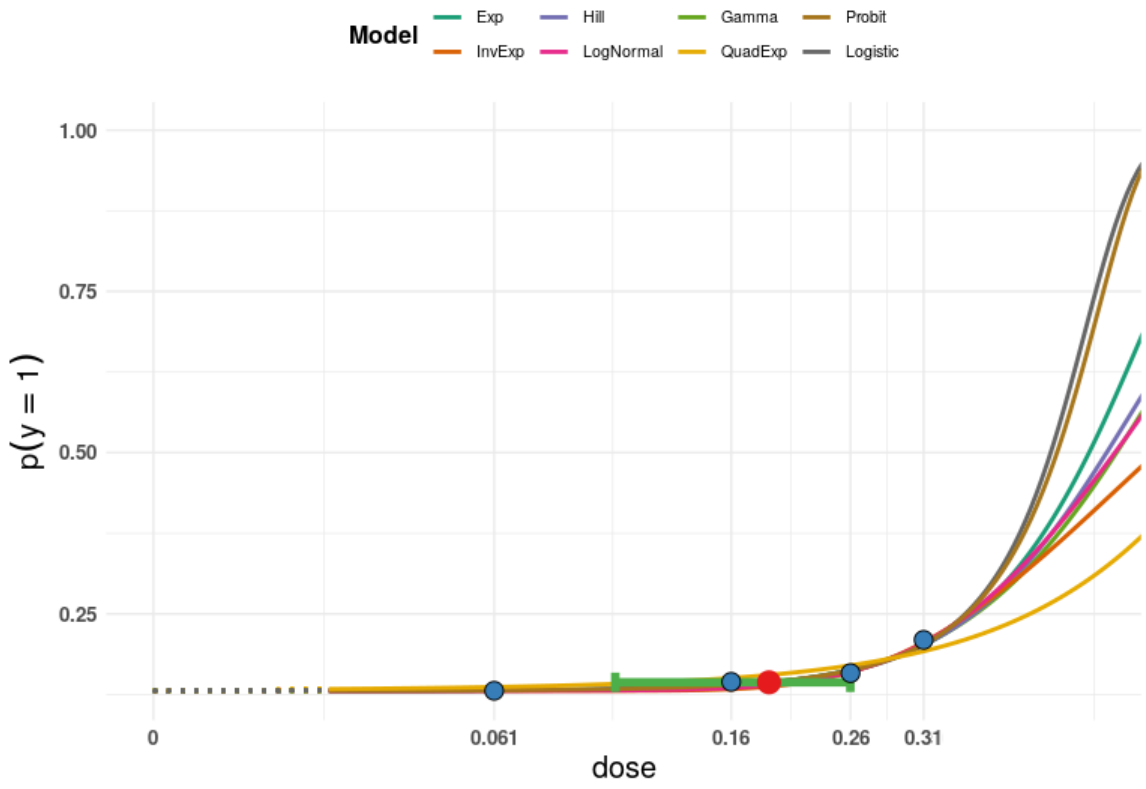
Estimated BMDs per model

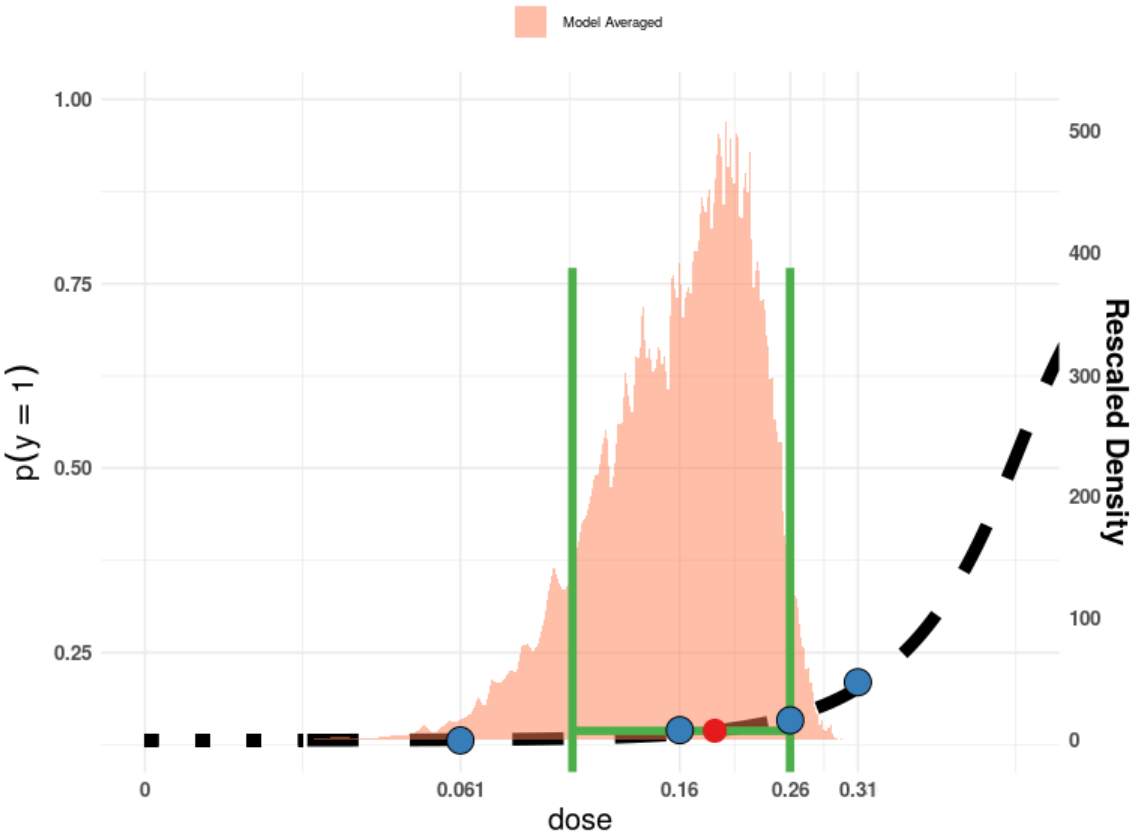
Model	BMDL	BMD	BMDU	Model Weights	Converged
E4_Q	0.109	0.188	0.259	0.138	1
IE4_Q	0.139	0.215	0.280	0.084	1
H4_Q	0.112	0.189	0.258	0.137	1
LN4_Q	0.131	0.207	0.272	0.112	1
G4_Q	0.114	0.188	0.248	0.166	1
QE4_Q	0.078	0.117	0.157	0.102	1
P4_Q	0.107	0.186	0.257	0.130	1
L4_Q	0.105	0.188	0.259	0.132	1

Plots of Fitted Models




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


Model
Exp
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
0.31
dose

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