

Supplemental data for the ML analyses

A) ProtTest model selection for the three sets of Vertebrate IR homologues.

1) Model selection for the IGF1R set of orthologues.

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*****
Best model according to AIC: JTT+G
*****
Model          deltaAIC*   AIC          AICw         -lnL
-----
JTT+G          0.00         18858.28     0.73         -9391.14
JTT+I+G       2.01         18860.28     0.27         -9391.14
WAG+G         145.41       19003.69     0.00         -9463.85
WAG+I+G       147.42       19005.70     0.00         -9463.85
JTT+I         191.61       19049.89     0.00         -9486.94
Dayhoff+G     237.47       19095.75     0.00         -9509.87
Dayhoff+I+G  239.47       19097.75     0.00         -9509.88
WAG+I         313.48       19171.76     0.00         -9547.88
Blosum62+G   384.49       19242.77     0.00         -9583.39
Blosum62+I+G 386.50       19244.78     0.00         -9583.39
VT+G          393.59       19251.87     0.00         -9587.94
VT+I+G       395.60       19253.88     0.00         -9587.94
Dayhoff+I    429.91       19288.19     0.00         -9606.09
JTT           472.33       19330.61     0.00         -9628.31
Blosum62+I   560.18       19418.46     0.00         -9671.23
WAG           578.90       19437.18     0.00         -9681.59
VT+I         645.22       19503.50     0.00         -9713.75
Dayhoff      727.97       19586.25     0.00         -9756.13
Blosum62     816.85       19675.13     0.00         -9800.57
VT           950.02       19808.30     0.00         -9867.15
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*: models sorted according to this column
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*****
Relative importance of parameters
*****
alpha (+G):    0.73
p-inv (+I):    0.00
alpha+p-inv (+I+G): 0.27
freqs (+F):    0.00

*****
Model-averaged estimate of parameters
*****
alpha (+G):    0.69
p-inv (+I):    0.30
alpha (+I+G):  0.69
p-inv (+I+G):  0.00

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Table: Weights(Ranking) of the candidate models under the different frameworks
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model          AIC          AICc-1       AICc-2       AICc-3       BIC-1       BIC-2       BIC-3
-----
JTT+G          0.73(1)      0.75(1)      0.77(1)      0.74(1)      0.97(1)      0.95(1)      0.98(1)
JTT+I+G       0.27(2)      0.25(2)      0.23(2)      0.26(2)      0.03(2)      0.05(2)      0.02(2)
WAG+G         0.00(3)      0.00(3)      0.00(3)      0.00(3)      0.00(3)      0.00(3)      0.00(3)
WAG+I+G       0.00(4)      0.00(4)      0.00(4)      0.00(4)      0.00(4)      0.00(4)      0.00(4)
JTT+I         0.00(5)      0.00(5)      0.00(5)      0.00(5)      0.00(5)      0.00(5)      0.00(5)
Dayhoff+G     0.00(6)      0.00(6)      0.00(6)      0.00(6)      0.00(6)      0.00(6)      0.00(6)
Dayhoff+I+G  0.00(7)      0.00(7)      0.00(7)      0.00(7)      0.00(7)      0.00(7)      0.00(7)
WAG+I         0.00(8)      0.00(8)      0.00(8)      0.00(8)      0.00(8)      0.00(8)      0.00(8)
Blosum62+G   0.00(9)      0.00(9)      0.00(9)      0.00(9)      0.00(9)      0.00(9)      0.00(9)
Blosum62+I+G 0.00(10)     0.00(10)     0.00(10)     0.00(10)     0.00(10)     0.00(10)     0.00(10)
VT+G         0.00(11)     0.00(11)     0.00(11)     0.00(11)     0.00(11)     0.00(11)     0.00(11)
VT+I+G       0.00(12)     0.00(12)     0.00(12)     0.00(12)     0.00(12)     0.00(12)     0.00(12)
Dayhoff+I    0.00(13)     0.00(13)     0.00(13)     0.00(13)     0.00(13)     0.00(13)     0.00(13)
JTT           0.00(14)     0.00(14)     0.00(14)     0.00(14)     0.00(14)     0.00(14)     0.00(14)
Blosum62+I   0.00(15)     0.00(15)     0.00(15)     0.00(15)     0.00(15)     0.00(15)     0.00(15)
WAG           0.00(16)     0.00(16)     0.00(16)     0.00(16)     0.00(16)     0.00(16)     0.00(16)
VT+I         0.00(17)     0.00(17)     0.00(17)     0.00(17)     0.00(17)     0.00(17)     0.00(17)
Dayhoff      0.00(18)     0.00(18)     0.00(18)     0.00(18)     0.00(18)     0.00(18)     0.00(18)
Blosum62     0.00(19)     0.00(19)     0.00(19)     0.00(19)     0.00(19)     0.00(19)     0.00(19)
VT           0.00(20)     0.00(20)     0.00(20)     0.00(20)     0.00(20)     0.00(20)     0.00(20)
-----
Relative importance of
parameters
AIC          AICc-1       AICc-2       AICc-3       BIC-1       BIC-2       BIC-3
-----
+G          0.73         0.75         0.77         0.74         0.97         0.95         0.98
+I          0.00         0.00         0.00         0.00         0.00         0.00         0.00
+I+G       0.27         0.25         0.23         0.26         0.03         0.05         0.02
+F         0.00         0.00         0.00         0.00         0.00         0.00         0.00
-----
Model-averaged estimate of
parameters
AIC          AICc-1       AICc-2       AICc-3       BIC-1       BIC-2       BIC-3
-----
alpha (+G)  0.69         0.69         0.69         0.69         0.69         0.69         0.69
p-inv (+I)  0.30         0.30         0.30         0.30         0.30         0.30         0.30
alpha (+I+G) 0.69         0.69         0.69         0.69         0.69         0.69         0.69
p-inv (+I+G) 0.00         0.00         0.00         0.00         0.00         0.00         0.00
-----
AIC : Akaike Information Criterion framework.
AICc-x: Second-Order Akaike framework.
BIC-x : Bayesian Information Criterion framework.
AICc/BIC-1: sample size as: number of sites in the alignment (946.0)
AICc/BIC-2: sample size as: Sum of position's Shannon Entropy over the whole alignment (441.7)
AICc/BIC-3: sample size as: align. length x num sequences x averaged (0-1)Sh. Entropy (2043.8)

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2) Model selection for the IR set of orthologues.

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*****
Best model according to AIC: JTT+G
*****
Model      deltaAIC*   AIC      AICw     -lnL
-----
JTT+G      0.00        21501.00  0.72     -10712.50
JTT+I+G    1.87        21502.88  0.28     -10712.44
WAG+G      163.79      21664.79  0.00     -10794.40
WAG+I+G    165.40      21666.40  0.00     -10794.20
Dayhoff+G  228.00      21729.00  0.00     -10826.50
Dayhoff+I+G 229.96     21730.96  0.00     -10826.48
JTT+I      302.29      21803.29  0.00     -10863.65
VT+G       439.22      21940.22  0.00     -10932.11
VT+I+G     441.22      21942.22  0.00     -10932.11
WAG+I      449.45      21950.45  0.00     -10937.23
Blosum62+G 455.08      21956.09  0.00     -10940.04
Blosum62+I+G 456.89     21957.90  0.00     -10939.95
Dayhoff+I  559.59      22060.59  0.00     -10992.30
Blosum62+I 728.09      22229.10  0.00     -11076.55
JTT        771.96      22272.96  0.00     -11099.48
VT+I       814.43      22315.44  0.00     -11119.72
WAG        896.02      22397.03  0.00     -11161.51
Dayhoff    1032.70     22533.70  0.00     -11229.85
Blosum62  1175.88     22676.88  0.00     -11301.44
VT        1301.25     22802.26  0.00     -11364.13
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*: models sorted according to this column

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*****
Relative importance of parameters
*****
alpha (+G): 0.72
p-inv (+I): 0.00
alpha+p-inv (+I+G): 0.28
freqs (+F): 0.00

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*****
Model-averaged estimate of parameters
*****
alpha (+G): 0.57
p-inv (+I): 0.33
alpha (+I+G): 0.60
p-inv (+I+G): 0.02

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Table: Weights(Ranking) of the candidate models under the different frameworks

model	AIC	AICc-1	AICc-2	AICc-3	BIC-1	BIC-2	BIC-3
JTT+G	0.72(1)	0.74(1)	0.75(1)	0.73(1)	0.97(1)	0.95(1)	0.98(1)
JTT+I+G	0.28(2)	0.26(2)	0.25(2)	0.27(2)	0.03(2)	0.05(2)	0.02(2)
WAG+G	0.00(3)	0.00(3)	0.00(3)	0.00(3)	0.00(3)	0.00(3)	0.00(3)
WAG+I+G	0.00(4)	0.00(4)	0.00(4)	0.00(4)	0.00(4)	0.00(4)	0.00(4)
Dayhoff+G	0.00(5)	0.00(5)	0.00(5)	0.00(5)	0.00(5)	0.00(5)	0.00(5)
Dayhoff+I+G	0.00(6)	0.00(6)	0.00(6)	0.00(6)	0.00(6)	0.00(6)	0.00(6)
JTT+I	0.00(7)	0.00(7)	0.00(7)	0.00(7)	0.00(7)	0.00(7)	0.00(7)
VT+G	0.00(8)	0.00(8)	0.00(8)	0.00(8)	0.00(8)	0.00(8)	0.00(8)
VT+I+G	0.00(9)	0.00(9)	0.00(9)	0.00(9)	0.00(9)	0.00(9)	0.00(9)
WAG+I	0.00(10)	0.00(10)	0.00(10)	0.00(10)	0.00(10)	0.00(10)	0.00(10)
Blosum62+G	0.00(11)	0.00(11)	0.00(11)	0.00(11)	0.00(11)	0.00(11)	0.00(11)
Blosum62+I+G	0.00(12)	0.00(12)	0.00(12)	0.00(12)	0.00(12)	0.00(12)	0.00(12)
Dayhoff+I	0.00(13)	0.00(13)	0.00(13)	0.00(13)	0.00(13)	0.00(13)	0.00(13)
Blosum62+I	0.00(14)	0.00(14)	0.00(14)	0.00(14)	0.00(14)	0.00(14)	0.00(14)
JTT	0.00(15)	0.00(15)	0.00(15)	0.00(15)	0.00(15)	0.00(15)	0.00(15)
VT+I	0.00(16)	0.00(16)	0.00(16)	0.00(16)	0.00(16)	0.00(16)	0.00(16)
WAG	0.00(17)	0.00(17)	0.00(17)	0.00(17)	0.00(17)	0.00(17)	0.00(17)
Dayhoff	0.00(18)	0.00(18)	0.00(18)	0.00(18)	0.00(18)	0.00(18)	0.00(18)
Blosum62	0.00(19)	0.00(19)	0.00(19)	0.00(19)	0.00(19)	0.00(19)	0.00(19)
VT	0.00(20)	0.00(20)	0.00(20)	0.00(20)	0.00(20)	0.00(20)	0.00(20)

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Relative importance of
parameters
+G      0.72      0.74      0.75      0.73      0.97      0.95      0.98
+I      0.00      0.00      0.00      0.00      0.00      0.00      0.00
+I+G    0.28      0.26      0.25      0.27      0.03      0.05      0.02
+F      0.00      0.00      0.00      0.00      0.00      0.00      0.00

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Model-averaged estimate of
parameters
alpha (+G) 0.57      0.57      0.57      0.57      0.57      0.57      0.57
p-inv (+I) 0.33      0.33      0.33      0.33      0.33      0.33      0.33
alpha (+I+G) 0.60      0.60      0.60      0.60      0.60      0.60      0.60
p-inv (+I+G) 0.02      0.02      0.02      0.02      0.02      0.02      0.02

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AIC : Akaike Information Criterion framework.

AICc-x: Second-Order Akaike framework.

BIC-x : Bayesian Information Criterion framework.

AICc/BIC-1: sample size as: number of sites in the alignment (946.0)

AICc/BIC-2: sample size as: Sum of position's Shannon Entropy over the whole alignment (490.4)

AICc/BIC-3: sample size as: align. length x num sequences x averaged (0-1)Sh. Entropy (2269.5)

3) Model selection for the IRR set of orthologues.

Best model according to AIC: JTT+G

Model	deltaAIC*	AIC	AICw	-lnL
JTT+G	0.00	14108.65	0.73	-7026.33
JTT+I+G	2.00	14110.65	0.27	-7026.33
JTT+I	109.39	14218.05	0.00	-7081.02
WAG+G	186.18	14294.84	0.00	-7119.42
WAG+I+G	188.18	14296.84	0.00	-7119.42
Dayhoff+G	218.53	14327.18	0.00	-7135.59
Dayhoff+I+G	220.53	14329.18	0.00	-7135.59
WAG+I	309.21	14417.86	0.00	-7180.93
JTT	345.54	14454.19	0.00	-7200.09
Dayhoff+I	345.69	14454.35	0.00	-7199.17
VT+G	401.38	14510.03	0.00	-7227.01
VT+I+G	403.38	14512.03	0.00	-7227.01
Blosum62+G	422.83	14531.48	0.00	-7237.74
Blosum62+I+G	424.83	14533.48	0.00	-7237.74
WAG	538.72	14647.37	0.00	-7296.69
VT+I	542.73	14651.38	0.00	-7297.69
Blosum62+I	545.11	14653.77	0.00	-7298.88
Dayhoff	604.66	14713.32	0.00	-7329.66
Blosum62	767.41	14876.06	0.00	-7411.03
VT	796.95	14905.61	0.00	-7425.80

 *: models sorted according to this column

 Relative importance of parameters

alpha (+G): 0.73
 p-inv (+I): 0.00
 alpha+p-inv (+I+G): 0.27
 freqs (+F): 0.00

 Model-averaged estimate of parameters

alpha (+G): 0.51
 p-inv (+I): 0.42
 alpha (+I+G): 0.51
 p-inv (+I+G): 0.00

 Table: Weights(Ranking) of the candidate models under the different frameworks

model	AIC	AICc-1	AICc-2	AICc-3	BIC-1	BIC-2	BIC-3
JTT+G	0.73(1)	0.74(1)	0.77(1)	0.74(1)	0.97(1)	0.95(1)	0.97(1)
JTT+I+G	0.27(2)	0.26(2)	0.23(2)	0.26(2)	0.03(2)	0.05(2)	0.03(2)
JTT+I	0.00(3)	0.00(3)	0.00(3)	0.00(3)	0.00(3)	0.00(3)	0.00(3)
WAG+G	0.00(4)	0.00(4)	0.00(4)	0.00(4)	0.00(4)	0.00(4)	0.00(4)
WAG+I+G	0.00(5)	0.00(5)	0.00(5)	0.00(5)	0.00(5)	0.00(5)	0.00(5)
Dayhoff+G	0.00(6)	0.00(6)	0.00(6)	0.00(6)	0.00(6)	0.00(6)	0.00(6)
Dayhoff+I+G	0.00(7)	0.00(7)	0.00(7)	0.00(7)	0.00(7)	0.00(7)	0.00(7)
WAG+I	0.00(8)	0.00(8)	0.00(8)	0.00(8)	0.00(8)	0.00(8)	0.00(8)
JTT	0.00(9)	0.00(9)	0.00(9)	0.00(9)	0.00(9)	0.00(9)	0.00(9)
Dayhoff+I	0.00(10)	0.00(10)	0.00(10)	0.00(10)	0.00(10)	0.00(10)	0.00(10)
VT+G	0.00(11)	0.00(11)	0.00(11)	0.00(11)	0.00(11)	0.00(11)	0.00(11)
VT+I+G	0.00(12)	0.00(12)	0.00(12)	0.00(12)	0.00(12)	0.00(12)	0.00(12)
Blosum62+G	0.00(13)	0.00(13)	0.00(13)	0.00(13)	0.00(13)	0.00(13)	0.00(13)
Blosum62+I+G	0.00(14)	0.00(14)	0.00(14)	0.00(14)	0.00(14)	0.00(14)	0.00(14)
WAG	0.00(15)	0.00(15)	0.00(15)	0.00(15)	0.00(15)	0.00(15)	0.00(15)
VT+I	0.00(16)	0.00(16)	0.00(16)	0.00(16)	0.00(16)	0.00(16)	0.00(16)
Blosum62+I	0.00(17)	0.00(17)	0.00(17)	0.00(17)	0.00(17)	0.00(17)	0.00(17)
Dayhoff	0.00(18)	0.00(18)	0.00(18)	0.00(18)	0.00(18)	0.00(18)	0.00(18)
Blosum62	0.00(19)	0.00(19)	0.00(19)	0.00(19)	0.00(19)	0.00(19)	0.00(19)
VT	0.00(20)	0.00(20)	0.00(20)	0.00(20)	0.00(20)	0.00(20)	0.00(20)

Relative importance of parameters	AIC	AICc-1	AICc-2	AICc-3	BIC-1	BIC-2	BIC-3
+G	0.73	0.74	0.77	0.74	0.97	0.95	0.97
+I	0.00	0.00	0.00	0.00	0.00	0.00	0.00
+I+G	0.27	0.26	0.23	0.26	0.03	0.05	0.03
+F	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Model-averaged estimate of parameters	AIC	AICc-1	AICc-2	AICc-3	BIC-1	BIC-2	BIC-3
alpha (+G)	0.51	0.51	0.51	0.51	0.51	0.51	0.51
p-inv (+I)	0.42	0.42	0.42	0.42	0.42	0.42	0.42
alpha (+I+G)	0.51	0.51	0.51	0.51	0.51	0.51	0.51
p-inv (+I+G)	0.00	0.00	0.00	0.00	0.00	0.00	0.00

 AIC : Akaike Information Criterion framework.
 AICc-x: Second-Order Akaike framework.
 BIC-x : Bayesian Information Criterion framework.
 AICc/BIC-1: sample size as: number of sites in the alignment (920.0)
 AICc/BIC-2: sample size as: Sum of position's Shannon Entropy over the whole alignment (295.2)
 AICc/BIC-3: sample size as: align. length x num sequences x averaged (0-1)Sh. Entropy (1024.5)

B) Tree bipartition support statistics.

Based on the Shimodaira-Hasegawa-like P values for branch support calculated for each of the trees found in 41 PhyML maximum likelihood searches under JTT+G (40 using random sequential addition seed trees, the remaining one using a BioNJ tree).

tree_file	n_bip.	min	max	mean	median	std_dev	variance	%_NRB < 0.7	%_PRB [0.7-0.85]	%_MRB [.85-.95]	%_WRB [.95-.99]	%_HRB ≥ 0.99
my_IRR_IGF1R_IR_Invert_prof,phy10	55	0,01	1	0,82	0,94	0,26	0,0657	18,18	14,55	25,45	14,55	27,27
my_IRR_IGF1R_IR_Invert_prof,phy11	55	0,08	1	0,83	0,94	0,25	0,0635	16,36	14,55	21,82	18,18	29,09
my_IRR_IGF1R_IR_Invert_prof,phy12	55	0,21	1	0,83	0,94	0,23	0,0529	21,82	9,09	23,64	16,36	29,09
my_IRR_IGF1R_IR_Invert_prof,phy13	55	0,1	1	0,84	0,94	0,23	0,0521	16,36	16,36	18,18	20	29,09
my_IRR_IGF1R_IR_Invert_prof,phy14	55	0,01	1	0,8	0,92	0,28	0,0797	20	14,55	23,64	14,55	27,27
my_IRR_IGF1R_IR_Invert_prof,phy15	55	0,17	1	0,82	0,92	0,24	0,0561	23,64	9,09	23,64	14,55	29,09
my_IRR_IGF1R_IR_Invert_prof,phy16	55	0,06	1	0,85	0,94	0,21	0,0423	12,73	21,82	18,18	18,18	29,09
my_IRR_IGF1R_IR_Invert_prof,phy17	55	0,01	1	0,83	0,93	0,24	0,0582	18,18	18,18	18,18	18,18	27,27
my_IRR_IGF1R_IR_Invert_prof,phy18	55	0,01	1	0,83	0,93	0,23	0,0513	20	18,18	16,36	20	25,45
my_IRR_IGF1R_IR_Invert_prof,phy19	55	0,29	1	0,87	0,93	0,17	0,0279	16,36	14,55	25,45	14,55	29,09
my_IRR_IGF1R_IR_Invert_prof,phy1	55	0,01	1	0,79	0,94	0,28	0,0807	25,45	12,73	18,18	14,55	29,09
my_IRR_IGF1R_IR_Invert_prof,phy20	55	0,05	1	0,82	0,94	0,25	0,0638	20	14,55	16,36	18,18	30,91
my_IRR_IGF1R_IR_Invert_prof,phy21	55	0,02	1	0,84	0,93	0,23	0,0525	12,73	20	23,64	16,36	27,27
my_IRR_IGF1R_IR_Invert_prof,phy22	55	0,26	1	0,83	0,93	0,21	0,0422	23,64	14,55	20	14,55	27,27
my_IRR_IGF1R_IR_Invert_prof,phy23	55	0	1	0,81	0,94	0,27	0,0713	20	14,55	20	18,18	27,27
my_IRR_IGF1R_IR_Invert_prof,phy24	55	0,01	1	0,81	0,93	0,28	0,0796	18,18	10,91	29,09	16,36	25,45
my_IRR_IGF1R_IR_Invert_prof,phy25	55	0,01	1	0,81	0,94	0,27	0,071	20	12,73	20	16,36	30,91
my_IRR_IGF1R_IR_Invert_prof,phy26	55	0,02	1	0,81	0,93	0,26	0,069	23,64	12,73	20	18,18	25,45
my_IRR_IGF1R_IR_Invert_prof,phy27	55	0,01	1	0,81	0,93	0,25	0,0618	18,18	21,82	20	12,73	27,27
my_IRR_IGF1R_IR_Invert_prof,phy28	55	0	1	0,83	0,93	0,25	0,0606	16,36	16,36	21,82	18,18	27,27
my_IRR_IGF1R_IR_Invert_prof,phy29	55	0	1	0,84	0,93	0,24	0,056	12,73	21,82	20	18,18	27,27
my_IRR_IGF1R_IR_Invert_prof,phy2	55	0,01	1	0,79	0,93	0,29	0,0852	21,82	12,73	21,82	18,18	25,45
my_IRR_IGF1R_IR_Invert_prof,phy30	55	0,01	1	0,8	0,94	0,28	0,0756	23,64	12,73	20	18,18	25,45
my_IRR_IGF1R_IR_Invert_prof,phy31	55	0,01	1	0,82	0,93	0,25	0,0632	18,18	14,55	23,64	16,36	27,27
my_IRR_IGF1R_IR_Invert_prof,phy32	55	0,02	1	0,81	0,94	0,27	0,0723	23,64	10,91	20	18,18	27,27
my_IRR_IGF1R_IR_Invert_prof,phy33	55	0,01	1	0,8	0,94	0,31	0,0936	20	14,55	18,18	18,18	29,09
my_IRR_IGF1R_IR_Invert_prof,phy34	55	0,01	1	0,79	0,93	0,29	0,0843	23,64	14,55	21,82	12,73	27,27
my_IRR_IGF1R_IR_Invert_prof,phy35	55	0,12	1	0,83	0,94	0,23	0,0521	21,82	10,91	20	18,18	29,09
my_IRR_IGF1R_IR_Invert_prof,phy36	55	0	1	0,8	0,93	0,28	0,0778	21,82	12,73	23,64	12,73	29,09
my_IRR_IGF1R_IR_Invert_prof,phy37	55	0,01	1	0,79	0,94	0,29	0,0859	21,82	16,36	21,82	14,55	25,45
my_IRR_IGF1R_IR_Invert_prof,phy38	55	0,02	1	0,82	0,93	0,25	0,0612	20	12,73	25,45	14,55	27,27
my_IRR_IGF1R_IR_Invert_prof,phy39	55	0,03	1	0,78	0,93	0,29	0,0851	25,45	9,09	23,64	14,55	27,27
my_IRR_IGF1R_IR_Invert_prof,phy3	55	0,01	1	0,82	0,93	0,25	0,0645	20	10,91	25,45	16,36	27,27
my_IRR_IGF1R_IR_Invert_prof,phy40	55	0,01	1	0,82	0,94	0,25	0,0613	16,36	23,64	16,36	14,55	29,09
my_IRR_IGF1R_IR_Invert_prof,phy4	55	0,17	1	0,82	0,94	0,25	0,0602	20	10,91	21,82	20	27,27
my_IRR_IGF1R_IR_Invert_prof,phy5	55	0,04	1	0,83	0,94	0,23	0,0507	18,18	20	18,18	16,36	27,27
my_IRR_IGF1R_IR_Invert_prof,phy6	55	0	1	0,81	0,94	0,28	0,0757	21,82	10,91	25,45	16,36	25,45
my_IRR_IGF1R_IR_Invert_prof,phy7	55	0,02	1	0,78	0,93	0,3	0,0911	25,45	9,09	21,82	18,18	25,45
my_IRR_IGF1R_IR_Invert_prof,phy8	55	0,12	1	0,85	0,93	0,22	0,0503	14,55	14,55	25,45	16,36	29,09
my_IRR_IGF1R_IR_Invert_prof,phy9	55	0,01	1	0,8	0,94	0,28	0,0807	23,64	12,73	20	14,55	29,09
my_IRR_IGF1R_IR_Invert_prof,phy_NJ	55	0	1	0,79	0,93	0,3	0,0925	21,82	10,91	21,82	16,36	29,09
	mean	0,04804	1	0,81634	0,93414	0,256585	0,06637804	19,955853	14,36975	21,463170	16,496585	27,713902
	median	0,01	1	0,82	0,93	0,25	0,0638	20	14,55	21,82	16,36	27,27

The data indicate a good overall tree resolution, with a mean median support value of 0.93, calculated over the 41 trees. Forty four percent of the cumulative 2255 bipartitions in the sample had a significant support value ($P \geq 0.95$), and 65% of them had a ($P \geq 0.85$). Notice that means and median values are very similar. The range of model lnL values was: 30836.65814 - 30870.89200, only 34 units of difference. The highest-scoring tree highlighted by shading.

C) Shimodaira-Hasegawa comparison of 41 user-supplied PhyML trees.

Fourty of them used random sequential addition seed trees and the remaining one a (default) BioNJ starter phylogeny. All were run with PhyML 2.4.5 under the best-approximating JTT+G model.

Analysis performed with Puzzle 5.2 [3] using the randomly chosen tree #6 for model parameter estimation.

Tree	log L	difference	S.E.	p-1sKH	p-SH	c-ELW	2sKH
1	-30920.22	19.13	28.9019	0.2540 +	0.8270 +	0.0032 -	+
2	-30918.11	17.02	32.7880	0.2980 +	0.8130 +	0.0195 +	+
3	-30921.04	19.95	28.6171	0.2240 +	0.7840 +	0.0049 -	+
4	-30909.99	8.90	18.1504	0.3060 +	0.9380 +	0.0179 +	+
5	-30916.65	15.56	26.1724	0.2780 +	0.8540 +	0.0187 +	+
6	-30901.09	0.00	<---- best	1.0000 +	1.0000 +	0.1544 +	best
7	-30933.54	32.46	29.8335	0.1520 +	0.5110 +	0.0000 -	+
8	-30918.16	17.07	31.9574	0.2930 +	0.8390 +	0.0090 +	+
9	-30921.24	20.15	21.7312	0.1810 +	0.7080 +	0.0326 +	+
10	-30911.82	10.73	23.0560	0.3120 +	0.8600 +	0.0621 +	+
11	-30926.76	25.67	32.6045	0.2020 +	0.6290 +	0.0089 +	+
12	-30928.11	27.02	31.5468	0.2130 +	0.6390 +	0.0042 -	+
13	-30925.87	24.78	30.1233	0.2080 +	0.6750 +	0.0076 +	+
14	-30918.64	17.55	28.5998	0.2500 +	0.8370 +	0.0160 +	+
15	-30915.19	14.11	27.9301	0.3000 +	0.8820 +	0.0120 +	rdm tree#15
16	-30928.55	27.46	29.0529	0.1750 +	0.5880 +	0.0183 +	+
17	-30910.53	9.45	19.1169	0.3160 +	0.9290 +	0.0271 +	+
18	-30923.15	22.06	29.9950	0.2360 +	0.7320 +	0.0083 +	+
19	-30922.78	21.69	28.0707	0.2340 +	0.7210 +	0.0204 +	+
20	-30927.55	26.46	31.0046	0.1940 +	0.6410 +	0.0084 +	+
21	-30905.19	4.10	22.8222	0.4290 +	0.9470 +	0.1050 +	+
22	-30913.79	12.70	22.0795	0.2720 +	0.8750 +	0.0129 +	+
23	-30910.28	9.19	19.0054	0.2990 +	0.9390 +	0.0187 +	+
24	-30922.79	21.70	29.3545	0.2400 +	0.7660 +	0.0036 -	+
25	-30922.89	21.81	31.2019	0.2660 +	0.7270 +	0.0087 +	+
26	-30930.51	29.42	32.5653	0.1780 +	0.5560 +	0.0054 -	+
27	-30916.59	15.50	28.0001	0.2800 +	0.8600 +	0.0069 -	+
28	-30912.32	11.23	16.7926	0.2360 +	0.9110 +	0.0065 -	+
29	-30925.54	24.45	22.9266	0.1330 +	0.6980 +	0.0026 -	+
30	-30925.80	24.71	23.5154	0.1600 +	0.7310 +	0.0012 -	+
31	-30918.39	17.30	29.2052	0.2850 +	0.8420 +	0.0113 +	+
32	-30917.78	16.69	27.6657	0.2900 +	0.8420 +	0.0116 +	+
33	-30913.84	12.75	27.6496	0.3250 +	0.9200 +	0.0167 +	+
34	-30907.55	6.46	21.4700	0.3640 +	0.9500 +	0.0450 +	+
35	-30918.02	16.93	30.6274	0.2670 +	0.8320 +	0.0123 +	+
36	-30911.59	10.50	23.7767	0.3380 +	0.8860 +	0.0444 +	+
37	-30910.64	9.55	28.3319	0.3550 +	0.8650 +	0.0840 +	+
38	-30925.24	24.15	29.6290	0.2140 +	0.6880 +	0.0047 -	+
39	-30911.88	10.79	26.1383	0.3220 +	0.8780 +	0.0620 +	+
40	-30924.83	23.74	35.7654	0.2460 +	0.6610 +	0.0144 +	+
41	-30909.60	8.51	20.2645	0.3250 +	0.8920 +	0.0685 +	+ BioNJ tree

The columns show the results and p-values of the following tests:

- 1sKH** - one sided KH test based on pairwise SH tests
- SH** - Shimodaira-Hasegawa test (1999) [2]
- ELW** - Expected Likelihood Weight (Strimmer-Rambaut 2002)[4]
- 2sKH** - two sided Kishino-Hasegawa test (1989)[1].

Plus signs denote the confidence sets. Minus signs denote significant exclusion. All tests used 5% significance level. 1sKH, SH, and ELW performed 1000 resamplings using the REL method.

1sKH and 2sKH are correct to the 2nd position after the the decimal point of the log-likelihoods.

As shown by the table above, all competing trees were congruent when evaluated by the very conservative Shimodaira-Hasegawa test. However, the more stringent expected likelihood weights test uncovered 11 significantly incongruent topologies. The lnL scores of the best tree (sarted from random seed tree #15) and that one found starting from the defual BioNJ tree are not significantly different.

D) PhyML tree search statistics.

D1) Sorted log likelihood scores for the ML trees obtained for each individual tree search initiated from a random tree (phy*_phym1) vs. that obtained for the standard search initiated from a BioNJ tree.

```
-30836.65814 = my_IRR_IGF1R_IR_Invert_prof.phy15_phym1_stat.txt
-30840.27766 = my_IRR_IGF1R_IR_Invert_prof.phy29_phym1_stat.txt
-30841.18697 = my_IRR_IGF1R_IR_Invert_prof.phy40_phym1_stat.txt
-30844.51886 = my_IRR_IGF1R_IR_Invert_prof.phy_MJ_phym1_stat.txt
-30845.52360 = my_IRR_IGF1R_IR_Invert_prof.phy6_phym1_stat.txt
-30845.70280 = my_IRR_IGF1R_IR_Invert_prof.phy13_phym1_stat.txt
-30845.76546 = my_IRR_IGF1R_IR_Invert_prof.phy19_phym1_stat.txt
-30845.88096 = my_IRR_IGF1R_IR_Invert_prof.phy25_phym1_stat.txt
-30845.91526 = my_IRR_IGF1R_IR_Invert_prof.phy30_phym1_stat.txt
-30846.11650 = my_IRR_IGF1R_IR_Invert_prof.phy5_phym1_stat.txt
-30848.04128 = my_IRR_IGF1R_IR_Invert_prof.phy35_phym1_stat.txt
-30848.57785 = my_IRR_IGF1R_IR_Invert_prof.phy2_phym1_stat.txt
-30849.78780 = my_IRR_IGF1R_IR_Invert_prof.phy8_phym1_stat.txt
-30851.61455 = my_IRR_IGF1R_IR_Invert_prof.phy3_phym1_stat.txt
-30852.35625 = my_IRR_IGF1R_IR_Invert_prof.phy14_phym1_stat.txt
-30854.20135 = my_IRR_IGF1R_IR_Invert_prof.phy23_phym1_stat.txt
-30854.57105 = my_IRR_IGF1R_IR_Invert_prof.phy17_phym1_stat.txt
-30854.93661 = my_IRR_IGF1R_IR_Invert_prof.phy34_phym1_stat.txt
-30855.36022 = my_IRR_IGF1R_IR_Invert_prof.phy38_phym1_stat.txt
-30855.83467 = my_IRR_IGF1R_IR_Invert_prof.phy22_phym1_stat.txt
-30856.37565 = my_IRR_IGF1R_IR_Invert_prof.phy39_phym1_stat.txt
-30857.06373 = my_IRR_IGF1R_IR_Invert_prof.phy18_phym1_stat.txt
-30857.07095 = my_IRR_IGF1R_IR_Invert_prof.phy11_phym1_stat.txt
-30857.25147 = my_IRR_IGF1R_IR_Invert_prof.phy10_phym1_stat.txt
-30857.59641 = my_IRR_IGF1R_IR_Invert_prof.phy4_phym1_stat.txt
-30860.00784 = my_IRR_IGF1R_IR_Invert_prof.phy27_phym1_stat.txt
-30860.29513 = my_IRR_IGF1R_IR_Invert_prof.phy31_phym1_stat.txt
-30860.44945 = my_IRR_IGF1R_IR_Invert_prof.phy12_phym1_stat.txt
-30860.49945 = my_IRR_IGF1R_IR_Invert_prof.phy26_phym1_stat.txt
-30861.82375 = my_IRR_IGF1R_IR_Invert_prof.phy21_phym1_stat.txt
-30862.07270 = my_IRR_IGF1R_IR_Invert_prof.phy7_phym1_stat.txt
-30862.30288 = my_IRR_IGF1R_IR_Invert_prof.phy9_phym1_stat.txt
-30862.53409 = my_IRR_IGF1R_IR_Invert_prof.phy37_phym1_stat.txt
-30862.77819 = my_IRR_IGF1R_IR_Invert_prof.phy32_phym1_stat.txt
-30863.40874 = my_IRR_IGF1R_IR_Invert_prof.phy36_phym1_stat.txt
-30864.61757 = my_IRR_IGF1R_IR_Invert_prof.phy24_phym1_stat.txt
-30865.27667 = my_IRR_IGF1R_IR_Invert_prof.phy1_phym1_stat.txt
-30866.44167 = my_IRR_IGF1R_IR_Invert_prof.phy33_phym1_stat.txt
-30866.98699 = my_IRR_IGF1R_IR_Invert_prof.phy28_phym1_stat.txt
-30867.14938 = my_IRR_IGF1R_IR_Invert_prof.phy20_phym1_stat.txt
-30870.89200 = my_IRR_IGF1R_IR_Invert_prof.phy16_phym1_stat.txt
-30836.65814 = 1
-30840.27766 = 1
-30841.18697 = 1
-30844.51886 = 1
-30845.52360 = 1
-30845.70280 = 1
-30845.76546 = 1
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-30862.07270 = 1
-30862.30288 = 1
-30862.53409 = 1
-30862.77819 = 1
-30863.40874 = 1
-30864.61757 = 1
-30865.27667 = 1
-30866.44167 = 1
-30866.98699 = 1
-30867.14938 = 1
-30870.89200 = 1
```

D2) Frequency of the lnL scores.

These data show that three trees were found that had a better score than that found by the default PhyML search (starting from a BioNJ seed tree), although not significantly better, as shown by the SH and c-ELW tests above. The fact that as many tree islands were found as searches were started indicates it gets stuck in different peaks that are in a narrow height range of lnL scores: -30836.65814 (best) to -30870.89200 (worst).

References not cited in the paper:

[1] Kishino H, Hasegawa M (1989) Evaluation of the maximum likelihood estimate of the evolutionary tree topologies from DNA sequence data, and the branching order in hominoidea. *J Mol Evol* 29(2): 170-179.

[2] Shimodaira H, Hasegawa M (1999) Multiple comparisons of log-likelihoods with applications to phylogenetic inference. *Mol Biol Evol* 16: 1114-1116.

[3] Schmidt HA, Strimmer K, Vingron M, von Haeseler A (2002) TREE-PUZZLE: maximum likelihood phylogenetic analysis using quartets and parallel computing. *Bioinformatics* 18(3): 502-504.

[4] Strimmer K, Rambaut A (2002) Inferring confidence sets of possibly misspecified gene trees. *Proc Biol Sci* 269(1487): 137-142.