

MrBayes стартовый экран

```
mc [dmitry@dmitry-F80Q]:/  
dmitry@dmitry-F80Q:/$ gimp &  
[1] 7001  
dmitry@dmitry-F80Q:/$ mb  
  
MrBayes v3.2.2 x86  
  
(Bayesian Analysis of Phylogeny)  
  
Distributed under the GNU General Public License  
  
Type "help" or "help <command>" for information  
on the commands that are available.  
  
Type "about" for authorship and general  
information about the program.  
  
MrBayes >  
MrBayes > |
```

Nexus - команды

```
mc [dmitry@dmitry-F80Q]:/  
Commands that should be in a NEXUS file (data  
block, trees block or taxa block) include:  
  
Begin          -- Denotes beginning of block in file  
Dimensions     -- Defines size of character matrix  
End            -- Denotes end of a block in file  
Endblock       -- Alternative way of denoting end of a block  
Format         -- Defines character format in data block  
Matrix         -- Defines matrix of characters in data block  
Taxlabels      -- Defines taxon labels  
Translate      -- Defines alternative names for taxa  
Tree           -- Defines a tree  
  
Note that this program supports the use of the shortest unambiguous  
spelling of the above commands (e.g., "exe" instead of "execute").  
-----  
MrBayes > |
```

Входной файл 1

```
mc [dmitry@dmitry-F80Q]:~/Data/renat
s.nex      [----]  0 L: [ 1+ 0  1/1033] *(0 /866741b) 0035 0x02[*][X]
#NEXUS
[created with the loop/stem utility]

begin data;
<----->dimensions ntax=64 nchar=11949;
<----->format datatype=dna gap=- missing=?;
<----->matrix
<----->1CVS-N2c <----->ACGCTTAACAACAAAACAGAGAAGAAAAAGACAGCGTCAATTGCAAAGCAAAAAAT
<----->MRV <-->ACGCTTAACAACAAGACTAAGAAAGAGAGCGACATCGTAGCCTACAAGTCCAAAAAGTAACACC
<----->H08_1320 <----->ACGCTTAACAACAAAATCAGAGAAGAAGCAGACAGCATCATTTGCAAAACAAAAAT
<----->CTN-1-31 <----->ACGCTTAACAACAAAATCAAAGAAGAAACAGACAGTGTCAATTGCAAAACAAAAAT
<----->RAVMMGN <----->ACGCTTAACAACACAGATCAAAGAAAAACAGACAGCGTCAATGGCAGAGCAAAAAAT
<----->Ni-CE <-->ACGCTTAACAACAAAACCAAAGAAGAAGTATACAGCGTCATTTGCAAAGCAAAAAATGTAACACC
<----->SHBRV-18 <----->ACGCTTAACAACAAAATCAGAGAAGAAGTAGACAGTGTCTTTACAGAGCAAAAAAT
<----->serotype1 <---->ACGCTTAACAACAAAACCAAAGAAGAAGCAGACAGCGTCAATTGCAAAGCAAAAAAT
<----->Nishigahara <-->ACGCTTAACAACAAAACCAAAGAAGAAGTATACAGCGTCATTTGCAAAGCAAAAAAT
<----->8648084 <----->ACGCTTAACAACAAAACCAAAGAAGAAGTATACAGCGTCATTTGCAAAGCAAAAAAT
<----->9627197 <----->ACGCTTAACAACACAGATCAAAGAAAAACAGACAGCGTCAATGGCAGAGCAAAAAAT
<----->BR-Pfx1 <----->ACGCTTAACAACAAAATCAAAGAAGAAGCAGACAGCGTCAATTGCAAAAGCAAAAAAT
<----->CQ92 <-->ACGCTTAACAACAAAATCAGAGAAGAAGCTGACAGCGTCACTTGCAAAACAAAAATGTAACACC
<----->isolateJ <----->ACGCTTAACAACAAAATCAGAGAAGAAGCAGACAGCGTCACTTGCAAAACAAAAAT
<----->SH06 <-->ACGCTTAACAACAAAATCATAGAAGAAGCAGACAGCGTCAATTGTAAAGCAAAAAATGTAACACC
1 Помощь 2 Сох-ть 3 Блок 4 Замена 5 Копия 6 Пер-ть 7 Поиск 8 Уда-ть 9 МенюМС 10 Выход
```

Входной файл 2

```
mc [dmitry@dmitry-F80Q:~/Data/renat
s.nex      [----] 0 L:[ 67+21 88/1033] *(766604/866741b) 0009 0x009      [*][X]
<----->CTN-1  >ACGCTTAACAACCAAAATCAAAGAAGAAACAGACAGTGTCAATTTGCAAAAACAAAAATGTAACACCCCTACAATGGATGCCGA
<----->2GX4  <->ACGCTTAACAACCAAAATCAGAGAAGAAGCAGACAGTGTCAATTTGCAAAAACAAAAATGTAACACCCCTACAATGGATGCCGA
<----->2JX08-LEP  <----->ACGCTTAACAACCAAAATCAGAGAAGAAGCAGACAGCGTCAATTTGCAAAAACAAAAATGTAACACCCCTACAATG
<----->Flury-45  <----->ACGCTTAACAACCAAAACCAAGAAGAAGCAGACAGCGTCAATTTGCAAAAGCAAAAAATGTAACACCCCTACAATG
<----->Flury-HEP  <----->ACGCTTAACAACCAAAACCAAGAAGAAGCAGACAGCGTCAATTTGCAAAAGCAAAAAATGTAACACCCCTACAATG
<----->;
end;

begin mrbayes;
<----->[Define pairs for the doublet model]
<----->Pairs      37:11913, 38:11912, 39:11911, 40:11910, 56:70, 57:69, 58:68, 59:67,.
<----->      74:169, 75:168, 76:167, 77:166, 79:164, 87:156, 88:155, 89:154,.
<----->      90:153, 91:152, 92:151, 93:150, 94:149, 95:148, 109:136, 110:135,.
<----->      111:134, 112:133, 113:132, 114:131, 116:129, 117:128, 200:210, 201:209,.
<----->      202:208, 223:284, 224:283, 225:282, 227:280, 228:279, 229:277,.
<----->      232:274, 233:273, 234:272, 236:268, 237:267, 238:266, 245:259, 246:258,.
<----->      247:257, 287:11816, 288:11815, 289:11814, 292:11812, 293:11811, 294:11810, 295:11
<----->      296:11808, 297:11807, 303:11806, 304:11805, 309:11801, 310:11800, 311:11799, 315:
<----->      316:11794, 317:11793, 318:11792, 319:11791, 325:349, 326:348, 327:347, 331:344,.
<----->      332:343, 334:342, 335:341, 336:340, 354:380, 355:379, 356:378, 357:377,.
<----->      358:376, 387:11571, 388:11570, 389:11569, 390:11568, 391:11567, 392:11566, 393:11
<----->      395:11563, 412:11548, 413:11547, 414:11546, 416:11544, 417:11543, 418:11542, 419:
<----->      421:11539, 422:11538, 423:11537, 429:498, 430:497, 431:496, 432:495, 433:494,.
<----->      436:493, 437:492, 438:491, 439:488, 440:487, 441:486, 442:485, 444:483,.
<----->      445:482, 447:480, 448:479, 454:472, 455:471, 456:470, 457:469, 459:468,.
<----->      507:11530, 508:11529, 509:11528, 510:11527, 511:11526, 512:11525, 513:11521, 514:
<----->      515:11519, 516:11518, 517:11517, 518:11516, 519:11515, 520:11514, 529:720, 530:71
<----->      531:718, 533:715, 534:714, 535:713, 537:710, 538:709, 539:708, 540:707,.
<----->      541:706, 542:705, 543:693, 544:692, 545:691, 546:690, 547:689, 562:634,.
<----->      563:633, 564:632, 565:631, 566:630, 568:628, 569:627, 573:623, 574:622,.
<----->      583:613, 584:612, 585:611, 586:610, 587:609, 588:608, 639:653, 641:651,.
<----->      642:650, 643:649, 644:648, 658:681, 659:680, 660:679, 661:678, 662:677,.
<----->      663:676, 724:11467, 725:11466, 726:11465, 727:11464, 728:11463, 735:11453, 736:11
<----->      737:11451, 738:11450, 744:767, 745:766, 746:765, 747:764, 748:763, 749:762,.

1Помощь 2Сох-ить 3Блок 4Замена 5Копия 6Пер-ить 7Тоиск 8Удалить 9МенюМС 10Выход
```

Входной файл - команды для MrBayes

```
mc [dmitry@dmitry-F80Q]:~/Data/renat
s nex      [----] 0 L:[1000+33 1033/1033] *(866741/866741b) <EOF>      [*][X]
<-----> 11596 11597 11598 11599 11608 11609 11611 11612 11613 11614 11620 11621 11622 1
<-----> 11634 11635 11636 11639 11640 11641 11642 11651 11652 11653 11654 11655 11656 1
<-----> 11665 11671 11672 11673 11681 11682 11683 11684 11686 11687 11697 11698 11699 1
<-----> 11709 11711 11712 11713 11714 11720 11721 11722 11729 11730 11731 11737 11738 1
<-----> 11759 11760 11761 11762 11763 11786 11787 11788 11789 11791 11792 11793 11794 1
<-----> 11808 11809 11810 11811 11812 11814 11815 11816 11820 11821 11822 11829 11830 1

<-----> set nowarn=yes;

<-----> [Define partitions]
<-----> partition smart = 2:stems,loops;
<-----> set partition = smart;
[! Model taking into account possible co-evolution in stems -----]
<-----> lset applyto=(1) nucmodel=doublet;
<-----> lset applyto=(2) nucmodel=4by4;
<-----> lset nst=6;

<-----> prset ratepr=variable;

<-----> mcmc nruns=2 nchains=1 ngen=2000000 file=loops.mb;
<-----> sumt burnin=10000;
<-----> sump burnin=10000;
[! SIMPLE Model -----]
<-----> lset applyto=(1) nucmodel=4by4;
<-----> lset nst=6;

<-----> prset ratepr=variable;

<-----> mcmc nruns=4 nchains=1 ngen=2000000 file=noloops.mb;
<-----> sumt burnin=10000;
<-----> sump burnin=10000;
end;
```

1 Помощь 2 Сох-ить 3 Блок 4 Замена 5 Копия 6 Пер-ить 7 Поиск 8 Удалить 9 Меню MS 10 Выход

Работа программы

```
mc [dmitry@dmitry-F80Q]:~/Data/renat
Chain 3 -- -1777.393537 -- 41.533077
Chain 4 -- -1808.374908 -- 41.533077

Using a relative burnin of 25.0 % for diagnostics

Chain results (500000 generations requested):

  0 -- [-1795.659] (-1781.329) (-1741.670) (-1797.612) * [-1730.201] (-1771.454) (-1777.3
94) (-1808.375)
  500 -- (-1431.199) (-1426.961) (-1444.689) [-1424.099] * (-1433.346) (-1413.450) [-1416.8
70] (-1413.578) -- 0:16:38
 1000 -- (-1389.280) (-1411.758) [-1399.630] (-1418.725) * (-1396.991) (-1416.413) [-1374.4
63] (-1381.750) -- 0:16:37
 1500 -- [-1365.174] (-1387.890) (-1363.084) (-1374.242) * (-1355.240) (-1389.716) [-1347.3
75] (-1349.238) -- 0:16:36
 2000 -- (-1331.495) (-1380.664) [-1334.979] (-1349.584) * (-1345.539) (-1358.087) (-1346.2
49) [-1332.884] -- 0:16:35
 2500 -- (-1315.563) (-1324.580) [-1323.708] (-1326.693) * (-1341.673) (-1338.132) [-1311.1
17] (-1319.454) -- 0:16:34
 3000 -- [-1312.270] (-1296.969) (-1323.540) (-1307.936) * (-1325.058) (-1332.783) (-1304.5
17) [-1286.098] -- 0:16:33
 3500 -- (-1285.361) [-1286.797] (-1300.200) (-1298.024) * (-1323.671) (-1314.144) (-1290.5
74) [-1279.597] -- 0:16:32
 4000 -- [-1273.000] (-1292.349) (-1290.957) (-1286.588) * (-1300.242) (-1301.603) (-1288.7
19) [-1278.337] -- 0:16:31
 4500 -- [-1259.029] (-1272.175) (-1280.718) (-1282.459) * (-1279.207) [-1272.463] (-1277.3
66) (-1265.798) -- 0:16:30
 5000 -- [-1248.841] (-1266.956) (-1276.093) (-1273.178) * (-1277.992) [-1270.027] (-1274.7
05) (-1263.001) -- 0:16:29

Average standard deviation of split frequencies: 0.108030

 5500 -- [-1246.005] (-1274.674) (-1268.075) (-1269.107) * (-1287.618) (-1264.607) [-1261.7
77] (-1265.167) -- 0:16:28
```

завершение анализа

```
mc [dmitry@dmitry-F80Q]:~/Data/renat
587) [-1242.723] -- 0:00:14
493500 -- [-1238.924] (-1253.936) (-1237.608) (-1243.823) * (-1234.175) [-1233.514] (-1238.
244) (-1235.872) -- 0:00:13
494000 -- [-1235.492] (-1238.025) (-1247.655) (-1251.338) * (-1240.197) (-1244.204) (-1236.
716) [-1236.304] -- 0:00:12
494500 -- (-1234.804) (-1245.597) [-1235.088] (-1246.440) * (-1230.840) (-1244.946) [-1240.
594] (-1237.807) -- 0:00:11
495000 -- (-1230.552) (-1239.078) [-1238.693] (-1256.402) * [-1234.853] (-1254.510) (-1236.
884) (-1235.106) -- 0:00:10

Average standard deviation of split frequencies: 0.007306

495500 -- (-1242.760) (-1238.937) [-1241.213] (-1243.814) * (-1238.797) (-1239.914) (-1244.
720) [-1235.012] -- 0:00:09
496000 -- (-1241.200) [-1232.956] (-1243.373) (-1245.550) * (-1232.398) (-1266.981) [-1242.
530] (-1234.680) -- 0:00:08
496500 -- (-1231.555) [-1234.590] (-1235.161) (-1244.621) * [-1240.347] (-1240.433) (-1245.
935) (-1234.435) -- 0:00:07
497000 -- (-1237.697) (-1233.934) [-1234.630] (-1250.061) * (-1238.360) (-1237.671) (-1247.
628) [-1231.662] -- 0:00:06
497500 -- (-1250.320) [-1234.912] (-1244.369) (-1250.735) * (-1230.575) [-1231.433] (-1244.
598) (-1237.339) -- 0:00:05
498000 -- (-1254.175) (-1243.721) (-1241.866) [-1244.773] * [-1238.031] (-1239.060) (-1251.
927) (-1233.847) -- 0:00:04
498500 -- (-1246.839) (-1239.467) (-1235.916) [-1246.559] * [-1236.945] (-1238.356) (-1246.
444) (-1238.486) -- 0:00:03
499000 -- (-1238.776) (-1241.762) (-1243.222) [-1244.091] * (-1251.189) [-1236.644] (-1244.
418) (-1246.113) -- 0:00:02
499500 -- (-1239.531) [-1244.638] (-1246.311) (-1239.048) * (-1244.222) (-1237.778) (-1254.
480) [-1240.568] -- 0:00:01
500000 -- [-1230.194] (-1236.677) (-1234.771) (-1237.302) * (-1236.631) (-1241.170) (-1243.
139) [-1239.183] -- 0:00:00

Average standard deviation of split frequencies: 0.007532

Continue with analysis? (yes/no):
```

Тестируемые предположения

шаперн	Uniform/Exponential/Fixed	<u>Uniform(0.0,200.0)</u>
Ratecorrpr	Uniform/Fixed	Uniform(-1.0,1.0)
Pinvarpr	Uniform/Fixed	Uniform(0.0,1.0)
Covswitchpr	Uniform/Exponential/Fixed	Uniform(0.0,100.0)
Symdirihyperpr	Uniform/Exponential/Fixed	Fixed(Infinity)
Topologypr	Uniform/Constraints/Fixed	Uniform
Br lenspr	Unconstrained/Clock/Fixed	Unconstrained:Exp(10.0)
Treeagepr	Exponential/Gamma/Fixed	Exponential(1.0)
Speciationpr	Uniform/Exponential/Fixed	Exponential(1.0)

constraints

```
>constraint golovanogi = golova nogi
```

```
>constraint nogolovanogi negative = golova nogi
```

включить топологическое ограничение:

```
>prset topologypr = constraints(golovanogi)
```

```
>mcmc
```

```
>sump
```

```
>prset topologypr = constraints(nogolovanogi)
```

```
>mcmc
```

```
>sump
```

constraints

```
>constraint golovanogi = golova nogi
```

```
>constraint nogolovanogi negative = golova nogi
```

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>prset topologypr = constraints(golovanogi)
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```
>sump
```

```
>prset topologypr = constraints(nogolovanogi)
```

```
>mcmc
```

```
>sump
```

constraints

```
>constraint golovanogi = golova nogi
```

```
>constraint nogolovanogi negative = golova nogi
```

включить топологическое ограничение:

```
>prset topologypr = constraints(golovanogi)
```

```
>mcmc
```

```
>sump
```

```
>prset topologypr = constraints(nogolovanogi)
```

```
>mcmc
```

```
>sump
```

Оценка качества анализа

```
mc [dmitry@dmitry-F80Q]:~/Data/renat
```

plateaus. Of course, this is not a guarantee that you are at stationarity. Also examine the convergence diagnostics provided by the 'sump' and 'sunt' commands for all the parameters in your model. Remember that the burn in is the number of samples to discard. There are a total of $n_{gen} / \text{samplefreq}$ samples taken during a MCMC analysis.

Overlay plot for all 4 runs:

(1 = Run number 1; 2 = Run number 2 etc.) 35% (several runs) the sites are under strong constraining selection ($\omega(-) = 0.086$). Only a small fraction of sites, around 4%, are under positive selection ($\pi(+)$). Examination of the positive selection probabilities and codon site ω value reveals which sites are most likely to be experiencing positive selection. For instance, the evidence is strong that sites (212, 243, 251, 14, 14, 3, 244, 14, 4, 192, 293, 294) = 0.998, $\omega = 2.21$.

4.3 Sampling Across the GTR Model Space

A standard approach to Bayesian phylogenetics is to first select an appropriate substitution model using a model testing approach, such as those implemented in `ModelTest` (Anisimova et al. 2000) or `jModelTest` (Darriba et al. 2012). An alternative, more elegant approach is to sample across the substitution model space in the Bayesian Estimated marginal likelihoods for runs sampled in `MrBayes` (Huelsenbeck and Ronquist 2001) or `RevBayes` (Huelsenbeck et al. 2012). (Use the harmonic mean for Bayes factor comparisons of models.)

Результат

```
mc [dmitry@dmitry-F80Q]:~/Data/renat
Overwriting file "stem129.nex.lstat"
Estimated marginal likelihoods for runs sampled in files
"nloops129.mb.run1.p", "nloops129.mb.run2.p", etc:
(Use the harmonic mean for Bayes factor comparisons of models)
(Values are saved to the file stem129.nex.lstat)

Run Arithmetic means, Harmonic mean about 85% (pi(-) ) of the sites are under
positive selection (pi(-) = 0.086 ). Only a small fraction of
sites, are under positive selection (pi(+) ). Examination of the
positive probability codon site omega values reveals which sites
are most likely to be experiencing positive selection. For instance, the evidence is
strong that site (292,293,294) is under positive selection (pr+(292,293,294) =
0.998 , omega(292,293,294) = 1.21 ).
Model parameter summaries over all 4 runs sampled in files
"nloops129.mb.run1.p", "nloops129.mb.run2.p" etc:
Summaries are based on a total of 3004 samples from 4 runs.
Each run produced 1001 samples of which 751 samples were included.
Parameter summaries saved to file "stem129.nex.pstat"
Overwriting file "stem129.nex.pstat"

4.2.8. Summary of the Model Space

95% HPD Interval
Parameter Mean Variance Lower Upper Median min ESS+ avg ESS
PSRF+
ModelTest or jModelTest (Posada, 1998, 2008). An alternative, more elegant
approach, is to sample across the substitution model space in the Bayesian
TL(all) 1.032381 0.004811 0.987273 1.175181 1.030231 751.00 751.00
1.000 MC analysis itself (Huelsenbeck et al., 2004), removing the need for a priori
r(A<->C){all} 0.100893 0.000420 0.064738 0.142813 0.099379 395.49 475.52
0.999 del testing. The purpose of this tutorial is to demonstrate how to set up an
```

Дерево

```
mc [dmitry@dmitry-F80Q]:~/Data/renat
|----- HN10 (2)
|----- SH06 (3)
|----- 9147FRA (4)
|----- Sanafox (5)
|----- 9001FRA (9)
|----- 9704ARG (10)
|----- 292293294 (12)
|----- SHBRV-18 (11)
|----- H-08-1320 (8)
Looking at the values, we get MRV (6) about 85% (pi(-)) of the sites are under
string constraining selection (omega(-) = 0.086). Only a small fraction of
sites, around 1%, are under positive selection (pi(+)). Examination of the
positive selection probabilities and codon site omega values reveals which sites
are most likely to be experiencing positive selection. For instance, the evidence is
string that site (291,293,294) is under positive selection (pi(292,293,294) =
0.998, omega(292,293,294) = 1.21).
|-----| 0.050 expected changes per site
4.3 Sampling Across the GTR Model Space
Calculating tree probabilities...
Credible sets of trees (187 trees sampled):
50 % credible set contains 4 trees
90 % credible set contains 46 trees
95 % credible set contains 78 trees
99 % credible set contains 157 trees (S, 2008). An alternative, more elegant
approach is to sample across the substitution model space in the Bayesian
setting burn-in to 2000
Summarizing parameters in 4 files (noloops129.mb.run1.p, the need for a priori
noloops129.mb.run2.p, etc)
Writing summary statistics to file noloops129.mb.pstat
```

BEAUTi & BEAST

mc [dmitry@dmitry-F80Q]:~/sandbox/BEASTv1.8.2/bin

Левая панель

Имя	Размер	Время	Правки
/			
/bin	4096	февр. 19 08:11	
/boot	12288	февр. 19 08:11	
/cdrom	4096	авг. 18 2014	
/dev	4120	февр. 21 07:32	
/etc	12288	февр. 22 08:54	
/home	4096	июня 2 2015	
/lib	4096	февр. 18 06:43	
/lost+found	16384	авг. 18 2014	
/media	4096	июня 23 2015	
/mnt	4096	апр. 11 2014	
/opt	4096	июля 23 2014	
/proc	0	февр. 21 15:31	
/root	4096	окт. 20 2014	
/run	820	февр. 21 07:49	
/sbin	12288	февр. 19 08:11	
/selinux	4096	июня 12 2012	
/srv	4096	июля 23 2014	
/sys	0	февр. 21 15:31	
/tmp	4096	февр. 22 09:17	
/usr	4096	февр. 10 13:59	
/var	4096	авг. 18 2014	
@initrd.img	33	февр. 10 14:00	
@initrd.img.old	33	дек. 23 10:06	
@vmlinuz	30	февр. 10 14:00	
@vmlinuz.old	30	дек. 23 10:06	

/usr

Правая панель

~/sandbox/BEASTv1.8.2/bin

Имя	Размер	Время	Правки
..			
*beast	653	марта 5 2015	
*beauti	573	марта 5 2015	
igr0.log	3346633	апр. 20 2015	
igr0.ops	1420	апр. 20 2015	
igr0.trees	35388K	апр. 20 2015	
igr0.xml	71644	апр. 20 2015	
igr1.log	3560867	апр. 17 2015	
igr1.ops	1420	апр. 17 2015	
igr1.trees	35404K	апр. 17 2015	
igr1.xml	72692	апр. 17 2015	
igr_start	286298	апр. 17 2015	
*loganalyser	596	марта 5 2015	
*logcombiner	596	марта 5 2015	
*treeannotator	598	марта 5 2015	
*treestat	599	марта 5 2015	

-BBERPX-

Совет: (F13 (или Shift-F3) вызывает просмотрщик в режиме необработанных данных:ori

dmitry@dmitry-F80Q:~/sandbox/BEASTv1.8.2/bin\$

1.Помощь 2.Меню 3.Просмотр 4.Правка 5.Копия 6.Перенос 7.Нактылог 8.Удалить 9.МенюМС 10.Выход