

# Metódy tvorby evolučných stromov

metóda tvorby stromov	vzdialenosti	typ dát DNA sekvencie (alebo iné znaky)
zhlukovací algoritmus	UPGMA neighbor-joining tree	
optimalizačné kritérium	minimum evolution tree	parsimónia maximum likelihood → Bayesova analýza

## Bayesova analýza



Bayes, T. 1763. An essay towards solving a problem in the doctrine of chances. *Phil. Trans. Roy. Soc. London* 53: 370-418.

[ 370 ]

quodque solum, certa nitri signa præbere, sed plura concurrere debere, ut de vero nitro producto dubium non relinquatur.

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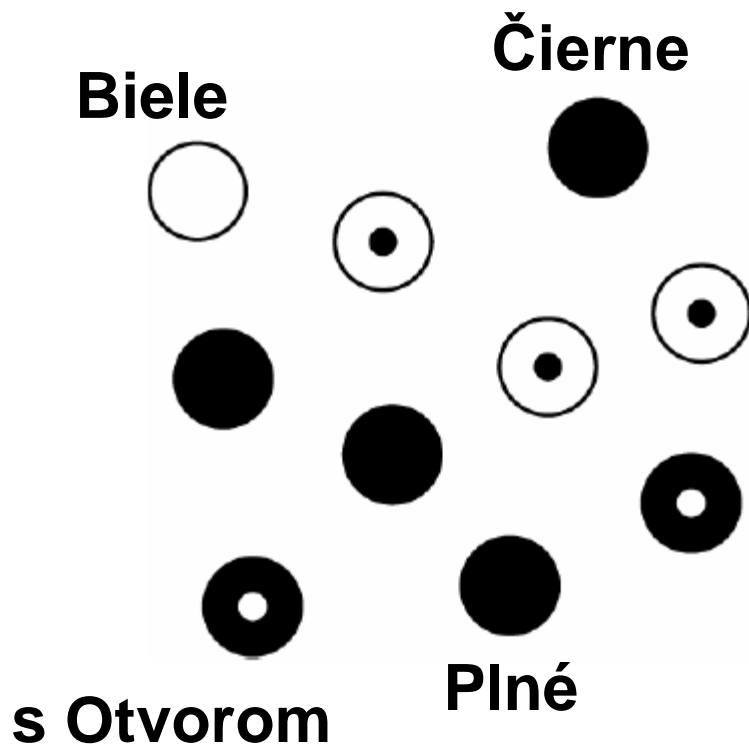
LII. *An Essay towards solving a Problem in the Doctrine of Chances. By the late Rev. Mr. Bayes, F. R. S. communicated by Mr. Price, in a Letter to John Canton, A. M. F. R. S.*

Dear Sir,

Read Dec. 23, 1763. **I** Now send you an essay which I have found among the papers of our deceased friend Mr. Bayes, and which, in my opinion, has great merit, and well deserves to be preserved. Experimental philosophy, you will find, is nearly interested in the subject of it; and on this account there seems to be particular reason for thinking that a communication of it to the Royal Society cannot be improper.

He had, you know, the honour of being a member of that illustrious Society, and was much esteemed by many in it as a very able mathematician. In an introduction which he has writ to this Essay, he says, that his design at first in thinking on the subject of it was, to find out a method by which we might judge concerning the probability that an event has to happen, in given circumstances, upon supposition that we know nothing concerning it but that, under the same circum-

## Spojená pravdepodobnosť



$$\Pr(B) = 0,4$$

$$\Pr(\check{C}) = 0,6$$

$$\Pr(O) = 0,5$$

$$\Pr(P) = 0,5$$

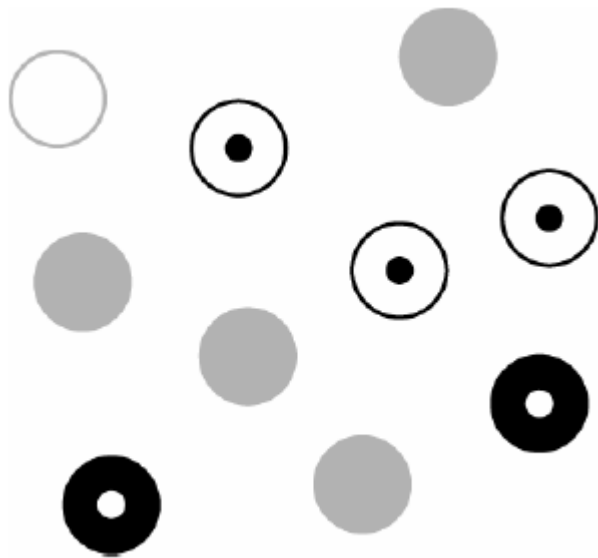
$$\Pr(\bullet\circ) = \Pr(\check{C},O) = 0,2$$

$$\Pr(\bullet) = \Pr(\check{C},P) = 0,4$$

$$\Pr(\odot) = \Pr(B,O) = 0,3$$

$$\Pr(\circ) = \Pr(B,P) = 0,1$$

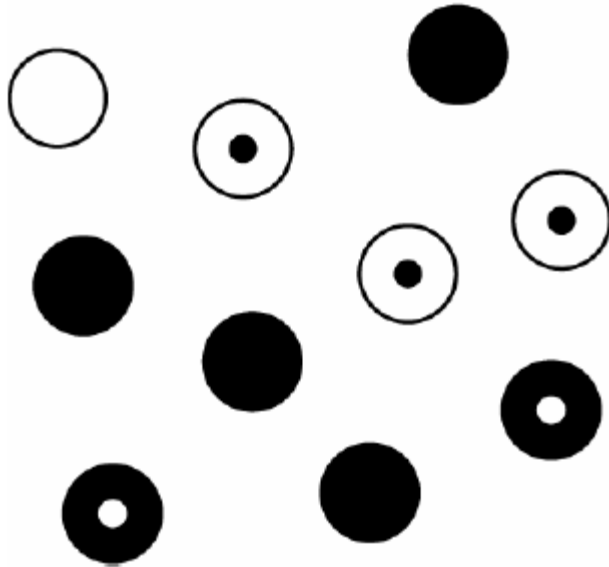
## Podmienečná pravdepodobnosť



$$\Pr(\check{C}|O) = 2/5 = 0,4$$

pravdepodobnosť Č  
za predpokladu, že platí O  
(t. j. vylúčime všetky P)

## Bayesovo pravidlo



$$\Pr(\check{C}, O) = 0,2 =$$

$$= \Pr(O) \times \Pr(\check{C}|O) = \Pr(\check{C}) \times \Pr(O|\check{C})$$

$$1/2 \times 2/5 = 3/5 \times 1/3$$

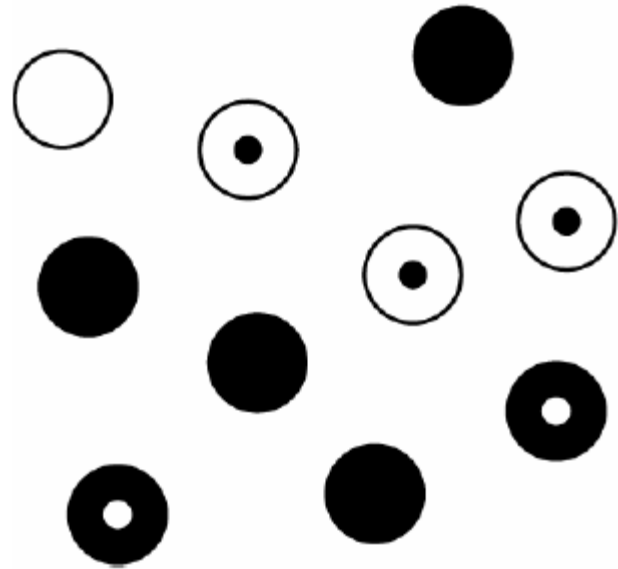
$$\Pr(\check{C}|O) = \frac{\Pr(\check{C}) \times \Pr(O|\check{C})}{\Pr(O)}$$

$$= \frac{3/5 \times 1/3}{1/2} = 2/5$$

## Marginálna pravdepodobnosť

$$\Pr(\check{C}|O) = \frac{\Pr(\check{C}) \times \Pr(O|\check{C})}{\Pr(O)}$$

$$\Pr(B|O) = \frac{\Pr(B) \times \Pr(O|B)}{\Pr(O)}$$



$$\Pr(O) = \Pr(B,O) + \Pr(\check{C},O) = [\Pr(B) \times \Pr(O|B)] + [\Pr(\check{C}) \times \Pr(O|\check{C})]$$

$$1/2 = 3/10 + 1/5 = [4/10 \times 3/4] + [3/5 \times 1/3]$$

## Bayesovo pravidlo

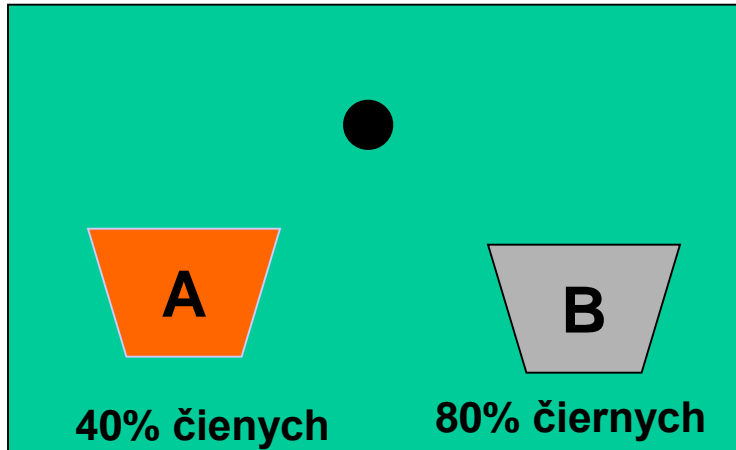
$$\Pr(\text{strom} \mid \text{dáta}) = \frac{\Pr(\text{dáta} \mid \text{strom}) \times \Pr(\text{strom})}{\Pr(\text{dáta})}$$

$$\Pr(\text{hypotéza} \mid \text{dáta}) = \frac{\Pr(\text{dáta} \mid \text{hypotéza}) \times \Pr(\text{hypotéza})}{\Pr(\text{dáta})}$$

- $\Pr(\text{strom} \mid \text{dáta})$  = posteriórna pravdepodobnosť  
= pravdepodobnosť, že strom je správny
- $\Pr(\text{dáta} \mid \text{strom})$  = vierohodnosť (likelihood) stromu
- $\Pr(\text{strom})$  = apriórna (prior) pravdepodobnosť stromu
- $\Pr(\text{dáta})$  = pravdepodobnosť dát (konštanta počítaná za všetky stromy, ktorá zaručuje, že suma posteriorných pravdepodobností = 1)

**Umožňuje počítat' pravdepodobnosti rôznych hypotéz vzhľadom k existujúcim dátam**

## Príklad: čierne a biele kamene



$$\begin{aligned}\Pr(D,H) &= \Pr(D)\Pr(H|D) \\ &= \Pr(H)\Pr(D|H)\end{aligned}$$

$$\Pr(H|D) = \Pr(H) \Pr(D|H) / \Pr(D)$$

dáta – vybrali sme čierny kameň  
hypotézy – ktorá urna to bola?

$\Pr(H|D)$  = posteriórna pravdepodobnosť, t.j. pravdepodobnosť  
hypotézy, za predpokladu známych dát

$\Pr(D|H)$  = vierohodnosť (likelihood) hypotézy, t.j. pravdepodobnosť  
dát, za predpokladu hypotézy

$\Pr(H)$  = apriórna (prior) pravdepodobnosť hypotézy

$\Pr(D)$  = nepodmienená pravdepodobnosť dát, t.j. suma všetkých  $\Pr(H)\Pr(D|H)$  pre  
všetky hodnoty H

Lewis, P. O. 2001b. Phylogenetic systematics turns over a new leaf.  
Trends Ecol. Evol. 16: 30-37.



## Vierohodnosť (likelihood)

**vierohodnosť je pravdepodobnosť, že kameň bude čierny, za predpokladu hypotézy o príslušnej urne**

**vierohodnosť (likelihood) pre urnu A je 0,4**

**vierohodnosť (likelihood) pre urnu B je 0,8**

**Pr (vybraný bol čierny kameň)**

**= (0.5)(0.4) + (0.5)(0.8) = 0.6** - suma všetkých  $\Pr(H)\Pr(D|H)$  pre všetky hodnoty H (urna A a urna B)

## **Posteriórna pravdepodobnosť**

**Pr (urna A / vybraný bol čierny kameň)**

**= (0.5)(0.4) / 0.6 = 1/3**

**Pr (urna B / vybraný bol čierny kameň)**

**= (0.5)(0.8) / 0.6 = 2/3**

**T.j. pravdepodobnosť, že kameň pochádza z urny B je 2/3, ide o upravenú verziu apriórnej pravdepodobnosti, ktorá bola 0,5**

V predošlom príklade sa jednalo o hypotézy s diskretnými hodnotami, pri Bayesovej analýze ide ale zväčša o kontinuálne parametre. V takých prípadoch pravdepodobnosti diskretných hypotéz nahrádzajú funkcie hustoty pravdepodobnosti.

$$\Pr(\theta | D) = \frac{\Pr(D | \theta) \Pr(\theta)}{\sum_{\theta} \Pr(D | \theta) \Pr(\theta)}$$

Vierohodnosť hypotézy  $\theta$

Apriórna pravdepodobnosť hypotézy  $\theta$

Posteriórna pravdepodobnosť hypotézy  $\theta$

Marginálna pravdepodobnosť dát

Apriórna  
hustota pravdepodobnosti

Vierohodnosť

$$f(\theta | D) = \frac{f(D | \theta) f(\theta)}{\int_{\theta} f(D | \theta) f(\theta) d\theta}$$

Posteriórna  
hustota pravdepodobnosti

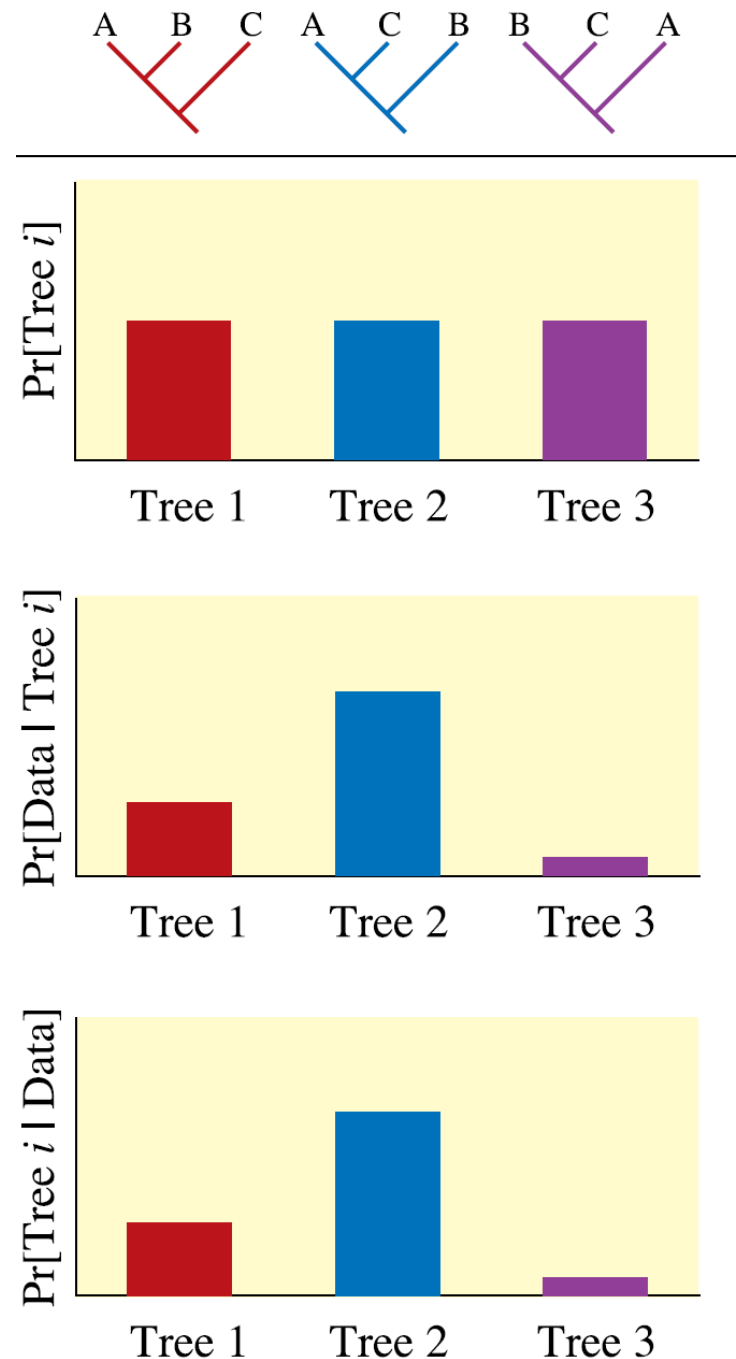
Marginálna pravdepodobnosť  
dát

Huelsenbeck, J. P., F. Ronquist, R. Nielsen & J. P. Bollneck. 2001. Bayesian inference of phylogeny and its impact on evolutionary biology. *Science* 294: 2310-2314.

**Apriórna pravdepodobnosť** – pravdepodobnosť stromu, predtým než sa robia akékoľvek pozorovania, väčšinou majú všetky stromy rovnakú pravdepodobnosť (môže byť aj iná – napr. na základe taxonomických poznatkov)

**Vierohodnosť (likelihood)** – proporčne závislá od pravdepodobnosti dát/pozorovaní (DNA alignment) pri danej topológii stromu; počíta sa s použitím modelov evolúcie znakov

**Posteriórna pravdepodobnosť stromu** – pravdepodobnosť stromu pri daných dátach/pozorovaniach; získa sa kombináciou apriórnej pravdepodobnosti a vierohodnosti pre každý strom s použitím Bayesovho pravidla



Pri počítaní **posteriórnych pravdepodobností** Bayesovým pravidlom nastáva problém, keď potrebujeme **sumarizovať informáciu o všetkých stromoch** a za všetky stromy všetky **dĺžkové parametre konárov** ako aj za všetky **parametre substitučných modelov**.

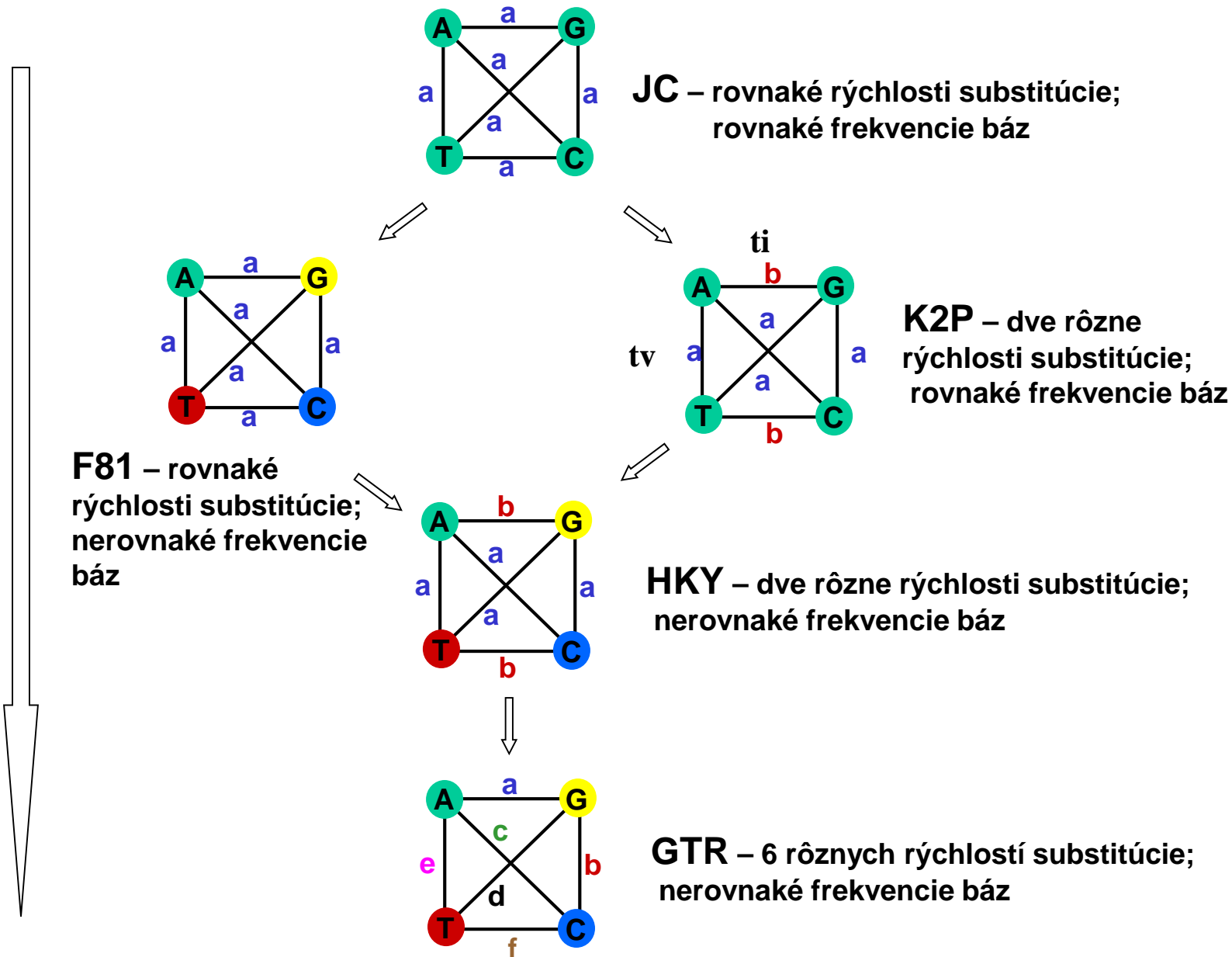
Preto sa využíva „**Markov chain**“ (reťaz), ktorá sa pohybuje v priestore definovanom parametrami modelu.

Každý **krok pri Markovovej reťazi zahŕňa náhodnú modifikáciu** topológie stromu, dĺžky konárov alebo parametra v substitučnom modeli. Ak je **posteriórna pravdepodobnosť** pre daný strom **väčšia**, tento krok sa akceptuje.

Ak je **posteriórna pravdepodobnosť menšia**, potom sa uplatní funkcia, ktorá je založená na pomere novej a starej posteriórnej pravdepodobnosti. Rozhodnutie či je krok akceptovaný alebo nie závisí od tohto pomeru.

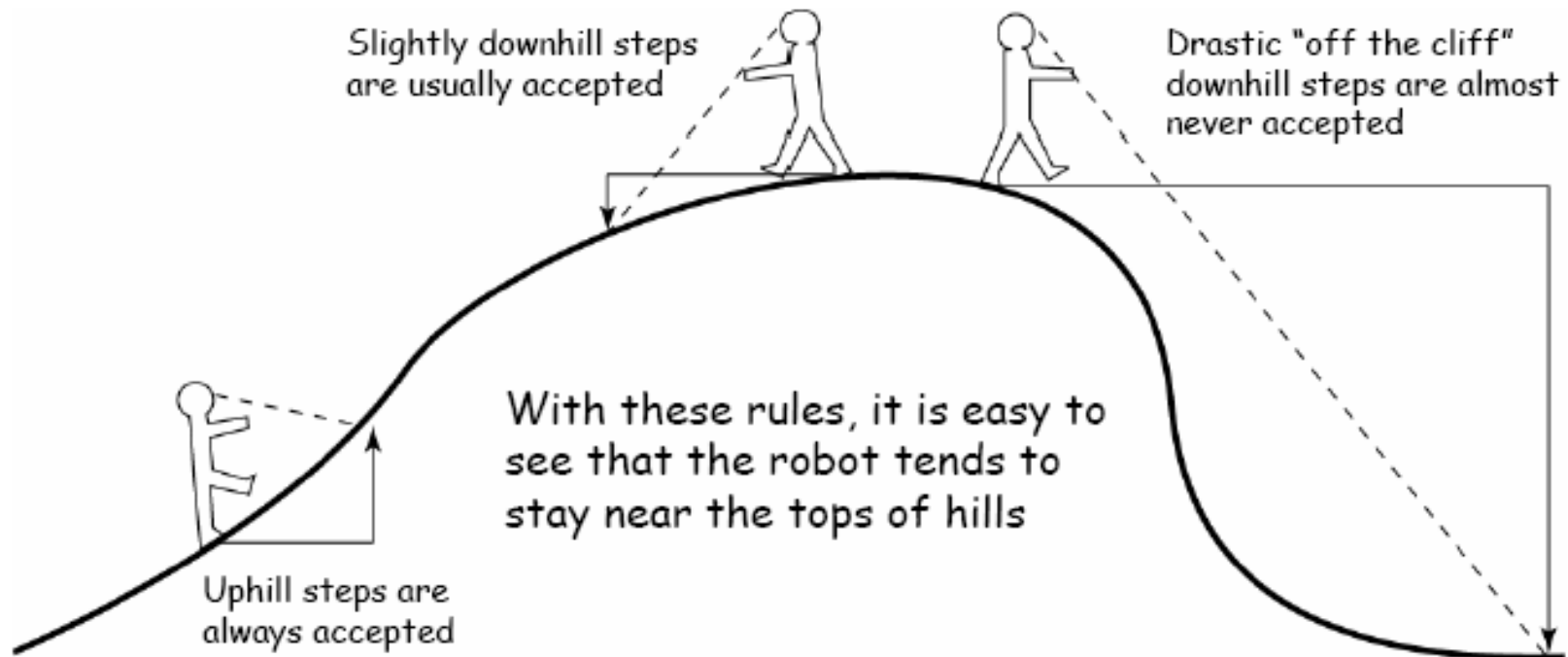
# Substitučné modely

Zvyšujúci sa počet parametrov modelu



# MCMC – Markov chain Monte Carlo metóda

## MCMC robot's rules

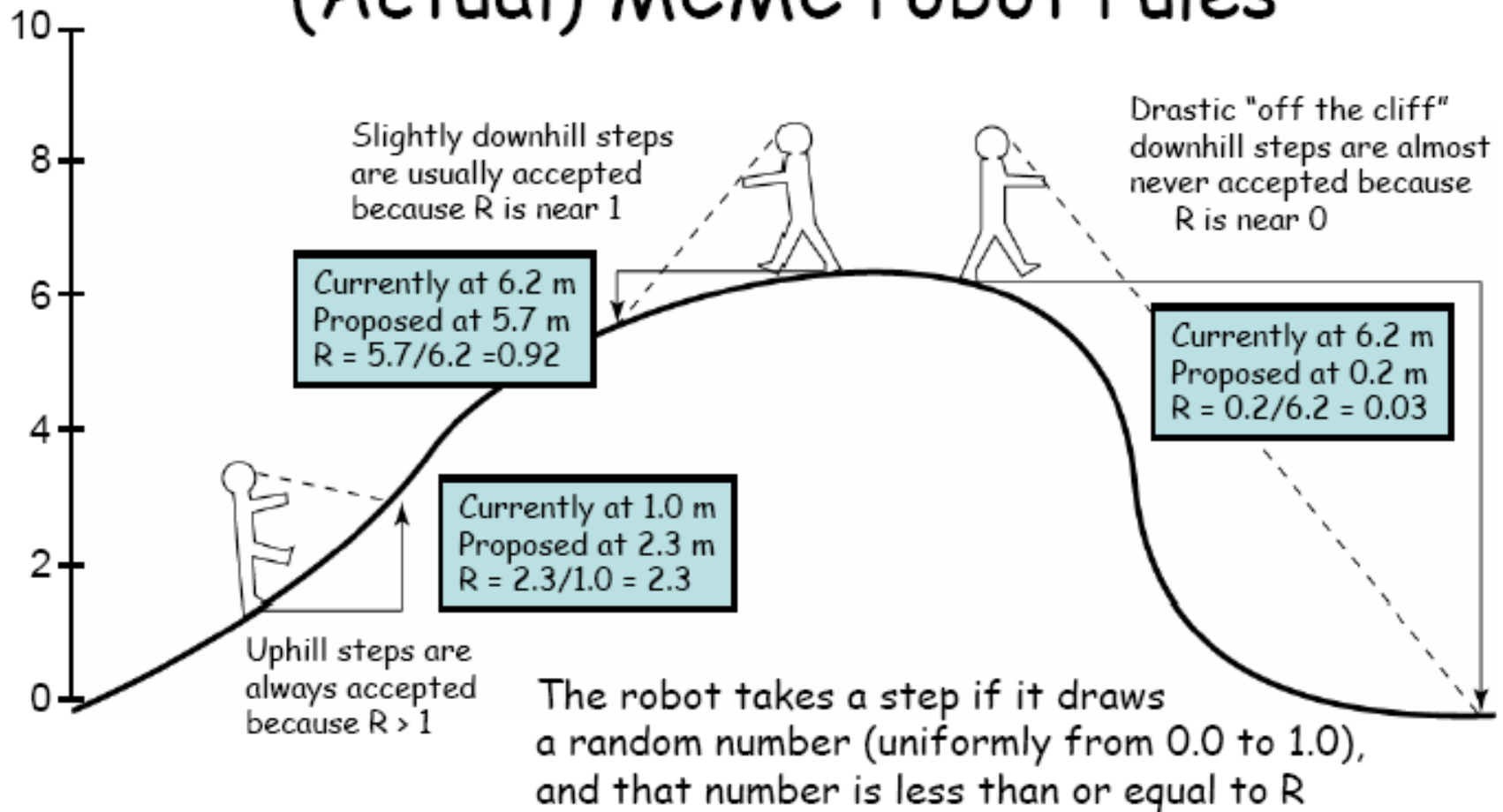


Lewis, P. O. 2001. Phylogenetic systematics turns over a new leaf. Trends Ecol. Evol. 16: 30-37.

Paul O. Lewis, Woods Hole Molecular Evolution Workshop, 2006

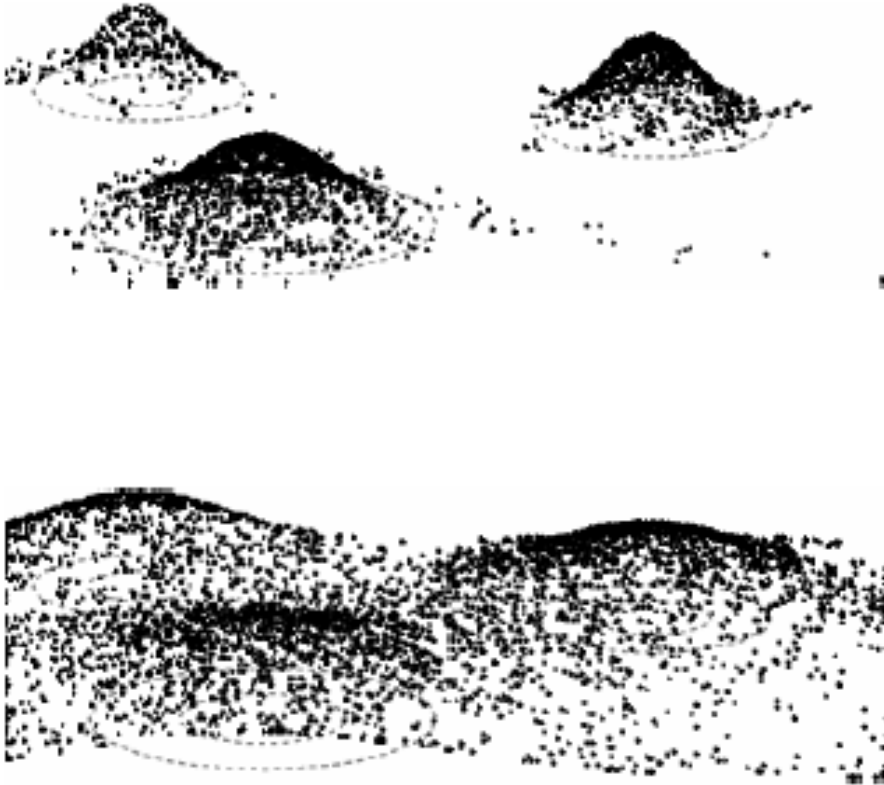
# MCMC – Markov chain Monte Carlo metóda

## (Actual) MCMC robot rules

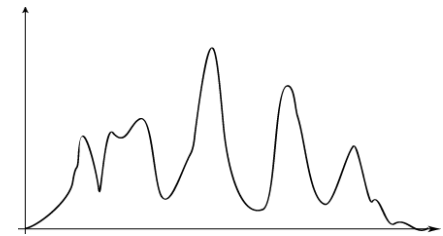




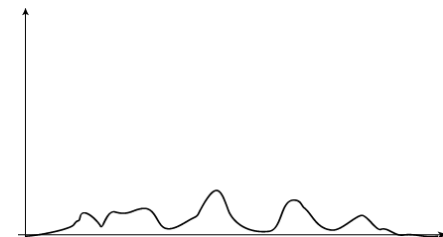
# MCMCMC – Metropolis coupled Markov chain Monte Carlo metóda



**Studená krajina,  
vysoké vrchy a hlboké  
doliny**



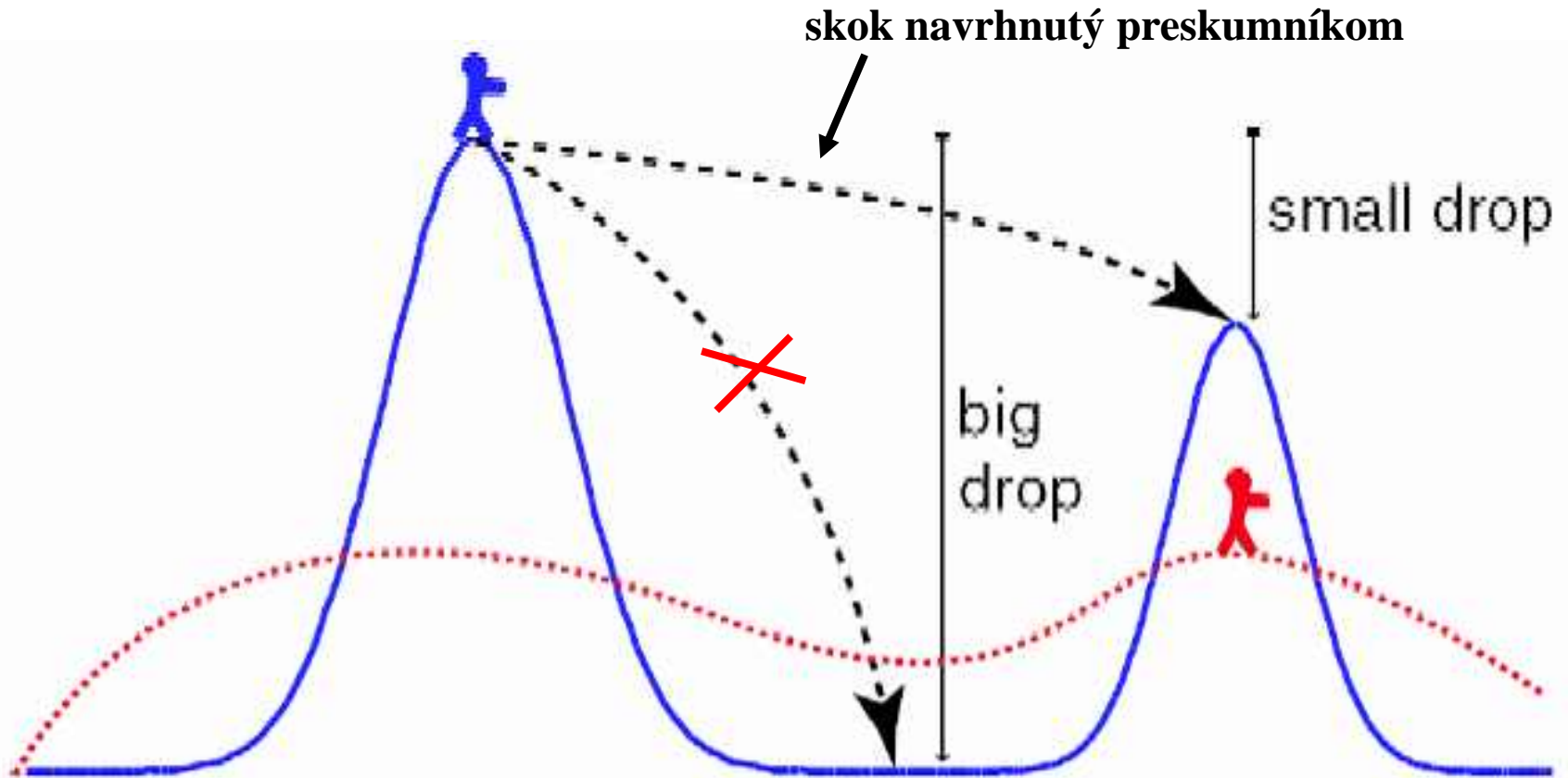
**Prehriata krajina,  
nízke vrchy a plytké  
doliny**



# MCMCMC –

## Metropolis coupled Markov chain Monte Carlo metóda

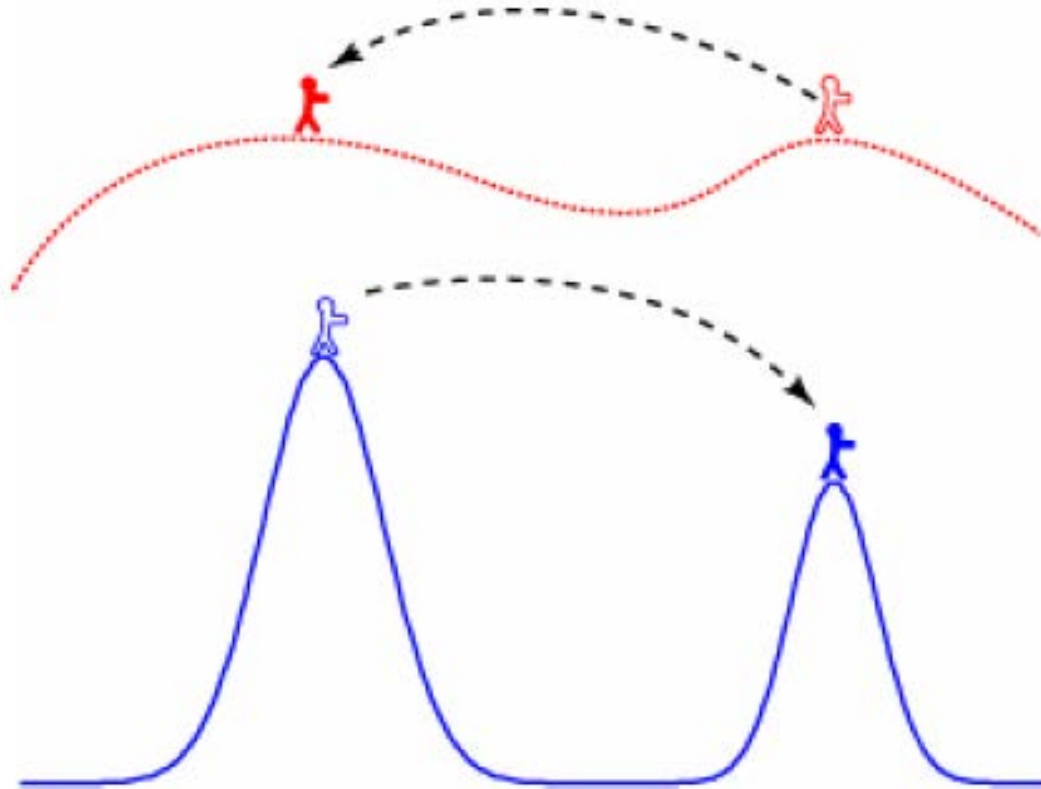
**Prehriata reťaz (heated chain) slúži studenej reťazi (cold chain) ako prieskumník**



## MCMCMC –

### Metropolis coupled Markov chain Monte Carlo metóda

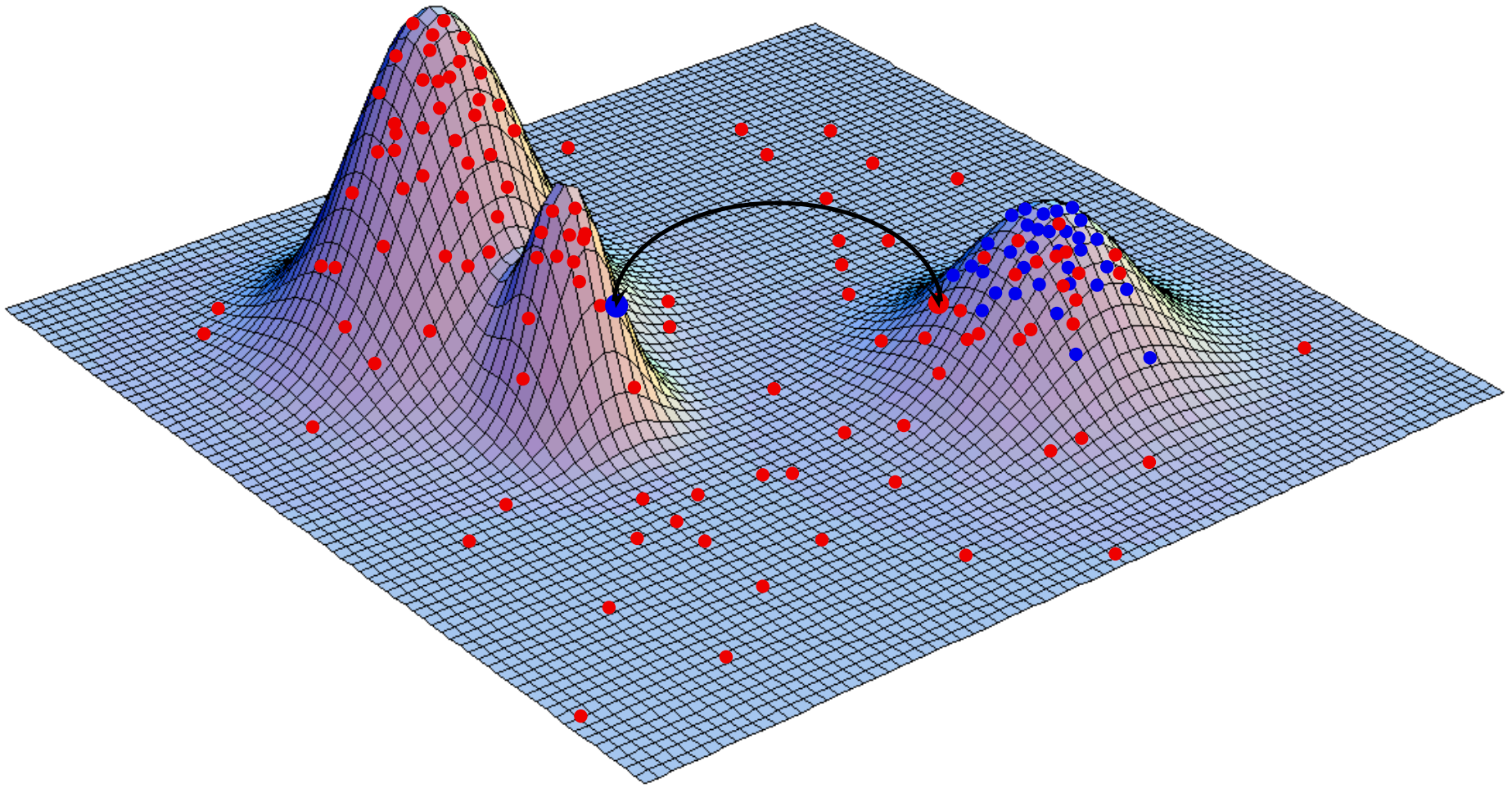
V každej generácii je istá pravdepodobnosť, že si **prehriata** a **studená** reťaz vymenia svoje pozície, studená reťaz sa takto môže dostať na vyšší vrch

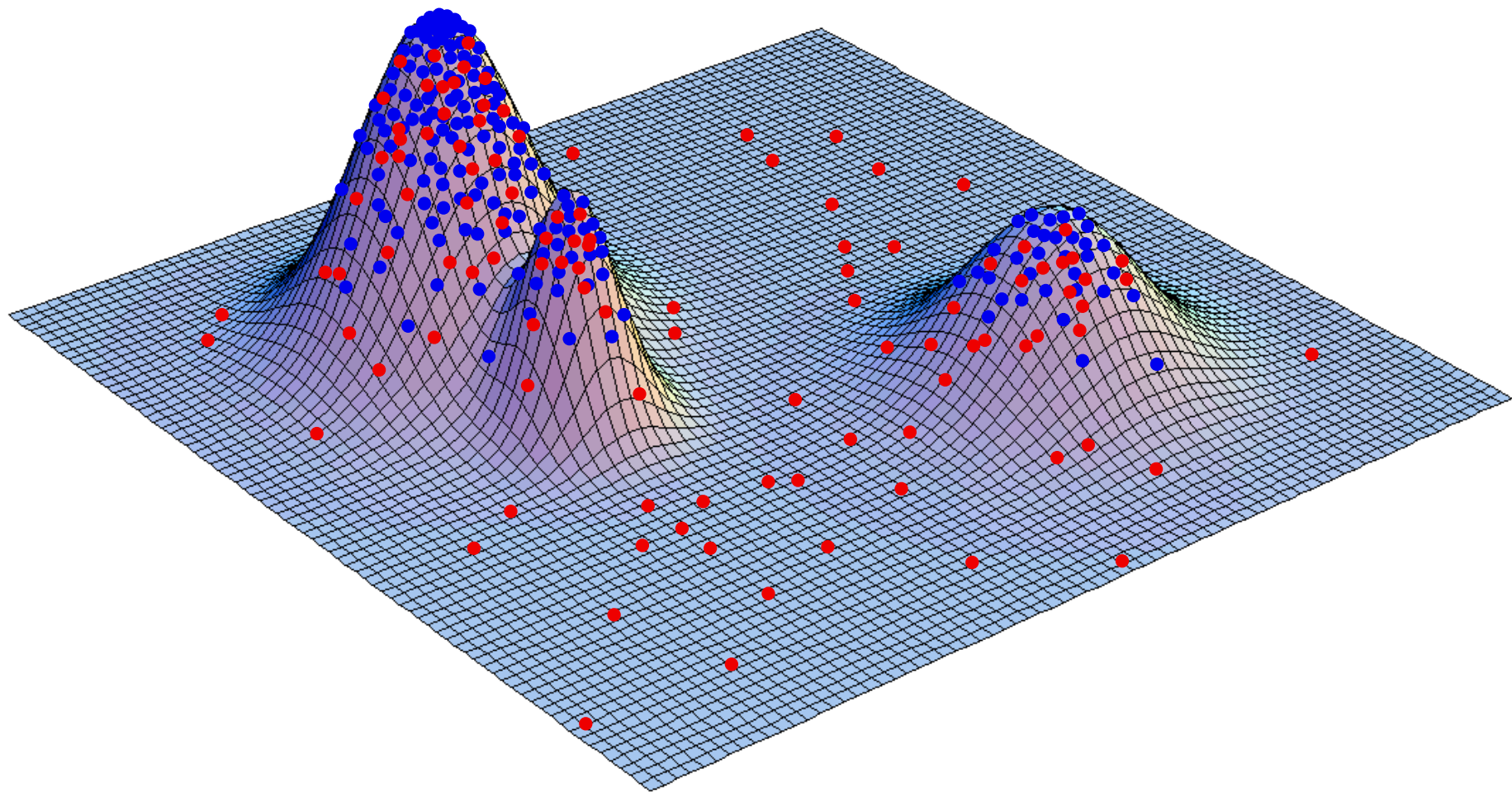


## MCMCMC –

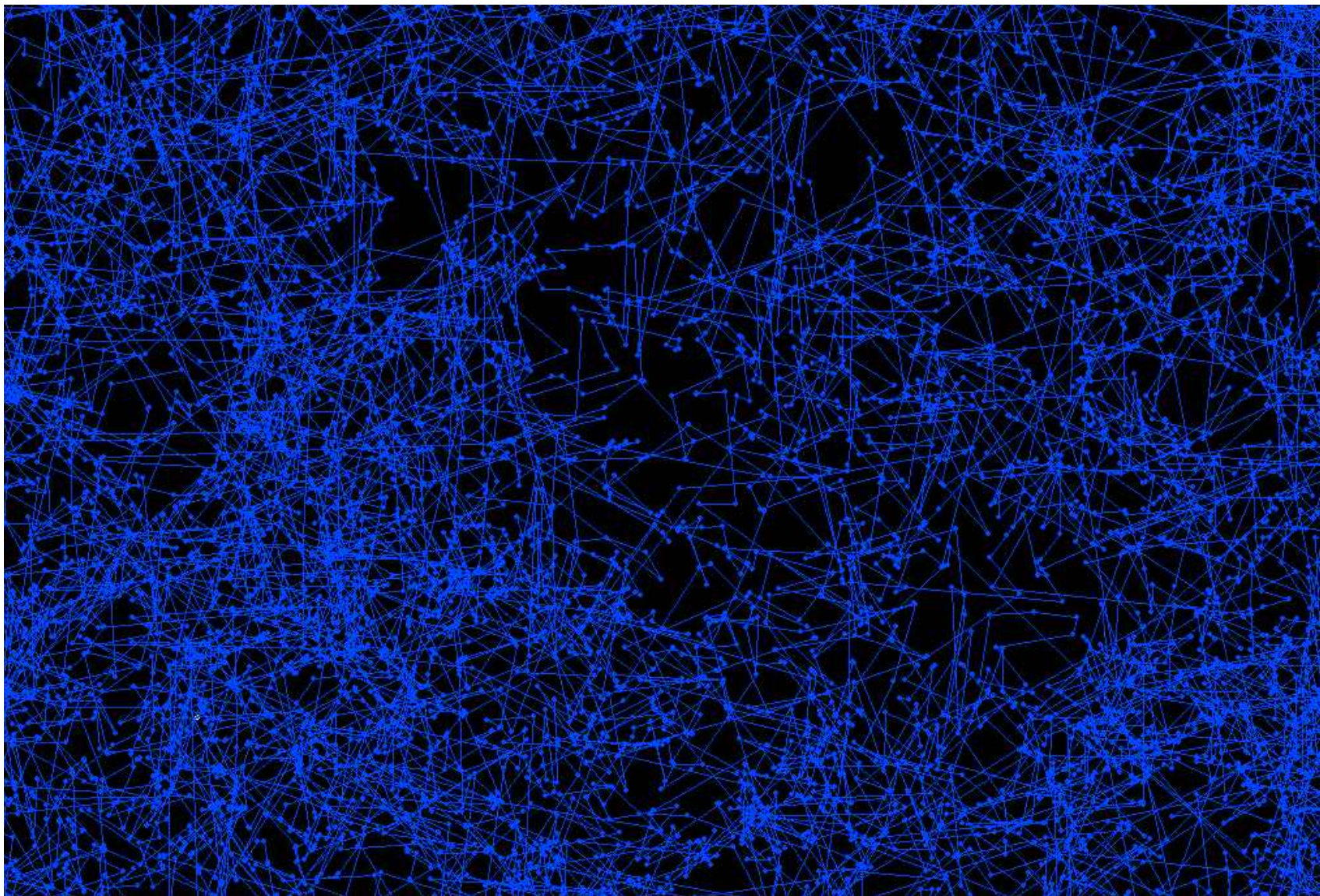
### Metropolis coupled Markov chain Monte Carlo metóda

V každej generácii je istá pravdepodobnosť, že si **prehriata** a **studená** reťaz vymenia svoje pozície, studená reťaz sa takto môže dostať na vyšší vrch





# MCMC – Markov chain Monte Carlo metóda



**Robot robí len náhodné kroky**

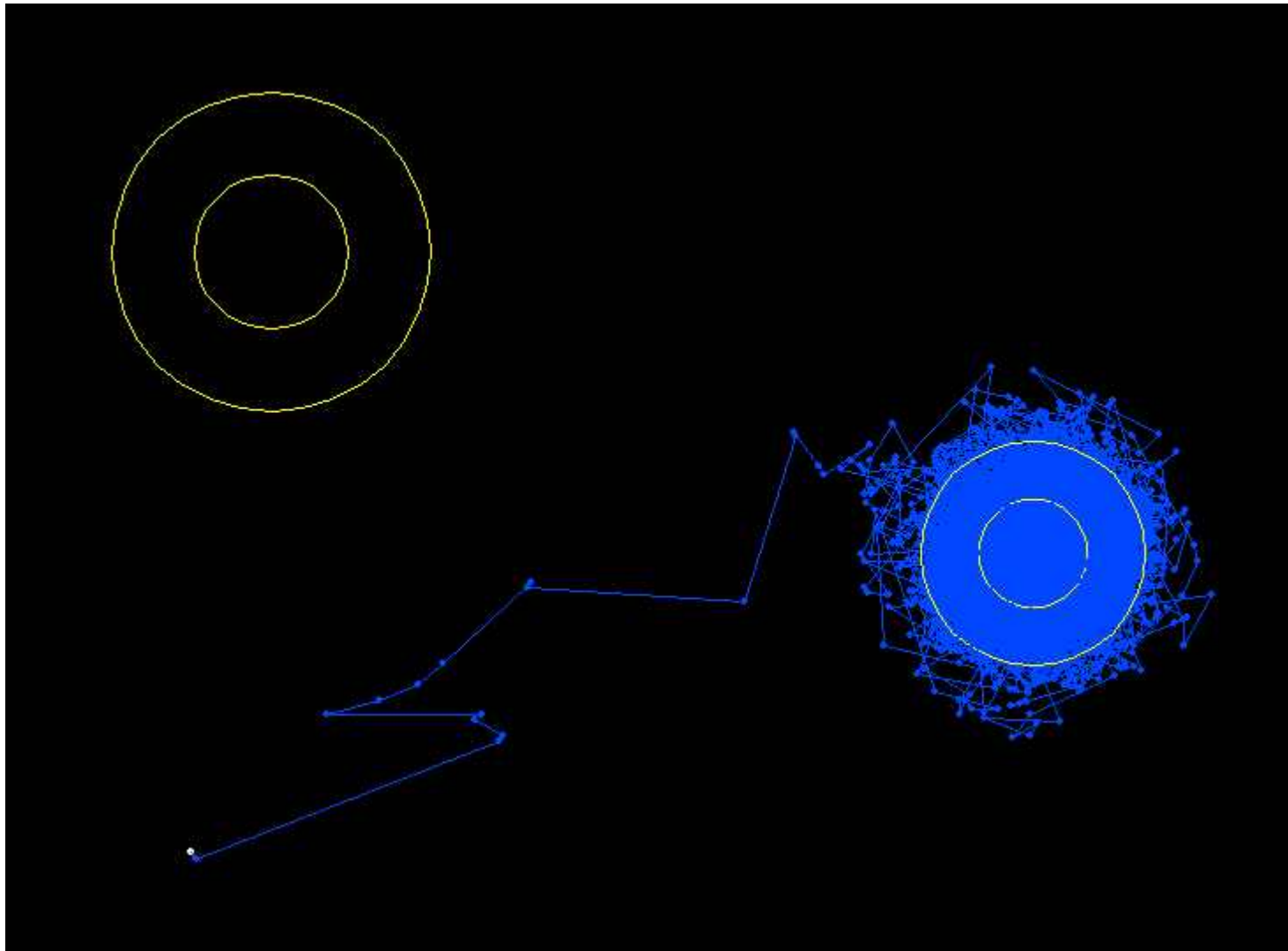
**vnútorný kruh – 50%**  
**vonkajší kruh – 95%**



**náhodný smer krokov, dĺžka  
krokov má gama distribúciu**

**V krajine sú dva vrchy a robot po niekoľkých krokoch  
(„burn-in period“) dôjde po jeden z vrchov ...**

## MCMC – Markov chain Monte Carlo metóda

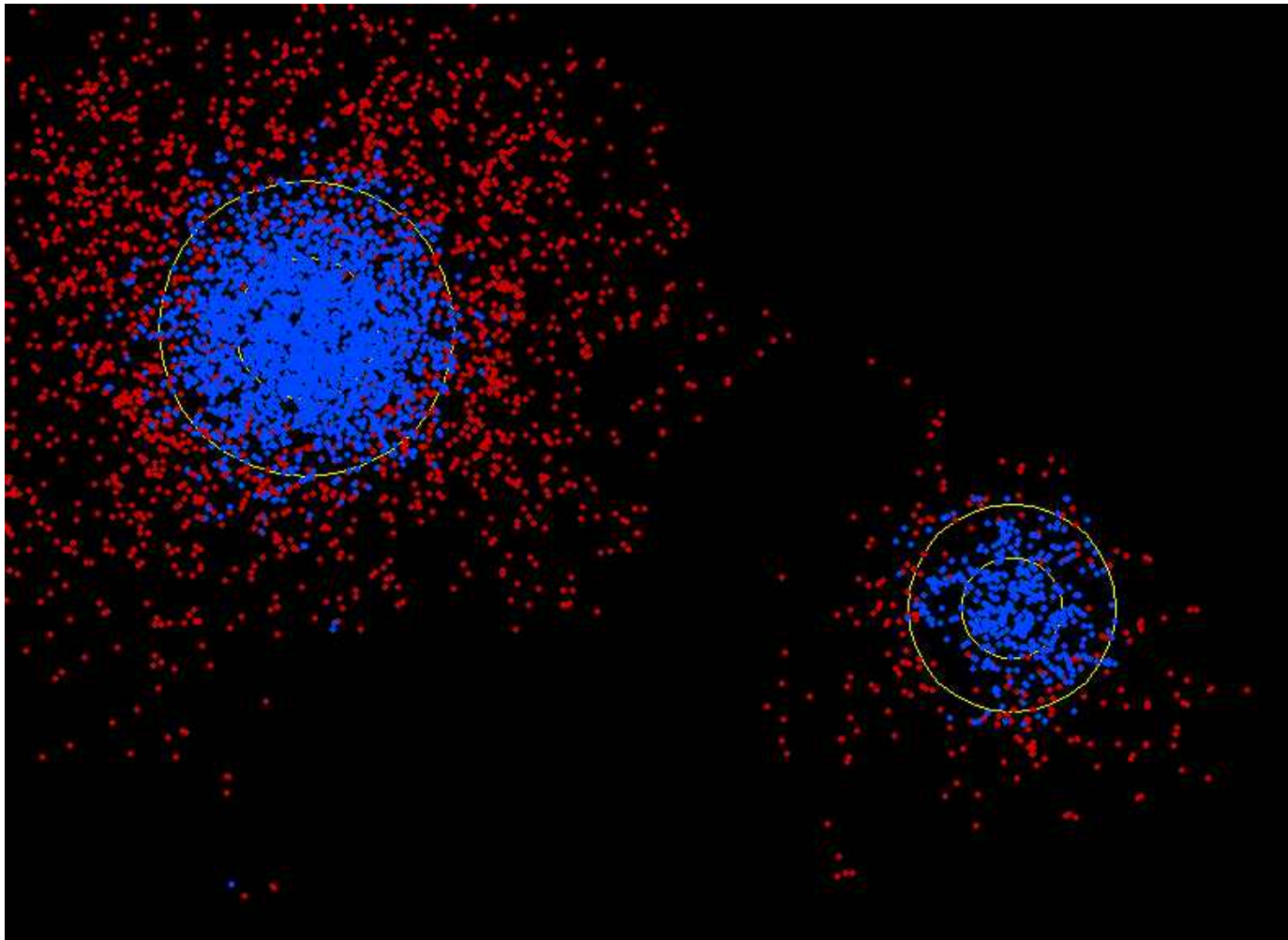


**... kde aj zostane, hoci v krajine je aj vyšší vrch**



# MCMCMC –

## Metropolis coupled Markov chain Monte Carlo metóda



**Prehriata reťaz** (kroky robota, ktorý funguje ako prieskumník),  
umožní **studenej reťazi** (robotovi) dosiahnuť vyšší vrch ...

## **MCMC – Markov chain Monte Carlo method**

**„Krajina“ – v skutočnosti evolučné stromy s určitou dĺžkou konárov a s ďalšími parametrami**

**„Výška vrchu“ – posteriórna hustota pravdepodobnosti je produktom:**

**vierohodnosti – pravdepodobnosti dát pri danom strome a hodnotách jeho parametrov (dĺžky konárov, substitučných parametrov, rýchlostí zmien na jednotlivých pozíciách)**

**apriórnej hustoty pravdepodobnosti**

# MCMC – Markov chain Monte Carlo metóda

## Jednotlivé kroky:

**Začne sa s náhodne vybraným stromom a arbitrárne zvolenými dĺžkami konárov a parametrami modelu**

**Každá generácia pozostáva z jednej náhodne vybranej možnosti z nasledovných dvoch:**

**Zvolí sa iný strom a ten sa buď prijme alebo odmietne**

**Zvolí sa iná hodnota parametra modelu a ten sa buď prijme alebo odmietne**

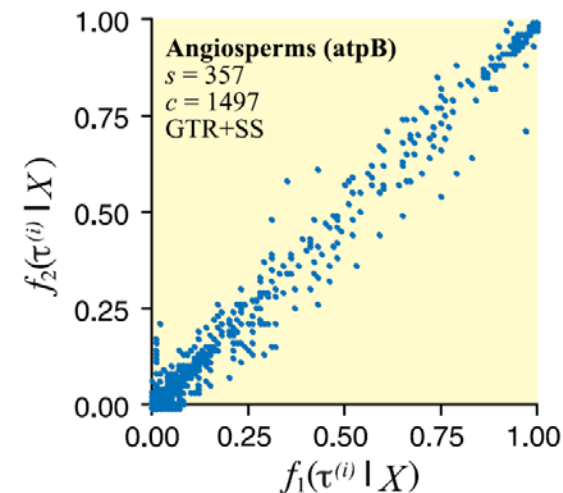
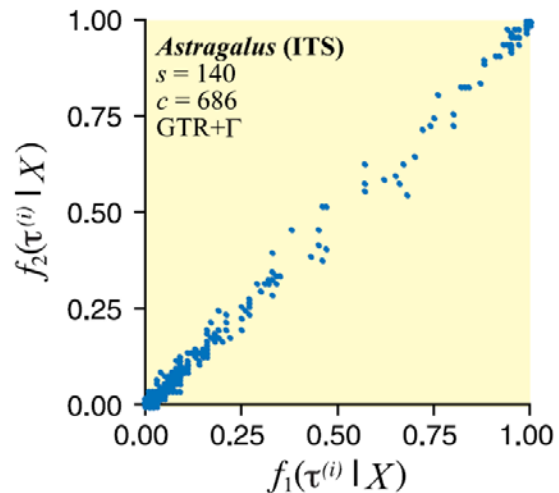
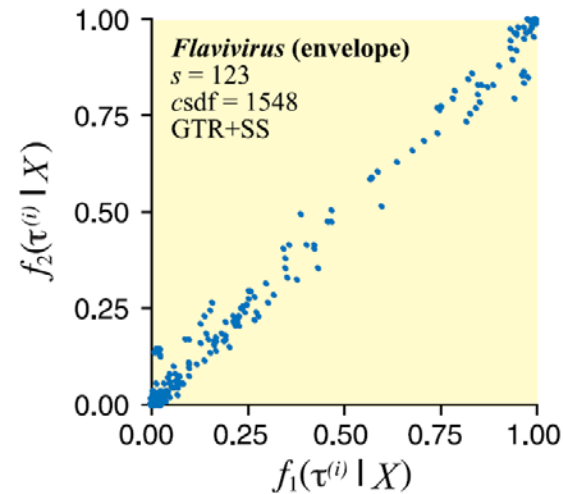
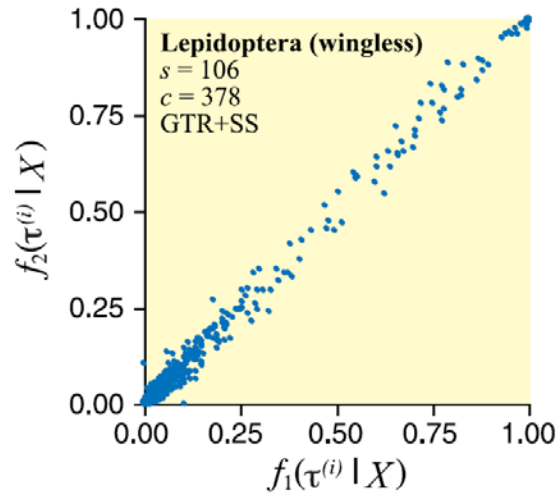
**Každých  $k$  generácií (napr. 100) sa zaznamená strom s jeho dĺžkami a všetkými parametrami modelu**

Po  $n$  generáciách sa Markov chain dostane do akéhosi **rovnovážneho stavu**, keď sa vyskytujú **určité topológie s ustálenou frekvenciou**. Táto frekvencia je vhodnou aproximáciou ich posteriórnej pravdepodobnosti.

V rovnovážnom stave sú **hodnoty vieryhodnosti viac-menej ustálené**.

Zo získaného výberu stromov je možné urobiť **konsenzuálny strom**.

Početnosť **koľkokrát sa príslušný clade objaví na stromoch** v tomto výbere stromov je v podstate ekvivalentná hodnote bootstrapu v ML analýze.



Posteriórne pravdepodobnosti jednotlivých „clades“ sú medzi dvomi nezávislými reťazami vysoko korelované – Metropolis coupled MCMC

Huelsenbeck, J. P., F. Ronquist, R. Nielsen & J. P. Bollneck. 2001. Bayesian inference of phylogeny and its impact on evolutionary biology. *Science* 294: 2310-2314.

Salemi, M. & Vandamme, A-M., eds. 2003. The Phylogenetic handbook. Cambridge University Press, Cambridge.

Hall, B. G. 2004. Phylogenetic trees made easy. Ed. 2. Sinauer Associates, Sunderland.

Felsenstein, J. 2004. Inferring phylogenies. Sinauer Associates, Sunderland.

Lewis, P. O. 2001b. Phylogenetic systematics turns over a new leaf. Trends Ecol. Evol. 16: 30-37.

Huelsenbeck, J. P., F. Ronquist, R. Nielsen & J. P. Bollneck. 2001. Bayesian inference of phylogeny and its impact on evolutionary biology. Science 294: 2310-2314.

# Software

## Applets that I use in teaching

Developing these applets helped me understand concepts, and I hope they are useful to you as well.

### Phylogenetics

- [Pagel's lambda, delta, and kappa](#)
- [Ornstein-Uhlenbeck vs. Brownian Motion](#)
- [Dirichlet base frequency distribution](#)

<https://plewis.github.io/software/>

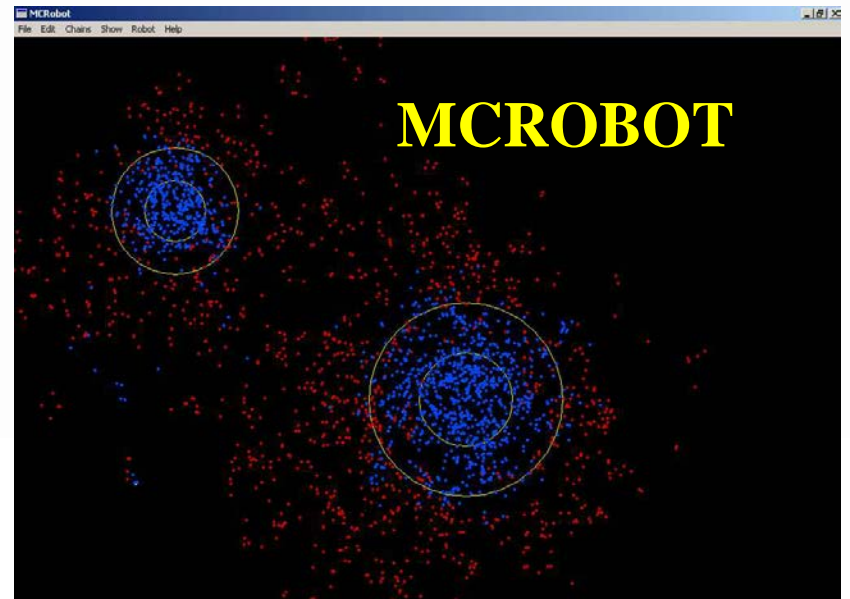
### Statistics

- [Density Rain](#)
- [MCMC](#)
- [Dirichlet Process Prior](#)

### Natural Selection

- [Natural selection ball-drop game](#)
- [Biston betularia \(1848-1898\)](#)
- [Biston betularia \(1959-2003\)](#)

### Population Genetics



# program MrBayes

<http://nbisweden.github.io/MrBayes/>



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[Links](#)

## MrBayes: Bayesian Inference of Phylogeny

MrBayes is a program for Bayesian inference and model choice across a wide range of phylogenetic and evolutionary models. MrBayes uses Markov chain Monte Carlo (MCMC) methods to estimate the posterior distribution of model parameters.

Program features include:

- A common command-line interface across Macintosh, Windows, and UNIX operating systems;
- Extensive help available from the command line;
- Analysis of nucleotide, amino acid, restriction site, and morphological data;
- Mixing of data types, such as molecular and morphological characters, in a single analysis;
- Easy linking and unlinking of parameters across data partitions;
- An abundance of evolutionary models, including 4x4, doublet, and codon models for nucleotide data and many of the standard rate matrices for amino acid data;
- Estimation of positively selected sites in a fully hierarchical Bayesian framework;
- Full integration of the BEST algorithms for the multi-species coalescent;
- Estimation of time calibrated (clock) trees using a variety of (strict and) relaxed-clock models;
- Support for complex combinations of positive, negative, and backbone constraints on topologies;
- Model jumping across the GTR model space and across fixed rate matrices for amino acid data;
- Monitoring of convergence during the analysis, and access to a wide range of convergence diagnostics tools after the analysis has finished;
- Rich summaries of posterior samples of branch and node parameters printed to majority rule consensus trees in FigTree format;
- Implementation of the stepping-stone method for accurate estimation of model likelihoods for Bayesian model choice using Bayes factors;
- The ability to spread jobs over a cluster of computers using MPI (for Macintosh (OS X) and UNIX environments only);
- Support for the BEAGLE library, resulting in dramatic speedups for codon and amino acid models on compatible hardware (NVIDIA graphics cards);
- Check pointing across all models, allowing the user to seamlessly extend a previous analysis or recover from a system crash;

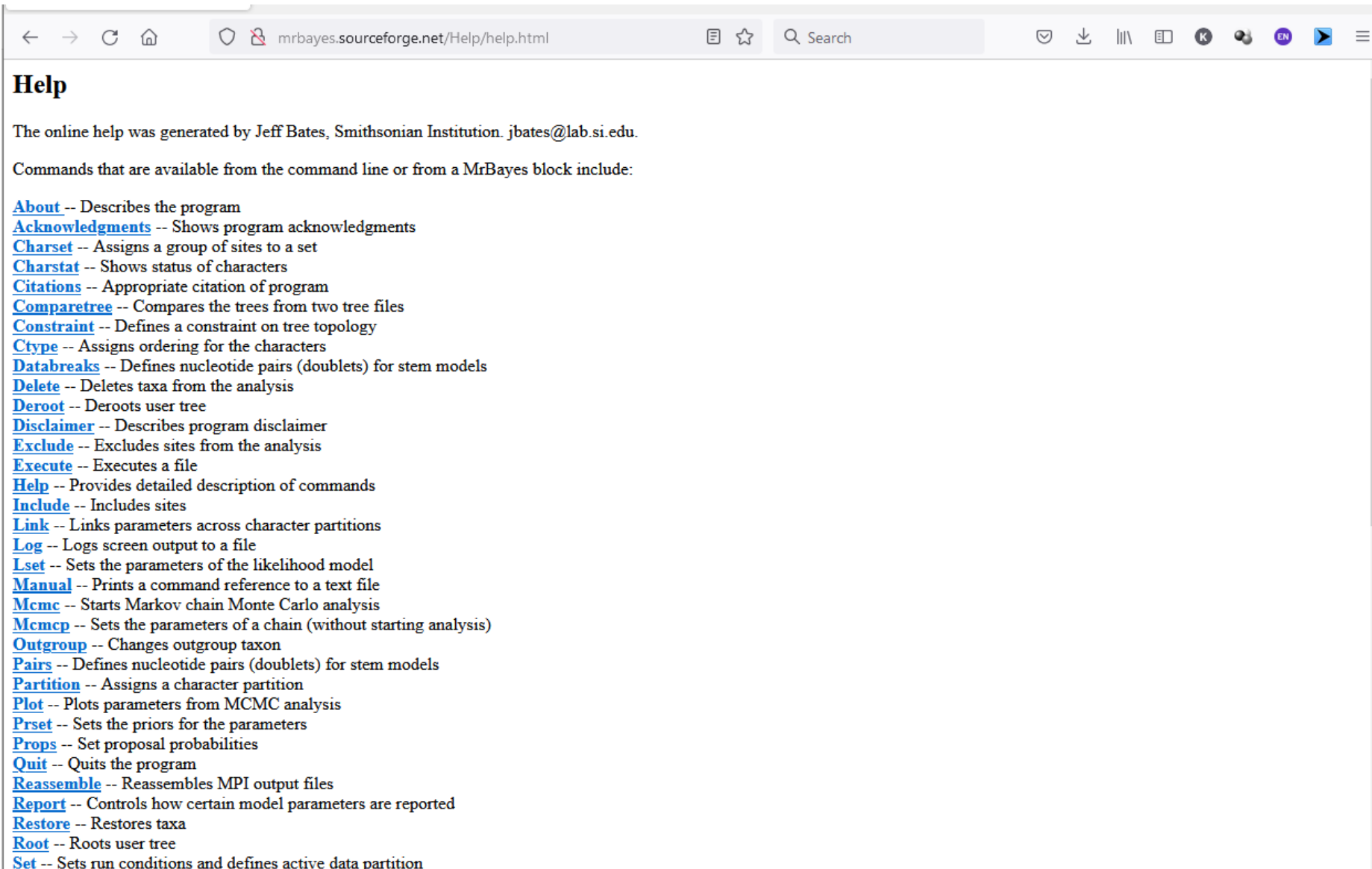




- Huelsenbeck JP and Ronquist F. 2001. MRBAYES: Bayesian inference of phylogenetic trees. *Bioinformatics* 17: 754-755.
- Huelsenbeck JP, Ronquist F, Nielsen R, Bollback JP. 2001. Bayesian inference of phylogeny and its impact on evolutionary biology. *Science* 294: 2310-2314.
- Archibald JK, Mort ME, Crawford DJ. 2003. Bayesian inference of phylogeny: a non-technical primer. *Taxon* 52: 187-191.
- Ronquist F. and Huelsenbeck JP. 2003. MrBayes 3: Bayesian phylogenetic inference under mixed models. *Bioinformatics* 19: 1572-1574.
- Ronquist F. 2004. Bayesian inference of character evolution. *Trends in ecology and Evolution* 19: 475-481.

Odkazy na ďalšie práce sú uvedené v príručke (MrBayes version 3.2 Manual), ktorá je zahrnutá v inštalačnom súbore.

http://mrbayes.sourceforge.net/Help/help.html



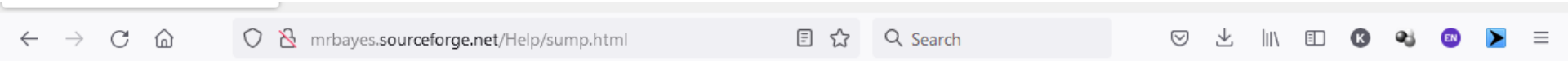
The screenshot shows a web browser window with the address bar containing "mrbayes.sourceforge.net/Help/help.html". The page title is "Help". The main content area contains the following text:

The online help was generated by Jeff Bates, Smithsonian Institution. [jbates@lab.si.edu](mailto:jbates@lab.si.edu).

Commands that are available from the command line or from a MrBayes block include:

- [About](#) -- Describes the program
- [Acknowledgments](#) -- Shows program acknowledgments
- [Charset](#) -- Assigns a group of sites to a set
- [Charstat](#) -- Shows status of characters
- [Citations](#) -- Appropriate citation of program
- [Comparetree](#) -- Compares the trees from two tree files
- [Constraint](#) -- Defines a constraint on tree topology
- [Ctype](#) -- Assigns ordering for the characters
- [Databreaks](#) -- Defines nucleotide pairs (doublets) for stem models
- [Delete](#) -- Deletes taxa from the analysis
- [Deroot](#) -- Deroots user tree
- [Disclaimer](#) -- Describes program disclaimer
- [Exclude](#) -- Excludes sites from the analysis
- [Execute](#) -- Executes a file
- [Help](#) -- Provides detailed description of commands
- [Include](#) -- Includes sites
- [Link](#) -- Links parameters across character partitions
- [Log](#) -- Logs screen output to a file
- [Lset](#) -- Sets the parameters of the likelihood model
- [Manual](#) -- Prints a command reference to a text file
- [Mcmc](#) -- Starts Markov chain Monte Carlo analysis
- [Mcmcp](#) -- Sets the parameters of a chain (without starting analysis)
- [Outgroup](#) -- Changes outgroup taxon
- [Pairs](#) -- Defines nucleotide pairs (doublets) for stem models
- [Partition](#) -- Assigns a character partition
- [Plot](#) -- Plots parameters from MCMC analysis
- [Prset](#) -- Sets the priors for the parameters
- [Props](#) -- Set proposal probabilities
- [Quit](#) -- Quits the program
- [Reassemble](#) -- Reassembles MPI output files
- [Report](#) -- Controls how certain model parameters are reported
- [Restore](#) -- Restores taxa
- [Root](#) -- Roots user tree
- [Set](#) -- Sets run conditions and defines active data partition

# http://mrbayes.sourceforge.net/Help/help.html



## Sump

During a [MCMC](#) analysis, [MrBayes](#) prints the sampled parameter values to a tab-delimited text file. This file has the extension ".p". The command 'Sump' summarizes the information in the parameter file. By default, the name of the parameter file is assumed to be the name of the last matrix-containing nexus file, but with a '.p' extension. You can set 'Sump' to summarize the information in any other parameter file by setting the 'filename' option to the appropriate file name. The 'Sump' command does not require a [matrix](#) to be read in first. When you invoke the 'Sump' command, three items are output: (1) a generation plot of the likelihood values; (2) estimates of the marginal likelihood of the model; and (3) a table with the mean, variance, and 95 percent credible interval for the sampled parameters. Each of these items can be switched on or off using the options 'Plot', 'Marglike', and 'Table'. By default, all three items are output but only to the screen. If output to a file is also desired, set 'Printtofile' to 'Yes'. The name of the output file is specified by setting the 'Outputname' option. When a new [matrix](#) is read in or when the [Mcmc](#) output filename or 'Sump' input filename is changed, the 'Sump' outputname is changed as well. If you want to output to another file than the default, make sure you specify the outputname every time you invoke 'Sump'. If the specified outputfile already exists, you will be prompted about whether you like to overwrite it or append to it. This behavior can be altered using 'Set nowarn=yes'; see the help for the [Set](#) command. When running 'Sump' you typically want to discard a specified number of samples from the beginning of the chain as the burnin. Note that the 'Burnin' value of the 'Sump' command is set separately from the 'Burnin' values of the [Sumt](#) and [Mcmc](#) commands. That is, if you issue

```
sump burnin = 4000
sumt burnin = 2000
sump
```

the burnin of the last 'Sump' command is 4000 and not 2000. The burnin values are reset to 0 every time a new [matrix](#) is read in. Similarly, 'Plot', 'Marglike' and 'Table' are all set to 'Yes' and 'Printtofile' to 'No' (the default values) when a new [matrix](#) is processed. If you have run several independent [MCMC](#) analyses, you may want to summarize and compare the samples from each of these runs. To do this, set 'Nruns' to the number of runs you want to compare and make sure that the '.p' files are named using the [MrBayes](#) convention (<filename>.run1.p, <filename>.run2.p, etc). When you run several independent analyses simultaneously in [MrBayes](#), the 'Nruns' and 'Filename' options are automatically set such that 'Sump' will summarize all the resulting output files.

### Options:

**Burnin** -- Determines the number of samples that will be discarded from the input file before calculating summary statistics. If there are several input files, the same number of samples will be discarded from each. Note that the burnin is set separately for the 'sump', 'sumt', and 'mcmc' commands.

**Nruns** -- Determines how many '.p' files from independent analyses that will be summarized. If Nruns > 1 then the names of the files are derived from 'Filename' by adding '.run1.p', '.run2.p', etc. If Nruns=1, then the single filename is obtained by adding '.p' to the 'Filename'.

**Filename** -- The name of the file to be summarized. This is the base of the file name to which endings are added according to the current setting of the 'Nruns' parameter. If 'Nruns' is 1, then only '.p' is added to the file name. Otherwise, the endings will be '.run1.p', '.run2.p', etc.

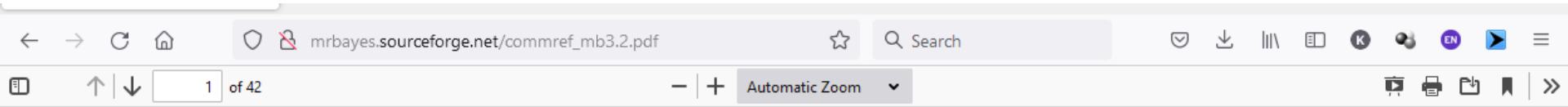
**Printtofile** -- Determines whether results will be printed to file.

**Outputname** -- Name of the file to which 'sump' results will be printed if 'Printtofile' is set to YES.

**Plot** -- Determines whether a likelihood plot should be output.

**Marglike** -- Determines whether estimates of marginal model likelihoods should be calculated. The marginal model likelihoods are useful in Bayesian model testing.

[http://mrbayes.sourceforge.net/commref\\_mb3.2.pdf](http://mrbayes.sourceforge.net/commref_mb3.2.pdf)



Command Reference for MrBayes ver. 3.2.5

(c) John P. Huelsenbeck, Fredrik Ronquist  
and Maxim Teslenko

```
*****  
* 1. Command summary *  
* * * * *  
*****
```

-----  
Commands that are available from the command  
line or from a MrBayes block include:

About	-- Describes the program
Acknowledgments	-- Shows program acknowledgments
Calibrate	-- Assigns dates to terminals or interior nodes
Charset	-- Assigns a group of sites to a set
Charstat	-- Shows status of characters
Citations	-- Citation of program, models, and methods
Comparetree	-- Compares the trees from two tree files
Constraint	-- Defines a constraint on tree topology
Ctype	-- Assigns ordering for the characters
Databreaks	-- Defines data breaks for autodiscrete gamma model
Delete	-- Deletes taxa from the analysis
Disclaimer	-- Describes program disclaimer
Exclude	-- Excludes sites from the analysis
Execute	-- Executes a file
Help	-- Provides detailed description of commands
Include	-- Includes sites
Link	-- Links parameters across character partitions
Log	-- Logs screen output to a file
Lset	-- Sets the parameters of the likelihood model
Manual	-- Prints a command reference to a text file
Mcmc	-- Starts Markov chain Monte Carlo analysis
Mcmcp	-- Sets parameters of a chain (without starting analysis)
Outgroup	-- Changes outgroup taxon
Pairs	-- Defines nucleotide pairs (doublets) for stem models
Partition	-- Assigns a character partition
Plot	-- Plots parameters from MCMC analysis

Príručka je zahrnutá v inštalačnom balíku MrBayes-3.2.7-WIN

Manual\_MrBayes\_v3.2.pdf - Adobe Acrobat Pro  
Súbor Úpravy Zobrazenie Okná Pomocník

Otvoriť Vytvoriť

Prispôbiť

1 / 174 204%

Nástroje Vyplniť a podpísať Poznámka

# MrBayes version 3.2 Manual: Tutorials and Model Summaries

Fredrik Ronquist, John Huelsenbeck, Maxim Teslenko and Johan Nylander

Draft version, February 2019

- MrBayes analýza
- postupné zadávanie príkazov
  - načítanie príkazov zahrnutých v *nexus* súbore

```
MrBayes 3.2.7a x86_64
(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 > _
```

Poznámka: príklady príkazov a výstupov sú z predošlej verzie programu, so súčasnou verziou sa bude pracovať v rámci cvičení

```
MrBayes > execute asarifolia_ITS.nex
```

# 1. načítanie *nexus* súboru

```
c:\Documents and Settings\Judita\My Documents\HEIDELBERG_old\Bayes\MrBayes3_0b4.exe
Type "help" or "help <command>" for information
on the commands that are available.

MrBayes > execute asarifolia_ITS.nex

Executing file "asarifolia_ITS.nex"
Macintosh line termination
Longest line length = 665
Parsing file
Expecting NEXUS formatted file
Reading data block
Allocated matrix
Matrix has 131 taxa and 628 characters
Data is Dna
Missing data coded as N
Gaps coded as -
Setting default partition (does not divide up characters).
Taxon 1 -> amaraBDA
Taxon 2 -> amaraROZ
Taxon 3 -> amC119
Taxon 4 -> amC1AS8
Taxon 5 -> am2BRG1
Taxon 6 -> amC0S4
Taxon 7 -> amLAI
Taxon 8 -> amFON4b
Taxon 9 -> am3U102
Taxon 10 -> am2U104
Taxon 11 -> amCOL0
Taxon 12 -> amCL0310
Taxon 13 -> fer1cB51
Taxon 14 -> fer1cB53
Taxon 15 -> fer1cB54
Taxon 16 -> fer3cB83
Taxon 17 -> fer4cB61
Taxon 18 -> fer4cB64
Taxon 19 -> fer4cB102
Taxon 20 -> fer5cB70
Taxon 21 -> fer5cB67
Taxon 22 -> fer5cB66
Taxon 23 -> fer4cB103
Taxon 24 -> fer4cB104
Taxon 25 -> fer3cB84
Taxon 26 -> fer3cB82
Taxon 27 -> fer3cB85
Taxon 28 -> fer2cB57
Taxon 29 -> fer2cB58
Taxon 30 -> fer1cB52
Taxon 31 -> fer1cB55
Taxon 32 -> asCOL02
Taxon 33 -> asCOL04
Taxon 34 -> asCOL07
Taxon 35 -> asCL0310
Taxon 36 -> asMCOL4
Taxon 37 -> asMCOL8
Taxon 38 -> asMCOL10
Taxon 39 -> asMCOL9
Taxon 40 -> asCH8
Taxon 41 -> asCH1
Taxon 42 -> asCH2
Taxon 43 -> asLIM3
Taxon 44 -> asLIM4
Taxon 45 -> asLIM6
Taxon 46 -> asLIM8
Taxon 47 -> asU1U9br
Taxon 48 -> asU1U10
Taxon 49 -> asU1U6
Taxon 50 -> asU1U8
Taxon 51 -> as3U102
Taxon 52 -> as3U109
Taxon 53 -> as3U104
Taxon 54 -> as3U103
Taxon 55 -> acrisUN
Taxon 56 -> acris2KPN
Taxon 57 -> acris724
Taxon 58 -> acrisIM3
Taxon 59 -> acrisUR
Taxon 60 -> teneraKS
Taxon 61 -> teneraGR
Taxon 62 -> teneraIAL
Taxon 63 -> seidlitzianaBES
```

```
c:\Documents and Settings\Judita\My Documents\HEIDELBERG_old\Bayes\MrBayes3_0
Type "help" or "help <command>" for information
on the commands that are available.

MrBayes > execute asarifolia_ITS.nex

Executing file "asarifolia_ITS.nex"
Macintosh line termination
Longest line length = 665
Parsing file
Expecting NEXUS formatted file
Reading data block
Allocated matrix
Matrix has 131 taxa and 628 characters
Data is Dna
Missing data coded as N
Gaps coded as -
Setting default partition (does not divide up characters).
Taxon 1 -> amaraBDA
Taxon 2 -> amaraROZ
Taxon 3 -> amC119
Taxon 4 -> amC1AS8
Taxon 5 -> am2BRG1
Taxon 6 -> amC0S4
Taxon 7 -> amLAI
Taxon 8 -> amFON4b
Taxon 9 -> am3U102
Taxon 10 -> am2U104
Taxon 11 -> amCOL0
Taxon 12 -> amCL0310
Taxon 13 -> fer1cB51
Taxon 14 -> fer1cB53
Taxon 15 -> fer1cB54
Taxon 16 -> fer3cB83
Taxon 17 -> fer4cB61
Taxon 18 -> fer4cB64
Taxon 19 -> fer4cB102
Taxon 20 -> fer5cB70
Taxon 21 -> fer5cB67
Taxon 22 -> fer5cB66
Taxon 23 -> fer4cB103
Taxon 24 -> fer4cB104
Taxon 25 -> fer3cB84
Taxon 26 -> fer3cB82
Taxon 27 -> fer3cB85
Taxon 28 -> fer2cB57
Taxon 29 -> fer2cB58
Taxon 30 -> fer1cB52
Taxon 31 -> fer1cB55
Taxon 32 -> asCOL02
Taxon 33 -> asCOL04
Taxon 34 -> asCOL07
Taxon 35 -> asCL0310
Taxon 36 -> asMCOL4
Taxon 37 -> asMCOL8
Taxon 38 -> asMCOL10
Taxon 39 -> asMCOL9
Taxon 40 -> asCH8
Taxon 41 -> asCH1
Taxon 42 -> asCH2
Taxon 43 -> asLIM3
Taxon 44 -> asLIM4
Taxon 45 -> asLIM6
Taxon 46 -> asLIM8
Taxon 47 -> asU1U9br
Taxon 48 -> asU1U10
Taxon 49 -> asU1U6
Taxon 50 -> asU1U8
Taxon 51 -> as3U102
Taxon 52 -> as3U109
Taxon 53 -> as3U104
Taxon 54 -> as3U103
Taxon 55 -> acrisUN
Taxon 56 -> acris2KPN
Taxon 57 -> acris724
Taxon 58 -> acrisIM3
Taxon 59 -> acrisUR
Taxon 60 -> teneraKS
Taxon 61 -> teneraGR
Taxon 62 -> teneraIAL
Taxon 63 -> seidlitzianaBES
Taxon 127 -> hirHEI
Taxon 128 -> hir4BRG4
Taxon 129 -> parviflSTR
Taxon 130 -> RoriPalustrisX98639
Taxon 131 -> RorippaheterophyllaX98638
Setting output file names to "asarifolia_ITS.nex.<p/t>"
Successfully read matrix
Exiting data block

MrBayes >
```

## 2. výber *outgroup* na zakorenenie stromov

```
Taxon 126 -> pectBJ4
Taxon 127 -> hirHEI
Taxon 128 -> hir4BRG4
Taxon 129 -> parvif1STR
Taxon 130 -> RoriPalustrisX98639
Taxon 131 -> RorippaheterophyllaX98638
Setting output file names to "asarifolia_ITS.nex.<p/t>"
Successfully read matrix
Exiting data block
```

```
MrBayes > outgroup 130
```

```
MrBayes > outgroup 130
```

```
Setting outgroup to taxon "RoriPalustrisX98639"
```

```
MrBayes >
```

## 3. uloženie výstupu do *log* súboru

```
MrBayes > log start filename=test.log
```

```
MrBayes > log start filename=test.log
```

```
Logging screen output to file "test.log"
```

```
MrBayes >
```



## 4. nastavenie parametrov modelu

help lset...zobrazenie parametrov a možností ich nastavenia

Parameter	Options	Current Setting
Nucmodel	4by4/Doublet/Codon	4by4
Nst	1/2/6	1
Code	Universal/Uertmt/Mycoplasma/ Yeast/Ciliates/Metmt	Universal
Rates	Equal/Gamma/Propinv/Invgamma/Adgamma	Equal
Ngammacat	<number>	4
Nbetacat	<number>	5
Omegavar	Equal/Ny98/M3	Equal
Covarion	No/Yes	No
Coding	All/Variable/Noabsencesites/ Nopresencesites	All
Parsmodel	No/Yes	No

#### 4. nastavenie parametrov modelu

1 = F81 model, 6 = GTR model

```
Could not find parameter logstart
MrBayes > log start filename=test.log
  Logging screen output to file "test.log"
MrBayes > lset nst=6 rates=gamma
```

```
MrBayes > lset nst=6 rates=gamma
  Setting Nst to 6
  Setting Rates to Gamma
  Successfully set likelihood model parameters
MrBayes > _
```

#### 5. nastavenie “prior settings” – nastavenie ďalších parametrov na základe apriórnych špecifikácií

help prset...zobrazenie parametrov a možností ich nastavenia

## 6. nastavenie parametrov analýzy

help mcmc...zobrazenie nastavení

Parameter	Options	Current Setting
Seed	<number>	1148882071
Ngen	<number>	1000000
Samplefreq	<number>	100
Swapfreq	<number>	1
Printfreq	<number>	100
Nchains	<number>	4
Temp	<number>	0.200000
Reweight Filename	<number>,<number> <name>	0.00 v 0.00 ^ asarifolia_ITS.nex.<p/t>
Burnin	<number>	0
Startingtree	Random/User	Random
Nperts	<number>	0
Savebrlens	Yes/No	No

MrBayes > \_

## 6. nastavenie parametrov analýzy - počet generácií, teplota

```
MrBayes > mcmc ngen=10000000 Temp=0.03 savebrlens=yes
```

```
MrBayes > mcmc ngen=10000000 Temp=0.03 savebrlens=yes
```

```
Setting number of generations to 10000000
```

```
Setting heating parameter to 0.030000
```

```
Setting program to save branch length information
```

```
Successfully set chain parameters
```

```
MrBayes > _
```

## 7. spustenie analýzy

```
MrBayes > mcmc ngen=10000000 Temp=0.03 savebrlens=yes
```

```
Setting number of generations to 10000000
```

```
Setting heating parameter to 0.030000
```

```
Setting program to save branch length information
```

```
Successfully set chain parameters
```

```
MrBayes > mcmc
```

# priebeh analýzy

```
MrBayes > mcmc
```

```
Running Markov chain
MCMC stamp = 9889988200
Model settings:
  Datatype   = DNA
  Nucmodel   = 4by4
  Nst        = 6
             Substitution rates, expressed as proportions
             of the rate sum, follow a Dirichlet
             (1.00,1.00,1.00,1.00,1.00,1.00)
  Covarion   = No
  # States   = 4
             State frequencies have a Dirichlet prior
  Rates      = Gamma
             Gamma shape parameter is uniformly dist-
             ributed on the interval (0.05,50.00).
             Gamma distribution is approximated using 4 categories.
```

```
Active parameters:
```

```
Parameters
-----
Revmat      1
Statefreq   2
Shape       3
Topology    4
Brlen       5
-----
```

```
1 -- Parameter = Revmat
   Prior      = Dirichlet(1.00,1.00,1.00,1.00,1.00,1.00)
2 -- Parameter = Statefreq
   Prior      = Dirichlet
3 -- Parameter = Shape
   Prior      = Uniform(0.05,50.00)
4 -- Parameter = Topology
   Prior      = All topologies equally probable a priori
5 -- Parameter = Brlen
   Prior      = Branch lengths are Unconstrained:Exponential(10.0)
```

```
Number of taxa = 131
```

```
Number of characters = 628
```

```
Compressing data matrix for division 1
```

```
Division 1 has 243 unique site patterns
```

```
The chain will use the following moves:
```

```
With prob. Chain will change
 3.70 % param. 1 (revmat) with multiplier
 3.70 % param. 2 (state frequencies) with Dirichlet proposal
 3.70 % param. 3 (gamma shape) with multiplier
55.56 % param. 4 (topology and branch lengths) with LOCAL
11.11 % param. 4 (topology and branch lengths) with extending TBR
11.11 % param. 5 (branch lengths) with multiplier
11.11 % param. 5 (branch lengths) with nodeslider
```

```
Creating parsimony (bitset) matrix for division 1
```

```
Initializing conditional likelihoods for terminals
```

```
Initializing conditional likelihoods for chains
```

```
Initial log likelihoods:
```

```
Chain 1 -- -10168.043333
Chain 2 -- -10389.666714
Chain 3 -- -10361.807983
Chain 4 -- -10319.898048
```

```
Chain results:
```

```
1 -- [-10168.043] (-10389.667) (-10361.846) (-10318.655)
100 -- [-9726.668] (-10074.274) (-10088.676) (-9946.870) -- 27:46:39
200 -- [-9534.361] (-9882.615) (-9864.944) (-9716.929) -- 27:46:38
```

```

9999400 -- (-2187.015) (-2190.527) [-2191.500] (-2234.304) -- 0:00:02
9999500 -- [-2194.541] (-2194.904) (-2193.479) (-2236.009) -- 0:00:02
9999600 -- (-2190.720) [-2189.221] (-2190.515) (-2239.931) -- 0:00:01
9999700 -- (-2190.148) (-2191.883) [-2185.789] (-2247.159) -- 0:00:01
9999800 -- [-2187.896] (-2189.191) (-2200.145) (-2250.243) -- 0:00:00
9999900 -- (-2181.179) (-2189.149) [-2190.183] (-2242.580) -- 0:00:00
10000000 -- [-2178.479] (-2190.152) (-2193.497) (-2241.901) -- 0:00:00

```

Continue with chain? (yes/no): no

Continue with chain? (yes/no): no

```

Chain completed in 43058 seconds
Chain used 75644.82 seconds of CPU time
Likelihood of best state for "cold" chain was -2153.07
Acceptance rates for the moves in the "cold" chain:
  With prob. Chain accepted changes to
    70.57 % param. 1 (reumat) with multiplier
    94.52 % param. 2 (reumat) with multiplier
    78.02 % param. 3 (reumat) with multiplier
    39.25 % param. 4 (state frequencies) with Dirichlet proposal
    54.67 % param. 5 (state frequencies) with Dirichlet proposal
    47.41 % param. 6 (state frequencies) with Dirichlet proposal
    90.66 % param. 7 (gamma shape) with multiplier
    25.68 % param. 8 (gamma shape) with multiplier
    90.33 % param. 9 (gamma shape) with multiplier
    93.15 % param. 10 (prop. invariants) with beta proposal
    61.37 % param. 11 (prop. invariants) with beta proposal
    90.48 % param. 12 (prop. invariants) with beta proposal
    67.55 % param. 13 (rate multiplier) with sliding window
    57.53 % param. 14 (topology and branch lengths) with LOCAL
    52.58 % param. 14 (topology and branch lengths) with extending TBR
    82.50 % param. 15 (branch lengths) with multiplier
    67.43 % param. 15 (branch lengths) with nodeslider

```

State exchange information:

	1	2	3	4
1		0.76	0.49	0.14
2	1668138		0.69	0.24
3	1667028	1667799		0.46
4	1666621	1665020	1665394	

Upper diagonal: Proportion of successful exchanges

Lower diagonal: Number of attempted exchanges

Chain information:

```

ID -- Heat
-----
1 -- 1.00 (cold chain)
2 -- 0.97
3 -- 0.94
4 -- 0.92

```

Heat = 1 / (1 + T \* (ID - 1))  
 (where T = 0.03 is the temperature and ID is the chain number)

*Acceptance rates for the moves in the cold chain* – existuje “palcové pravidlo” podľa ktorého by sa mali hodnoty hýbať v rozmedzí 10-70%

**State exchange information** – dolný riadok hornej diagonály obsahuje

*Acceptance rates for the swaps between chains separated by only one heating step* – rovnako existuje “palcové pravidlo” podľa ktorého by sa mali hodnoty hýbať v rozmedzí 0.1-0.7

uvedené parametre môžeme meniť úpravou teploty

```
Acceptance rates for the moves in the "cold" chain:
```

```
With prob. Chain accepted changes to
 57.98 % param. 1 (revmat) with multiplier
 15.49 % param. 2 (state frequencies) with Dirichlet proposal
 17.89 % param. 3 (gamma shape) with multiplier
 55.62 % param. 4 (prop. invariants) with beta proposal
 38.94 % param. 5 (topology and branch lengths) with LOCAL
 45.06 % param. 5 (topology and branch lengths) with extending TBR
 71.63 % param. 6 (branch lengths) with multiplier
 49.50 % param. 6 (branch lengths) with nodeslider
```

```
State exchange information:
```

	1	2	3	4
1		0.06	0.00	0.00
2	1697		0.06	0.00
3	1710	1647		0.07
4	1658	1631	1657	

```
Upper diagonal: Proportion of successful exchanges
Lower diagonal: Number of attempted exchanges
```

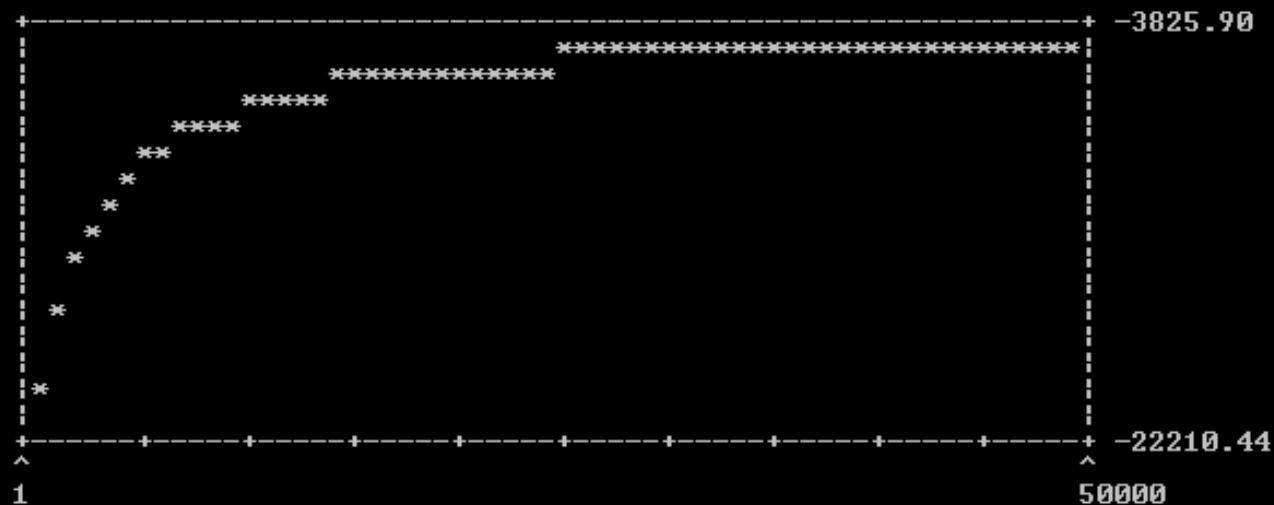
## 8. sumarizácia výstupu – *likelihood scores* jednotl. stromov

sump

```
MrBayes > sump
```

```
Summarizing parameters in file asarifolia_ITS.nex.p
DOS line termination
Longest line length = 59
Found 501 parameter lines in file "asarifolia_ITS.nex.p"
All 501 lines will be summarized (starting at line 3)
(Only the last set of lines will be read, in case multiple
parameter blocks are present in the same file.)
501 rows and 7 columns in each row
Successfully read 501 lines from last parameter block
```

Below is a rough plot of the generation (x-axis) versus the log probability of observing the data (y-axis). You can use this graph to determine what the burn-in for your analysis should be. When the log probability starts to plateau you may be at stationarity. Sample trees and parameters after the log probability plateaus. Of course, this is not a guarantee that you are at stationarity. When possible, run multiple chains starting from random trees; if the inferences you make for independent chains are the same, this is reasonable evidence that the chains have converged. Remember that the burn in is the number of samples to discard. There are a total of  $\text{ngen} / \text{samplefreq}$  samples taken during a MCMC analysis.

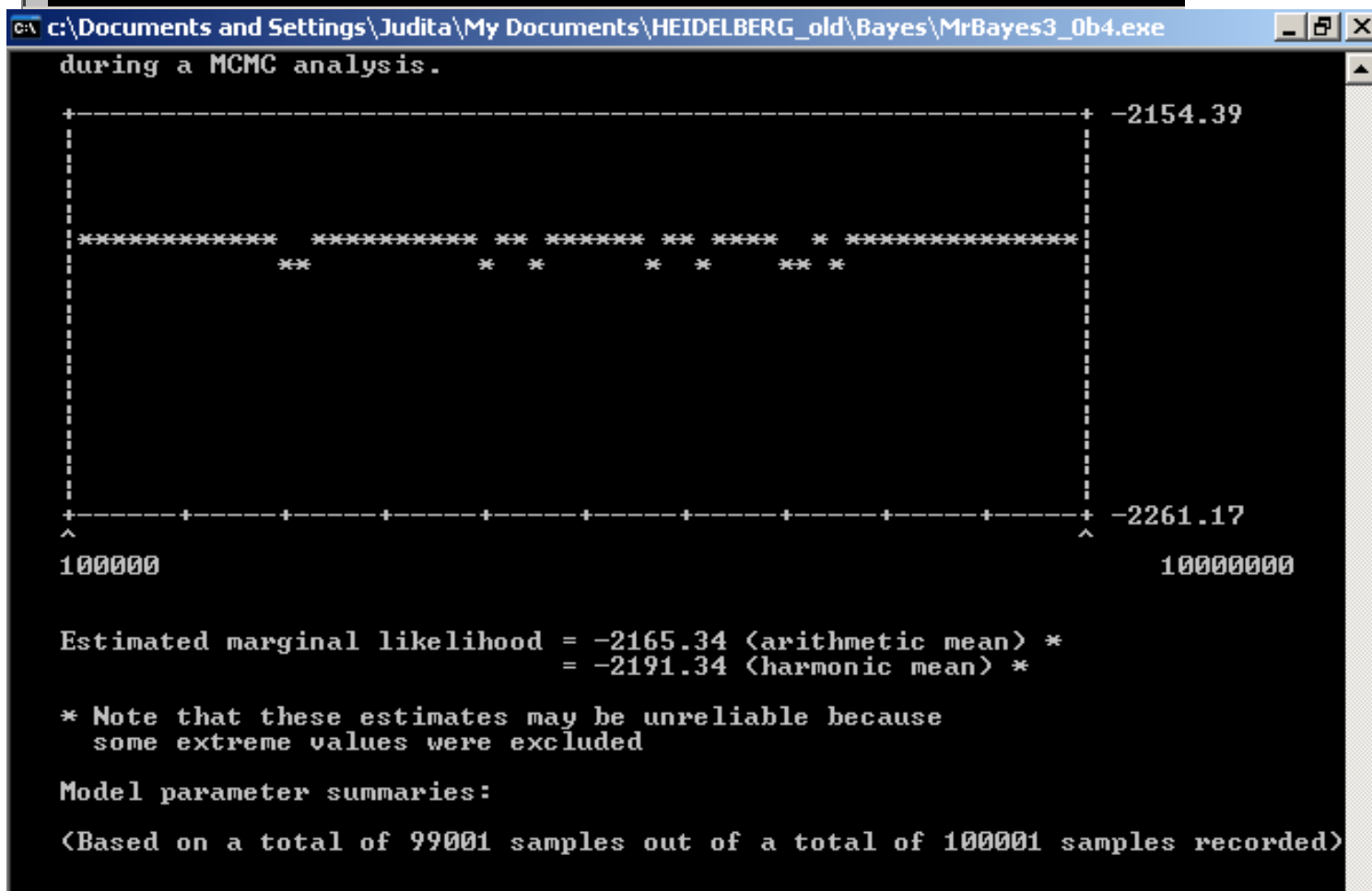




8. sumarizácia výstupu – vyradenie ca. 10% počiatočných stromov,  
kontrola *likelihood scores*

```
MrBayes > sump burnin=1000

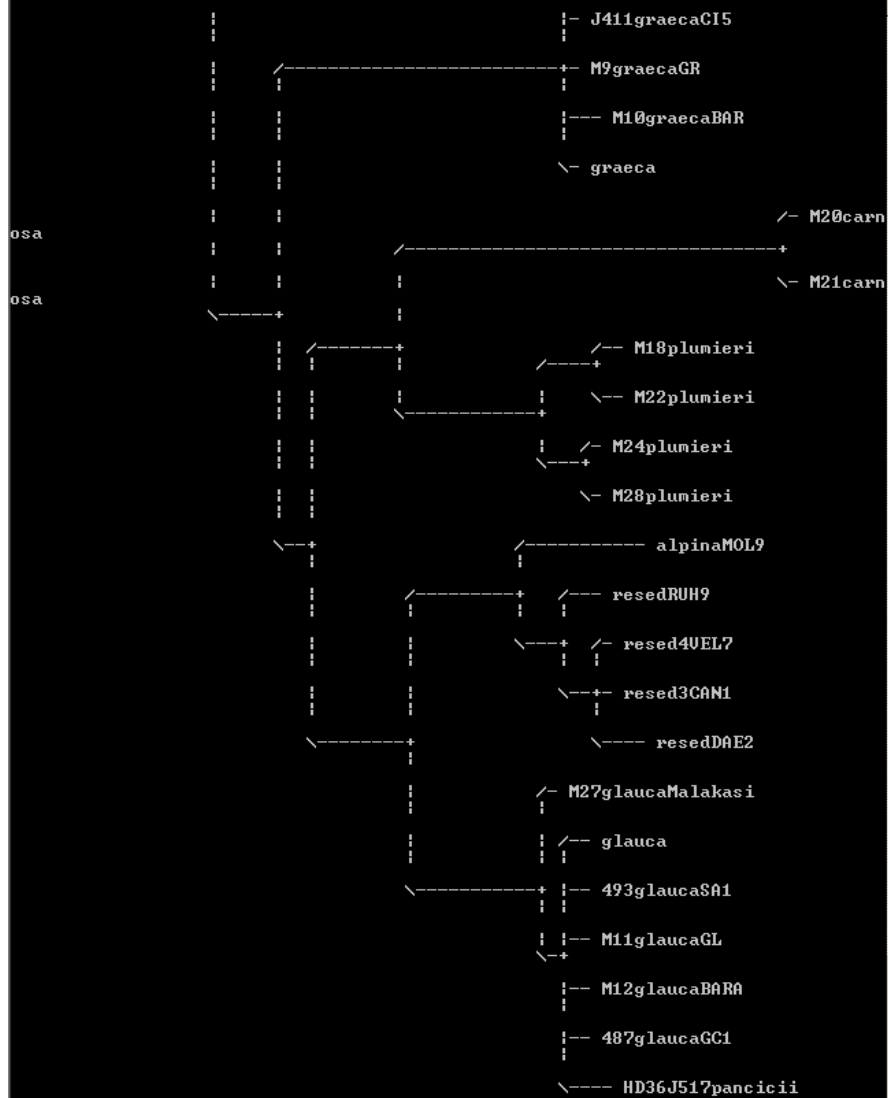
Setting sump burnin to 1000
Summarizing parameters in file maritITSBay.nex.p
DOS line termination
Longest line length = 412
```



8. sumarizácia výstupu – vyradenie ca. 10% počiatočných stromov, výpočet konsenzuálneho stromu

sumt

```
-----  
MrBayes > sumt burnin=1000  
  
Setting sumt burnin to 1000  
Summarizing trees in file maritITSBay.nex.t  
DOS line termination  
Longest line length = 1432  
Found one tree block in file "maritITSBay.nex.t" with 100001 trees in last block  
  
Tree reading status:  
  
0      10      20      30      40      50      60      70      80      90  
100  
v-----v-----v-----v-----v-----v-----v-----v-----v-----  
---v  
*****
```



Credible sets of trees (98958 trees sampled):  
50 % credible set contains 49458 trees  
90 % credible set contains 89058 trees  
95 % credible set contains 94008 trees  
99 % credible set contains 97968 trees

Výstup analýzy – súbory:

\*.p – zapísané parametre modelu pre jednotlivé generácie stromov

\*.t – zapísaná topológia stromov a dĺžky vetiev

\*.con – zapísaný konsenzuálny strom s hodnotami *posterior probabilities* pre jednotlivé vetvy (-> program TreeView)

```
[ID: ·2458661562] ¶
Gen>LnL>TL » pi (A) » pi (C) » pi (G) » pi (T) » ¶
1>-22210.442 » 25.878 » 0.250000 » 0.250000 » 0.250000 » 0.250000 » ¶
100>-21578.668 » 25.086 » 0.250000 » 0.250000 » 0.250000 » 0.250000 » ¶
200>-21038.146 » 24.438 » 0.250000 » 0.250000 » 0.250000 » 0.250000 » ¶
300>-20346.150 » 23.501 » 0.250000 » 0.250000 » 0.250000 » 0.250000 » ¶
400>-19905.772 » 22.928 » 0.250000 » 0.250000 » 0.250000 » 0.250000 » ¶
500>-19399.796 » 22.128 » 0.250000 » 0.250000 » 0.250000 » 0.250000 » ¶
600>-18826.467 » 21.337 » 0.250000 » 0.250000 » 0.250000 » 0.250000 » ¶
700>-18378.499 » 20.720 » 0.250000 » 0.250000 » 0.250000 » 0.250000 » ¶
800>-18083.160 » 20.163 » 0.250000 » 0.250000 » 0.250000 » 0.250000 » ¶
900>-17667.410 » 19.454 » 0.252511 » 0.240379 » 0.246962 » 0.260148 » ¶
1000 » -17396.425 » 19.073 » 0.252511 » 0.240379 » 0.246962 » 0.260148 » ¶
1100 » -17111.373 » 18.622 » 0.252511 » 0.240379 » 0.246962 » 0.260148 » ¶
1200 » -16736.481 » 18.146 » 0.252511 » 0.240379 » 0.246962 » 0.260148 » ¶
1300 » -16397.315 » 17.720 » 0.252511 » 0.240379 » 0.246962 » 0.260148 » ¶
1400 » -16051.652 » 17.225 » 0.252511 » 0.240379 » 0.246962 » 0.260148 » ¶
1500 » -15755.588 » 16.773 » 0.252511 » 0.240379 » 0.246962 » 0.260148 » ¶
1600 » -15510.693 » 16.306 » 0.252511 » 0.240379 » 0.246962 » 0.260148 » ¶
1700 » -15183.653 » 15.714 » 0.252511 » 0.240379 » 0.246962 » 0.260148 » ¶
1800 » -14880.723 » 15.206 » 0.252511 » 0.240379 » 0.246962 » 0.260148 » ¶
1900 » -14510.636 » 14.691 » 0.252511 » 0.240379 » 0.246962 » 0.260148 » ¶
2000 » -14300.939 » 14.321 » 0.247201 » 0.243404 » 0.246420 » 0.262975 » ¶
2100 » -14015.828 » 13.945 » 0.247201 » 0.243404 » 0.246420 » 0.262975 » ¶
2200 » -13873.806 » 13.738 » 0.244453 » 0.248604 » 0.240938 » 0.266006 » ¶
2300 » -13727.609 » 13.492 » 0.244453 » 0.248604 » 0.240938 » 0.266006 » ¶
2400 » -13460.856 » 13.159 » 0.244453 » 0.248604 » 0.240938 » 0.266006 » ¶
2500 » -13223.727 » 12.846 » 0.244453 » 0.248604 » 0.240938 » 0.266006 » ¶
2600 » -13068.844 » 12.554 » 0.244453 » 0.248604 » 0.240938 » 0.266006 » ¶
2700 » -12919.087 » 12.327 » 0.244453 » 0.248604 » 0.240938 » 0.266006 » ¶
2800 » -12819.285 » 12.081 » 0.244453 » 0.248604 » 0.240938 » 0.266006 » ¶
2900 » -12690.801 » 11.929 » 0.244453 » 0.248604 » 0.240938 » 0.266006 » ¶
```

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\*.p – zapísané parametre modelu pre jednotlivé generácie stromov

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```
.....114.rapCN, ¶
.....115.rapPO, ¶
.....116.gallaecica, ¶
.....117.barPE1, ¶
.....118.barsO1, ¶
.....119.barPE3, ¶
.....120.bar1KA, ¶
.....121.aus369, ¶
.....122.ausALIT, ¶
.....123.imprB1, ¶
.....124.impatSCH3, ¶
.....125.pectBN19, ¶
.....126.pectBJ4, ¶
.....127.hirHEI, ¶
.....128.hir4BRG4, ¶
.....129.parviflSTR, ¶
.....130.RoriPalustrisX98639, ¶
.....131.RorippaheterophyllaX98638; ¶
...tree.rep.1.= (((((((((((((((((((((((((((((((111, 93, ((113, 63), (48, (127, (90, 79))))))))), (69, (77, (17, 86))))), (76, (47, (99, 45))))), (4
...tree.rep.100.= (((((((((((((((((((((((((((((((48, (111, (21, ((87, (4, 104)), 33), (22, 122))))), 5), ((60, 120), (11)), (100, 86)), 24), 51), 52)
...tree.rep.200.= (((((((((((((((((((((((((((((((38, ((71, 77), 15), ((72, (2, 19)), 41))), (121, (((((((((((((((((((48, (111, ((33, ((22, 122), 21))), (87, (4, 104))))))
...tree.rep.300.= (((((((38, ((71, 77), 15), ((72, (2, 19)), 41))), 108), (121, (((((((((((51, (((48, ((60, 120), (11), 5)), ((111, (87, (4, 1
...tree.rep.400.= (((((((38, (15, ((71, 77), ((72, (2, 19)), 41))), 108), (121, (((((((18, (((73, ((51, (((48, ((60, 120), (11), 5)), ((11
...tree.rep.500.= ((93, (31, (36, 105))), (((((((38, (72, 41))), ((71, 77), (2, 19))), 15), 108), (121, (((((((18, (((73, (((34, 45), ((64, 57)
...tree.rep.600.= ((31, (93, (36, 105))), (((((((38, (72, 41))), ((71, 77), (2, 19))), 15), 108), ((121, (((((((18, (((73, (((34, 45), ((64, 57),
...tree.rep.700.= ((31, (93, (36, 105))), (((((((38, (72, 41))), (2, ((71, 77), 19))), (15, 108)), ((121, (((((((18, (((73, (((34, 45), ((64, 57),
...tree.rep.800.= ((31, (93, (36, 105))), (((((((2, ((71, 77), (38, (72, 41))), 19))), (15, 108)), ((121, (((((((18, (((73, (((34, 45), ((64, 57),
...tree.rep.900.= ((31, (93, (36, 105))), ((2, ((71, 77), (38, (72, 41))), 19))), ((121, (((((((18, (((97, (((73, (((34, (64, 57), 54))), 45), (
...tree.rep.1000.= ((31, (93, (36, 105))), ((2, ((71, 77), (38, (72, 41))), 19))), ((121, (((((((18, (((73, (((51, ((86, ((48, (87, ((122, (
...tree.rep.1100.= ((31, (93, (36, 105))), ((2, ((71, 77), (38, (72, 41))), 19))), ((121, ((18, (((((((73, (8, ((51, ((86, ((48, (87, ((122, (
...tree.rep.1200.= ((93, 31), ((2, ((71, 77), (38, (72, 41))), 19))), ((121, ((18, (((((((73, ((51, ((86, ((48, (87, ((122, (21, (22, 33))))
...tree.rep.1300.= ((93, 31), ((2, ((71, 77), (38, (72, 41))), 19))), ((124, 69), 102), 56), ((121, ((18, (((((((51, ((86, ((48, (87, (4, (
...tree.rep.1400.= ((93, 31), ((2, ((71, 77), (38, (72, 41))), 19))), ((124, 69), 102), 56), ((121, (((((((18, (((61, (109, 58))), 131), ((88,
...tree.rep.1500.= ((93, 31), ((2, ((71, 77), (38, (72, 41))), 19))), ((124, 69), 102), 56), ((2, ((71, 77), (38, (72, 41))), 19))), ((121, (((((((18, (((61, (109, 58))), 131), ((88,
...tree.rep.1600.= ((93, 31), (((124, 69), 102), 56), ((2, ((71, 77), (38, (72, 41))), 19))), ((121, (((((((18, (((109, 61), 58), 131), ((88,
...tree.rep.1700.= ((93, 31), (((124, 69), 102), 56), ((2, ((71, 77), (38, (72, 41))), 19))), ((121, (((((((18, (((88, 78), ((61, (109, 58))), ((
...tree.rep.1800.= ((93, 31), (((124, 69), 102), 56), ((2, ((71, 77), (38, (72, 41))), 19))), ((121, (((((((18, (((88, 78), ((61, (109, 58))), ((
...tree.rep.1900.= ((93, 31), (((124, 69), 102), 56), (((71, 77), (38, 41), 72))), 19), (2, ((121, (((((((28, 43), 47), 84), ((7, ((18, (((88
...tree.rep.2000.= ((93, 31), (((124, 69), 102), 56), ((71, 77), (38, 41), 72))), ((2, (121, (((((((28, 43), 47), 84), ((7, ((18, (((88, 78),
...tree.rep.2100.= ((93, 31), (((124, 69), 102), 56), ((71, 77), (38, 41), 72))), ((2, ((121, (((((((28, 43), 47), 84), ((7, ((18, (((88, 78),
...tree.rep.2200.= ((36, ((93, 31), (((124, 69), 102), 56), ((71, 77), (38, 41), 72))), (((115, (65, 63))), 2, (((28, 43), 47), 84), ((7, ((
...tree.rep.2300.= ((36, ((93, 31), (((124, 69), 102), 56), ((71, 77), (38, 41), 72))), (((115, (65, 63))), 2, (((70, 66), 15), ((28, 43, 4
...tree.rep.2400.= ((36, ((93, 31), ((69, (124, 102)), 56), ((71, 77), (38, 41), 72))), (((115, (65, 63))), 2, (((15, ((28, 43), 47), 84), ((
...tree.rep.2500.= ((36, ((93, 31), ((69, 56), (124, 102)), ((71, 77), (38, 41), 72))), 106), 2, ((115, (65, 63))), ((15, ((28, 43), 47),
...tree.rep.2600.= ((36, ((93, 31), ((69, 56), (124, 102)), ((71, 77), (38, 41), 72))), 106), (19, 2, ((115, ((108, 121), 96), ((68, (55, 62)
```