Introduction to RevBayes

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With massive borrowings from
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What is RevBayes?

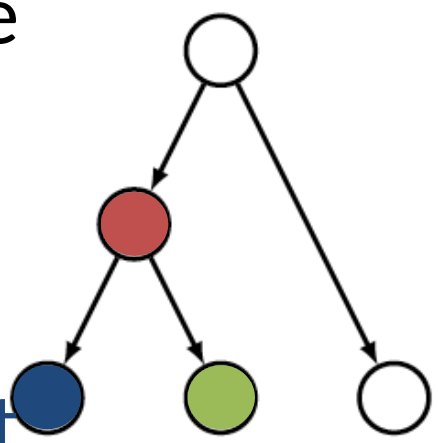
- Software for Bayesian statistical analyses
- Strong focus on phylogenetic models
- Strong focus on MCMC algorithms (Metropolis-Hastings, MCMCMC)
- C++ core for efficiency
- Interpreted R-like language for interactivity
- Built with probabilistic graphical models in mind

Useful pointers

- http://revbayes.github.io/
- http://revbayes.github.io/tutorials/
- https://revbayes.github.io/documentation/
- http://revbayes.github.io/download
- https://github.com/revbayes
- https://groups.google.com/g/revbayes-users

Graphical models in RevBayes

- Graphical models provide a simple way to represent probabilistic models
- They are also a powerful way to identify conditionally independent variables:
  - In RevBayes, objects are programmed in such a way that algorithms naturally benefit from conditional independence



The Rev language

- R-like
- Type inference
- Object-oriented
- Completions
- Case-sensitive
- Math functions:

```
exp(1)
ln(1)
sqrt(16)
power(2,2)
```

- Distributions:
-

```
dexp(x=1,lambda=1)      # exponential distribution density function
qexp(0.5,1)             # exponential distribution quantile function
rexp(n=10,1)            # random draws from an exponential distribution
dnorm(-2.0,0.0,1.0)     # normal distribution density function
rnorm(n=10,0,1)         # random draws from a normal distribution
```

The Rev language: useful functions

- Structure of a variable :

```
str(a)                          # printing the structure information of 'a'
   _variable    = a
   _RevType     = Natural
   _RevTypeSpec = [ Natural, Integer, RevObject ]
   _value       = 1
   _dagType     = Constant DAG node
   _children    = [ ]
   .methods = void function ()
```

- Type of a variable :

```
type(a)
    Natural
```

- Help: `?mean`
- Working directory: `getwd()`
- What's in my environment: `ls()`
- What commands are available? `ls(all=TRUE)`
- Sourcing a file: `source("file")`

Variable declaration in Rev

- 2 main types of variables:
  - Environment variable: name = « MyAnalysis »
  - Model variables:
    - Constant variable: c <- 1
    - Deterministic variable: d := exp(c)
    - Stochastic variable: x ~ dnExponential(c)

A little practical exercise

Start revbayes

In the terminal :

```
rb
```

Let’s explore the variable types

```
a<-1
b<-2
x~dnNormal(mean=a,sd=b)
print(x)
y:=x*x
z<-x*x
x.redraw();print("x: "+x);print("y: "+y);print("z: "+z)
x.redraw();print("x: "+x);print("y: "+y);print("z: "+z)
y.redraw()
z.redraw()
```

Let's explore the variable types

```
a<-1
```
Constant node

```
b<-2
```
Constant node

```
x~dnNormal(mean=a,sd=b)
```
Stochastic node

```
print(x)
y:=x*x
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Deterministic node

```
z<-x*x
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Constant node

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    - Stochastic variable: x ~ dnExponential(c)

  - More fun with stochastic variables:

```
x                                # print value of stochastic node 'x'
x.probability()                  # print the probability if 'x'
x.lnProbability()                # print the log-probability if 'x'
str(x)                           # printing all the information of 'x'
```

The Rev language: more details

- Vectors: `v <- v(1,2,3)` or: `w <- [1,2,3]` or:

```
z[1] <-1
z[2] <-2
z[3] <-3
```

- Convenience functions:

```
1:10
rep(10,1)
seq(1,20,2)
```

- Vectors are objects:

```
v.methods()
```

- Control structures:
  - for loops
  - while loops

```
sum <- 0
for (i in 1:100) {
   sum <- sum + i
}
sum
```

Anatomy of a phylogenetic MCMC analysis

How do we set up inference with MCMC for a simple phylogenetic model in RevBayes ?

Anatomy of a phylogenetic MCMC analysis

```
########
# Data #
########
# We read the sequence alignment:
data = readDiscreteCharacterData("...")
n_branches = 2 * data.ntaxa() - 3
```

Anatomy of a phylogenetic MCMC analysis

```
########
# Data #
########
# We read the sequence alignment:
data = readDiscreteCharacterData("...")
n_branches = 2 * data.ntaxa() - 3

###############################
# Model of sequence evolution #
###############################
# Uniform prior on topologies
topology ~ dnUniformTopology(...)

# Exponential priors on branch lengths
for (i in 1:n_branches) {
 bls[i] ~ dnExponential(10)
}
# Putting branch lengths and topology together
psi := treeAssembly(topology, bls)
# We define a JC rate matrix:
Q <- fnJC(4)
# The sequences are drawn from a CTMC running
along the tree
seq ~ dnPhyloCTMC( tree=psi, Q=Q, type="DNA" )
# We condition the CTMC on the sequence
alignment.
seq.clamp( data )
# We declare the model as one big object that
we are going to use in the MCMC:
my_model = model(psi)
```

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```
#########
# Moves #
#########
# We create a vector of moves to store them
all:
moves = VectorMoves()
# Move on the topology
moves.append(mvNNI(topology, weight=10.0))
# We define moves on the branch lengths, one
for each branch.
for (i in 1:n_branches) {
   moves.append(mvScaleBactrian(bls[i],
tune=TRUE))
}
```

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#################
# MCMC analysis #
#################
# Now we define monitors to keep track of
what's happening during the MCMC.
# One monitor to store the parameter
distributions into a file:
monitors[1] = mnModel(filename="...",
printgen=10, separator = TAB)
# We create an MCMC object:
analysis = mcmc(my_model, monitors, moves,
...)
# We run the MCMC for 20,000 iterations:
analysis.run(20000)
```

Anatomy of a phylogenetic MCMC analysis

DATA

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MODEL

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MCMC

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Advice on organizing an analysis

- create a folder for the analysis
- put data in a folder « `data` »
- put the scripts in a folder « `scripts` »
- store the output files in « `analyses` » or « `output` »
- to run an analysis from the terminal:

```
rb scripts/myscript.rev
```

- or, from within rb :

```
source("scripts/myscript.rev")
```