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| BASIC SET UP  1. Describe what is happening in these lines of code | setOption("useScaling","true")  NUM\_STATES = 2  NUM\_HIDDEN = 2  NUM\_RATES = NUM\_STATES \* NUM\_HIDDEN  observed\_phylogeny <- readTrees("basicdata/poleult.tre")[1]  data <- readCharacterDataDelimited("basicdata/pole\_datadis.csv",  stateLabels=2,  type="NaturalNumbers",  delimiter=",",  headers=TRUE)  data\_exp <- data.expandCharacters( NUM\_HIDDEN )  taxa <- observed\_phylogeny.taxa()  root\_age <- observed\_phylogeny.rootAge()  # set my move index  mvi = 0  mni = 0 |
| DIVERSIFICATION RATES  2. Draw the fixed, stochastic and deterministic nodes determined by the RevBayes code for speciation and extinction | ## Number of surviving lineages is 165  mx=(ln(165/2)/observed\_phylogeny.rootAge())  sx= 0.05  rate\_mean <- exp(mx+sx^2)  rate\_sd <- sqrt(exp(2\*mx+sx^2)\*exp(sx^2-1))  #Key point: The way we define the states in RevBayes is by letter. Therefore, 1=0A, 2=1A, 3=0B, and 4=1B  speciation\_alpha ~ dnNormal(mean=rate\_mean,sd=rate\_sd)  moves[++mvi] = mvSlide(speciation\_alpha,delta=0.20,tune=true,weight=3.0)  extinction\_alpha ~ dnNormal(mean=rate\_mean,sd=rate\_sd)  moves[++mvi] = mvSlide(extinction\_alpha,delta=0.20,tune=true,weight=3.0)  speciation\_beta ~ dnExp(1.0)  moves[++mvi] = mvScale(speciation\_beta,lambda=0.20,tune=true,weight=2.0)  ### Create an normal distributed variable for the turnover rate  extinction\_beta ~ dnNormal(0.0,1.0)  moves[++mvi] = mvSlide(extinction\_beta,delta=0.20,tune=true,weight=2.0)  for (j in 1:NUM\_HIDDEN) {  for (i in 1:NUM\_STATES) {  if ( j == 1) {  speciation[i] := exp( speciation\_alpha )  extinction[i] := exp( extinction\_alpha )  } else {  index = i+(j\*NUM\_STATES)-NUM\_STATES  speciation[index] := speciation[index-NUM\_STATES] \* exp( speciation\_beta )  extinction[index] := exp( extinction\_alpha + extinction\_beta )  }  }  } |
| TRANSITION RATES BETWEEN OBSERVED STATES  3. Draw the fixed, stochastic and deterministic nodes determined by the RevBayes code for transition rates between states 0 and 1 | shape\_pr := 0.5  rate\_pr := 1  #### First create a 4x4 matrix full of zeros  for (i in 1:4) {  for (j in 1:4) {  q[i][j] := 0.0  }  }  #Key point: The way we define the states in RevBayes is by letter. Therefore, 1=0A, 2=1A, 3=0B, and 4=1B  q\_01 ~ dnGamma(shape=shape\_pr, rate=rate\_pr)  moves[++mvi] = mvScale(q\_01, weight=2 )  q\_10 ~ dnGamma(shape=shape\_pr, rate=rate\_pr)  moves[++mvi] = mvScale(q\_10, weight=2 )  q[1][2] :=q\_01  q[3][4] :=q\_01  q[2][1] :=q\_10  q[3][4] :=q\_10 |
| TRANSITION RATES BETWEEN HIDDEN STATES  4. Draw the fixed, stochastic and deterministic nodes determined by the RevBayes code for transition rates between states A and B  #Key point: The way we define the states in RevBayes is by letter. Therefore, 1=0A, 2=1A, 3=0B, and 4=1B | hidden\_rate1 ~ dnExponential(rate\_pr)  moves[++mvi] = mvScale(hidden\_rate1,lambda=0.2,tune=true,weight=5)  hidden\_rate2 ~ dnExponential(rate\_pr)  moves[++mvi] = mvScale(hidden\_rate2,lambda=0.2,tune=true,weight=5)  #### Here the hidden rates should go (alpha,beta, alpha, beta) for assymetric models  q[1][3] := hidden\_rate1  q[2][4] := hidden\_rate1  q[3][1] := hidden\_rate2  q[4][2] := hidden\_rate2  ### Note, we could go a step further and define even 4 different hidden rates  ######################################################################  # Create the rate matrix for the combined observed and hidden states #  ######################################################################  rate\_matrix := fnFreeK(q, rescaled=false, matrixExponentialMethod="scalingAndSquaring") |
| ROOT FREQUENCIES  5. Draw the fixed, stochastic and deterministic nodes determined by the RevBayes code to calculate the root frequencies | rate\_category\_prior ~ dnDirichlet( rep(1,NUM\_RATES) )  moves[++mvi] = mvBetaSimplex(rate\_category\_prior,tune=true,weight=2)  moves[++mvi] = mvDirichletSimplex(rate\_category\_prior,tune=true,weight=2)  ### Sampling bias  ### fix this to 165/450  sampling <- observed\_phylogeny.ntips()/450 |
| FULL HiSSE MODEL  6. As a large group we will come back to this point to determine the full graphical model for HiSSE | cidmodel ~ dnCDBDP(rootAge = root\_age,  speciationRates = speciation,  extinctionRates = extinction,  Q = rate\_matrix,  pi = rate\_category\_prior,  rho = sampling)  ### clamp the model with the "observed" tree  cidmodel.clamp( observed\_phylogeny )  cidmodel.clampCharData( data\_exp ) #note the clamping on the expanded dataset |

