razzo choices

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Overview

Parameter selection

- MBD regime vs nu & q
- # taxa and % extinct vs lambda and mu

Inference models selection

- Generative and best non-generative vs simplest and most complex

Parameter selection

MBD parameters: lambda, mu, nu, q

Compound parameters: # taxa, % extinct taxa, MBD regime

Choices, <u>in this order</u>:

- **MBD regime** vs nu & q
- **# taxa and % extinct** vs lambda and mu

= Richel's favorite   = Giovanni's favorite

MBD regime vs nu & q

MB regime	# MB events	q	nu
Few intense MB events	2	1	T / 2
Intermediate	4	0.5	T / 4
Many weak MB events	8	0.25	T / 8

Do/don't select full/reconstructed trees with observable/unobservable number of MB events

Do/don't track full/reconstructed trees with observable/unobservable number of MB events

nu: MB event trigger rate
q: fraction of lineages that speciate during MB event
T: crown age

nu	q
T / 2	1
T / 4	0.5
T / 8	0.25

In all 9 combinations

<u>Do</u>/<mark>don't</mark> select <u>full/reconstructed</u> trees with <u>observable/unobservable</u> number of MB events

<u>Do</u>/don't track full/<mark>reconstructed</mark> trees with <mark>observable</mark>/<u>unobservable</u> number of MB events

nu: MB event trigger rate
q: fraction of lineages that speciate during MB event
T: crown age

taxa and % extinct vs lambda and mu

Known: nu and q

# extant taxa	% extinct
50	0
100	25
200	50

Do/don't select
the precise number of extant taxa.
Do/don't select
the precise percentage
of taxa to go extinct.

In all 9 combinations

Equation
$\langle n\_taxa \rangle = f(lambda, mu, nu, q)$
must be derived

Do/don't track
the precise number of extant taxa.
Do/don't track
the precise percentage
of taxa to go extinct.

taxa and % extinct vs <u>lambda and mu</u>

Known: nu and q

lambda	mu
0.4	0.0
0.6	0.1
0.8	0.2

In all 9 combinations

Do/don't select/limit
a precise number of extant taxa.
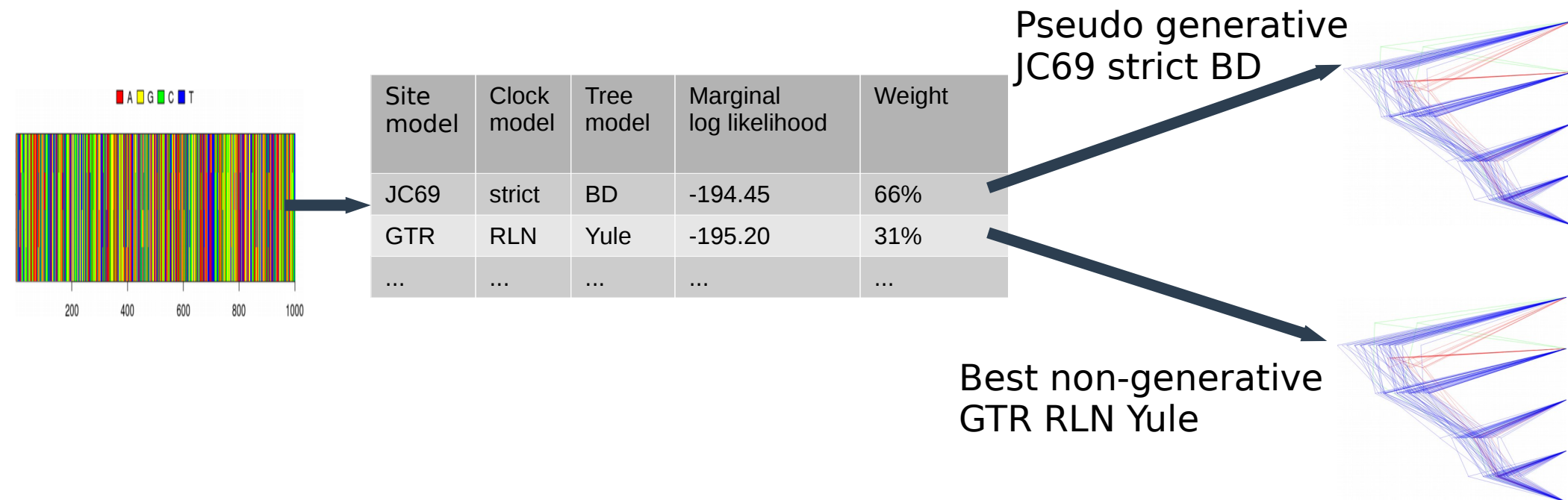Do/don't select
a precise percentage
of taxa to go extinct.

Do/don't track
the precise number of extant taxa.
Do/don't track
the precise percentage
of taxa to go extinct.

lambda: speciation rate
mu: extinction rate

Inference models selection

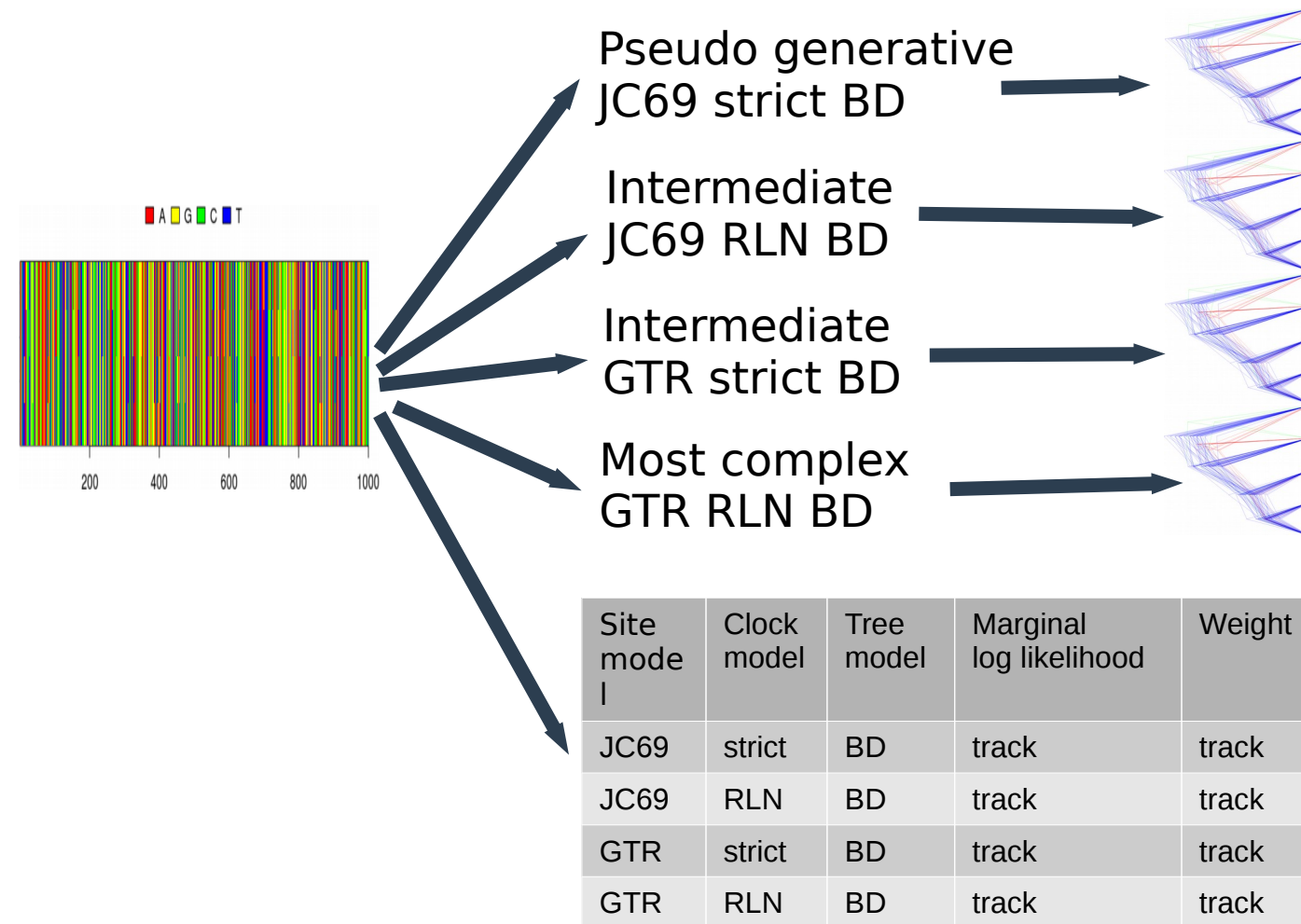**Generative and best non-generative vs simplest and most complex**

Generative and best non-generative vs simplest and most complex

Site model	Clock model	Tree model	Marginal log likelihood	Weight
JC69	strict	BD	-194.45	66%
GTR	RLN	Yule	-195.20	31%
...	...	...	...	...

Pseudo generative
JC69 strict BD

Best non-generative
GTR RLN Yule

Pseudo generative
JC69 strict BD

Intermediate
JC69 RLN BD

Intermediate
GTR strict BD

Most complex
GTR RLN BD

Site model	Clock model	Tree model	Marginal log likelihood	Weight
JC69	strict	BD	track	track
JC69	RLN	BD	track	track
GTR	strict	BD	track	track
GTR	RLN	BD	track	track

Other decisions

- **Number of different alignments per tree: 1, 2, more**

- **Number of BEAST2 runs per alignment: 1, 2, more**

- **Number of MBD trees per parameter setting: 10, 100, 1000, calculate from experiment time**

- **DNA alignment length: 100, 1000, 10k, 100k**