

# **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, in this order:**

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



# 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

# MBD regime vs nu & q

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

In all 9 combinations

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

# # taxa and % extinct vs lambda and mu

**Known: nu and q**

# extant taxa	% extinct
50	0
100	25
200	50

In all 9 combinations

Do/don't select  
the precise number of extant taxa.  
Do/don't select  
the 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.

# # taxa and % extinct vs lambda and mu

**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.

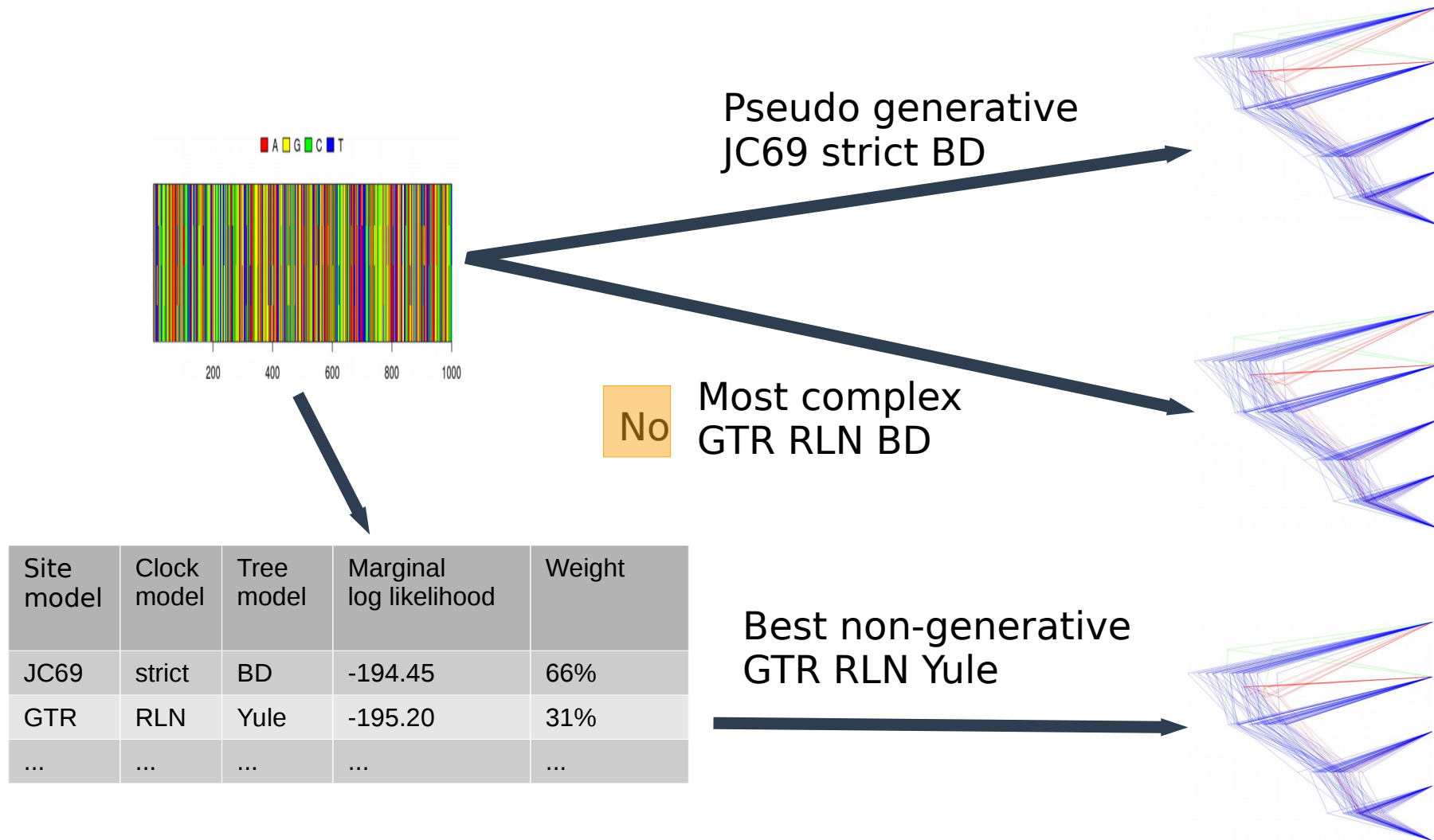
Do/don't track  
the precise number of extant taxa.  
Do/don't track  
the precise percentage  
of taxa to go extinct.

# Inference models selection

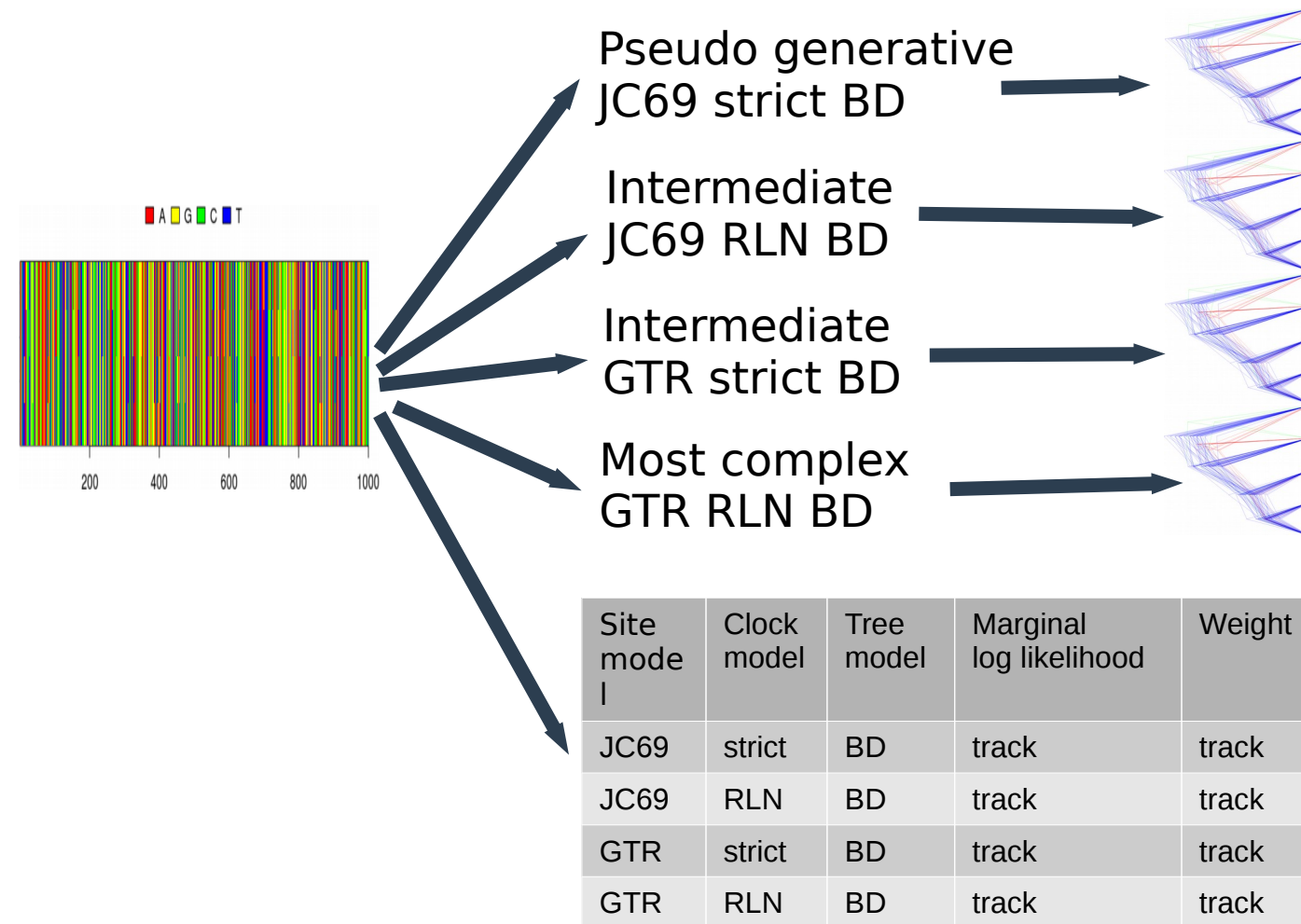
**Generative and best non-generative vs simplest and most complex**



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



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



# 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