Input

tabular data file e.g., Parquet, CSV,

JSON. etc.

<u>"genome</u>s" raw sim output w/ genome hex strinas

chronological sort



<u>"unpack</u>ed"

chunk

extract and decode hstrat markers

NumPy 9 Numba

"exploded"

pybind11

build trie

extend and

consolidate

collapse dropped unifs

postprocess

- collapse all unifurcations

Polars

- estimate taxon origin times

- convert to alife standard

Output tabular data file

"phylogeny"

alife data standard

format

JSON, etc.

e.g., Parquet, CSV,