Input

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

"fossils" raw sim output w/ genome hex

strinas

JSON. etc.

chunk

chronological sort



<u>"unpack</u>ed"





build trie

collapse dropped unifs





- collapse all

postprocess

unifurcations

- estimate taxon origin times

- convert to alife

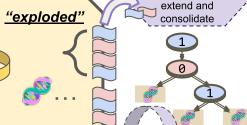
Output

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

"phylogeny"

alife data standard format





standard