

# User input

# Results

**Enter cross-sectional data**

Upload file

Enter genotype frequencies manually

**Cross-sectional data**

Modify cross-sectional data

Analyze  
("Run evamtools")

"Advanced options":  
Choice of methods  
(OT, OncoBN,  
CBN, MCCBN,  
H-ESBCN, MHN,  
HyperTraPS-CT, BML)  
and methods' parameters

**Fitted EvAM model(s)**

- DAG (& rates/conditional probs.)
- MHN log- $\Theta$  matrix
- HyperTraPS influences
- BML paths & edge probs.

**Predictions from fitted models**

- Transition probabilities → Probabilities paths of progression
- Transition rates
- Predicted genotype relative frequencies → Finite genotype samples
- Motifs and timings (HyperTraPS)

**Generate cross-sectional data from CPM models**

- DAG and rates/cond. probs: OT, OncoBN, CBN, H-ESBCN
- MHN log- $\Theta$  matrix

Modify models

Simulate data from model

Sample size  
Observational noise  
Model deviations (epos,  $\epsilon$ : OT, OncoBN)

Download

Output file  
(analyzed data,  
fitted models,  
tabular output)