

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- Θ 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- Θ matrix

Simulate data from model

Sample size
Observational noise
Model deviations (epos, ϵ : OT, OncoBN)

Download

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

1

3.3

2

2

3.1

3.2

2

1

3.2

3.3

3.3