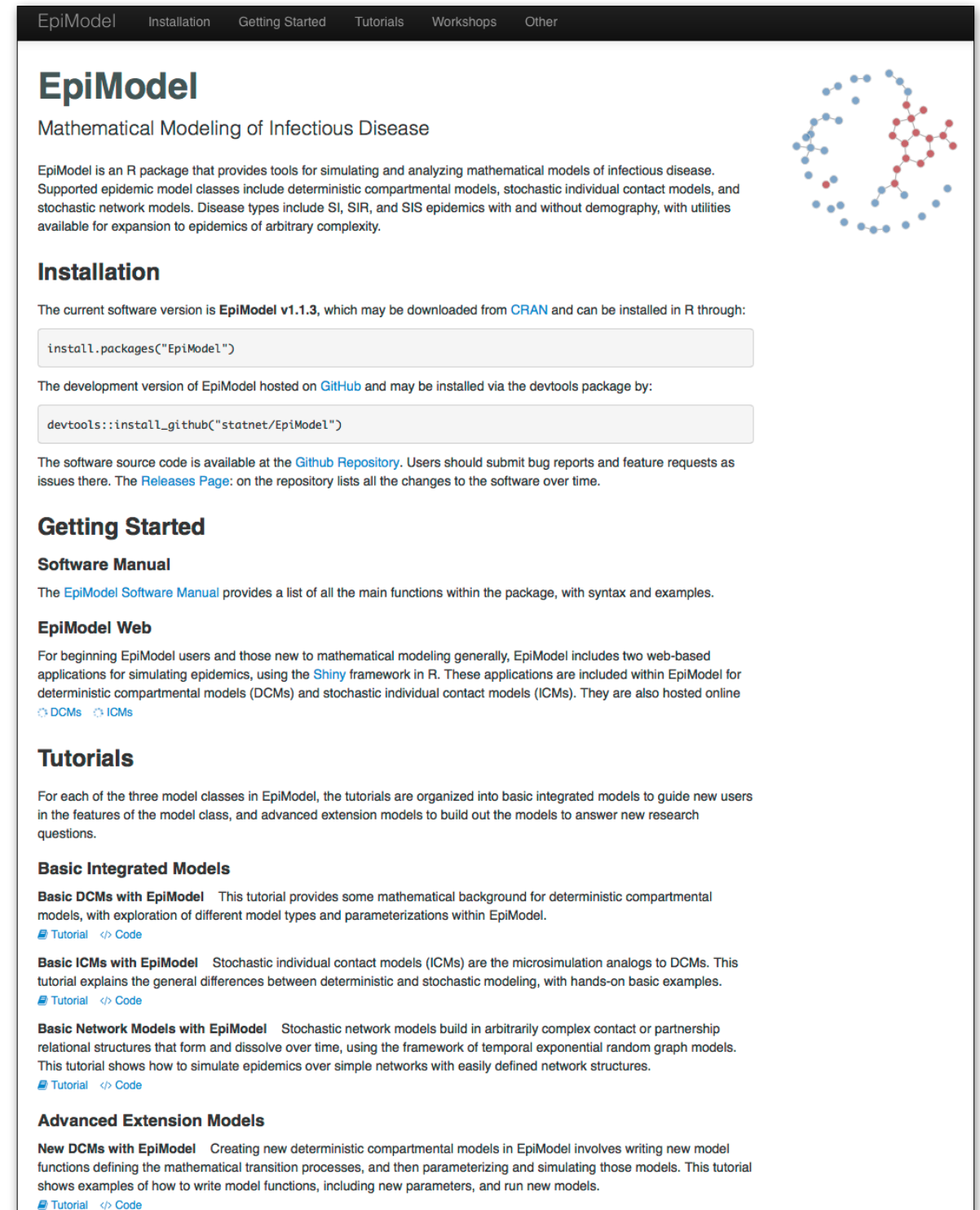


Introduction to EpiModel

Network Models for HIV/STI Transmission Dynamics with EpiModel

June 27, 2017

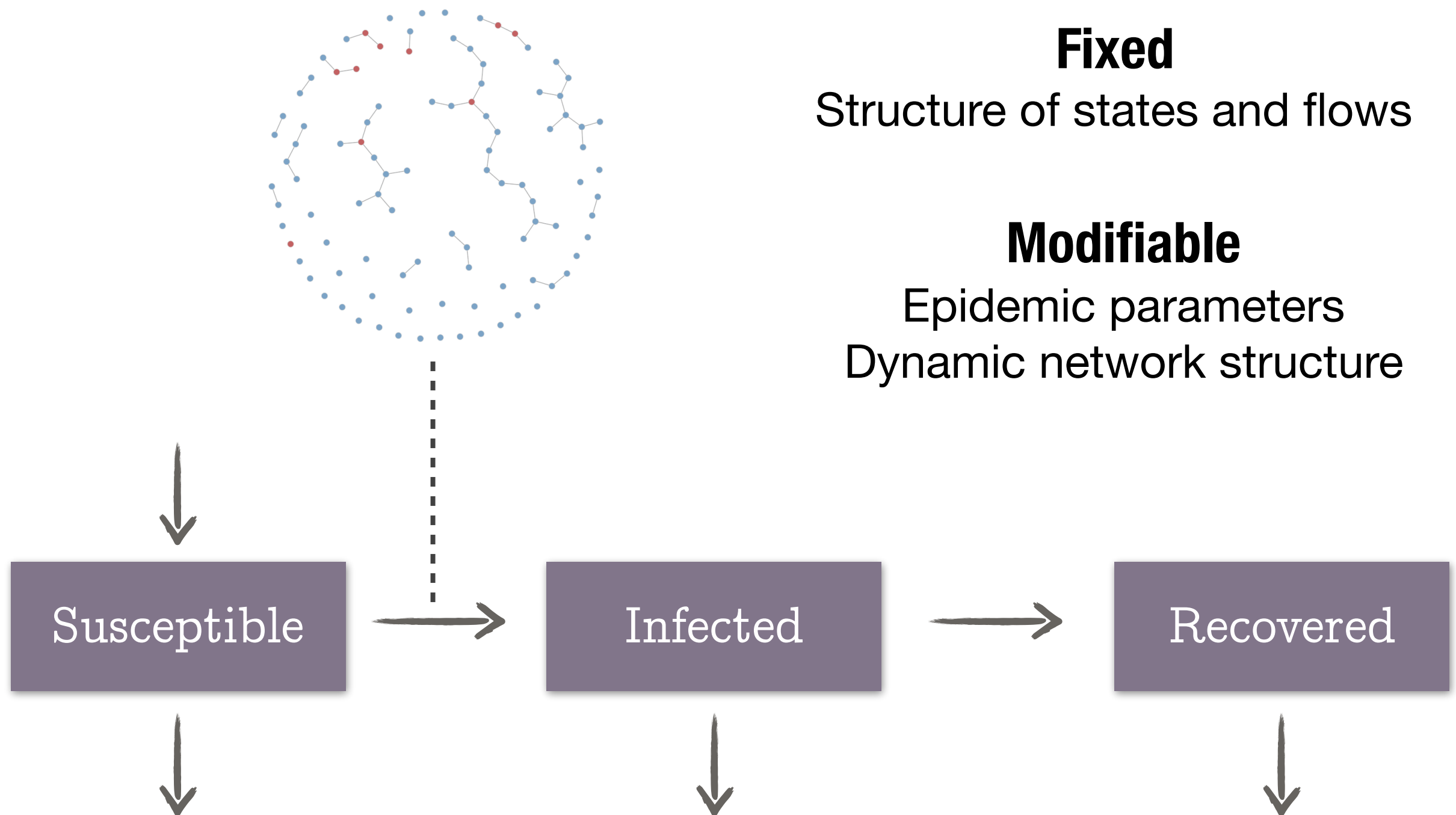
- Open-source software platform for epidemic modeling
- Tools for building, simulating, and analyzing models
- Three model classes
 - Deterministic compartmental models
 - Stochastic ABMs
 - Stochastic network models
- <http://epimodel.org/>

The screenshot shows the EpiModel website with a navigation bar at the top containing links for EpiModel, Installation, Getting Started, Tutorials, Workshops, and Other. The main heading is 'EpiModel' followed by the subtitle 'Mathematical Modeling of Infectious Disease'. A paragraph describes EpiModel as an R package for simulating and analyzing mathematical models of infectious disease, listing supported model classes and disease types. To the right is a network diagram with blue and red nodes. The 'Installation' section provides the current version (v1.1.3) and instructions for installing from CRAN or via devtools from GitHub, with corresponding R code snippets. The 'Getting Started' section includes links to the Software Manual, EpiModel Web (with links to DCMs and ICMs), and Tutorials. The 'Basic Integrated Models' section contains three subsections: 'Basic DCMs with EpiModel', 'Basic ICMs with EpiModel', and 'Basic Network Models with EpiModel', each with a brief description and links to the tutorial and code. The 'Advanced Extension Models' section includes 'New DCMs with EpiModel'.

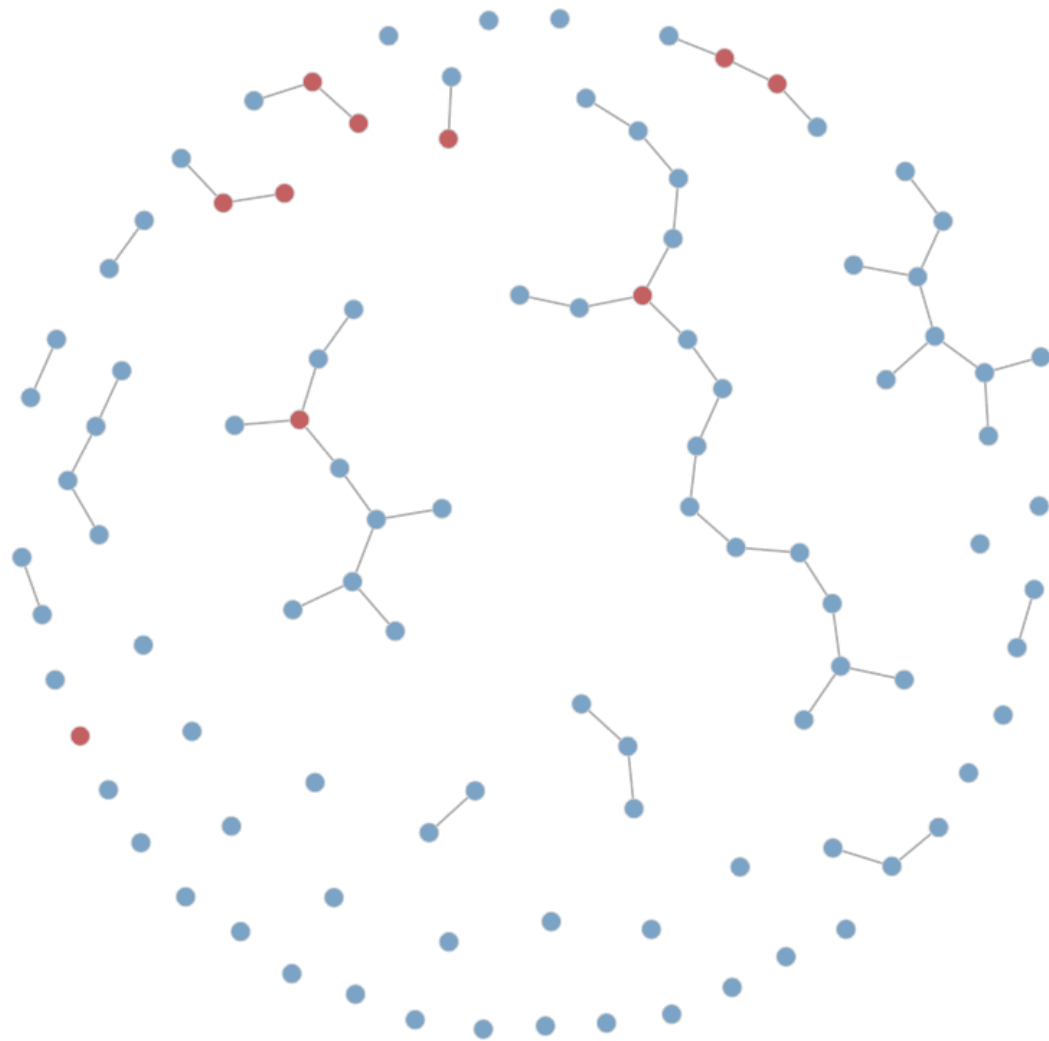
Learning vs Research Extensions

- EpiModel designed to be a tool for both **teaching** and **research**
- Software “**integrated**” **epidemic models** over basic disease types (SI, SIS, SIR) to learn the fundamentals of network modeling
- Not (necessarily) designed for novel research questions, but still allow for **broad flexibility** in parameterizing dynamic networks

Base Epidemic Models



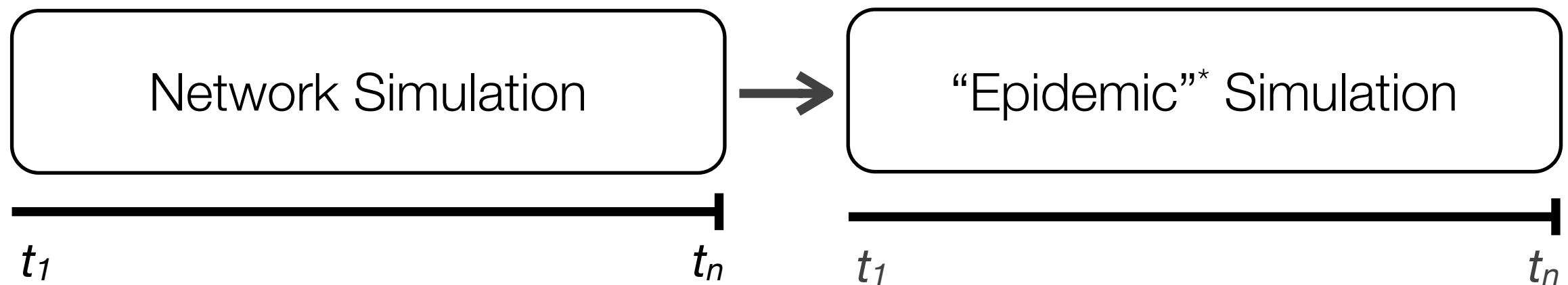
Closed Population



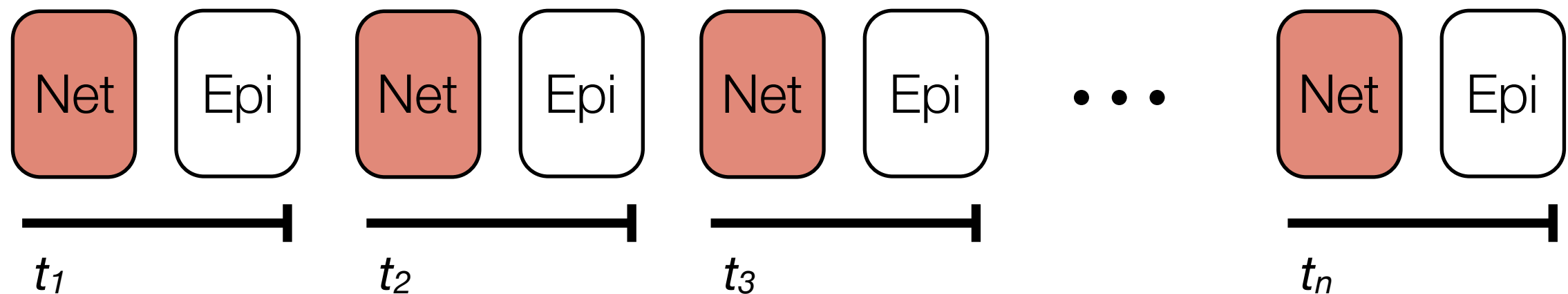
- Simplification conceptually and computationally
- Assumes no temporal feedback from exogenous dynamics on network structure
 - No demographic flows
 - No disease terms in the TERGM
 - No behavioral adaptation

Model Dependence

Independent Models



Dependent Models



"Epidemic" = biological, behavioral, demographic, etc., changes*

EpiModel Workflow for Base Models

1. Construct the (empty) network data structure
2. Parameterize the TERGM (formation and dissolution formulas and target statistics)
3. Fit the TERGM, and diagnose the model fit
4. Parameterize the epidemic model
5. Simulate the epidemic
6. Analyze the simulation data

EpiModel Workflow for Base Models

1. Construct the (empty) network data structure:
`network.initialize, set.vertex.attribute`
2. Parameterize the TERGM (formation and dissolution formulas and target statistics): `dissolution_coefs`
3. Fit the TERGM, and diagnose the model fit: `netest, netdx`
4. Parameterize the epidemic model: `param.net, init.net, control.net`
5. Simulate the epidemic: `netsim`
6. Analyze the model data: `print, plot, summary, as.data.frame, ...`