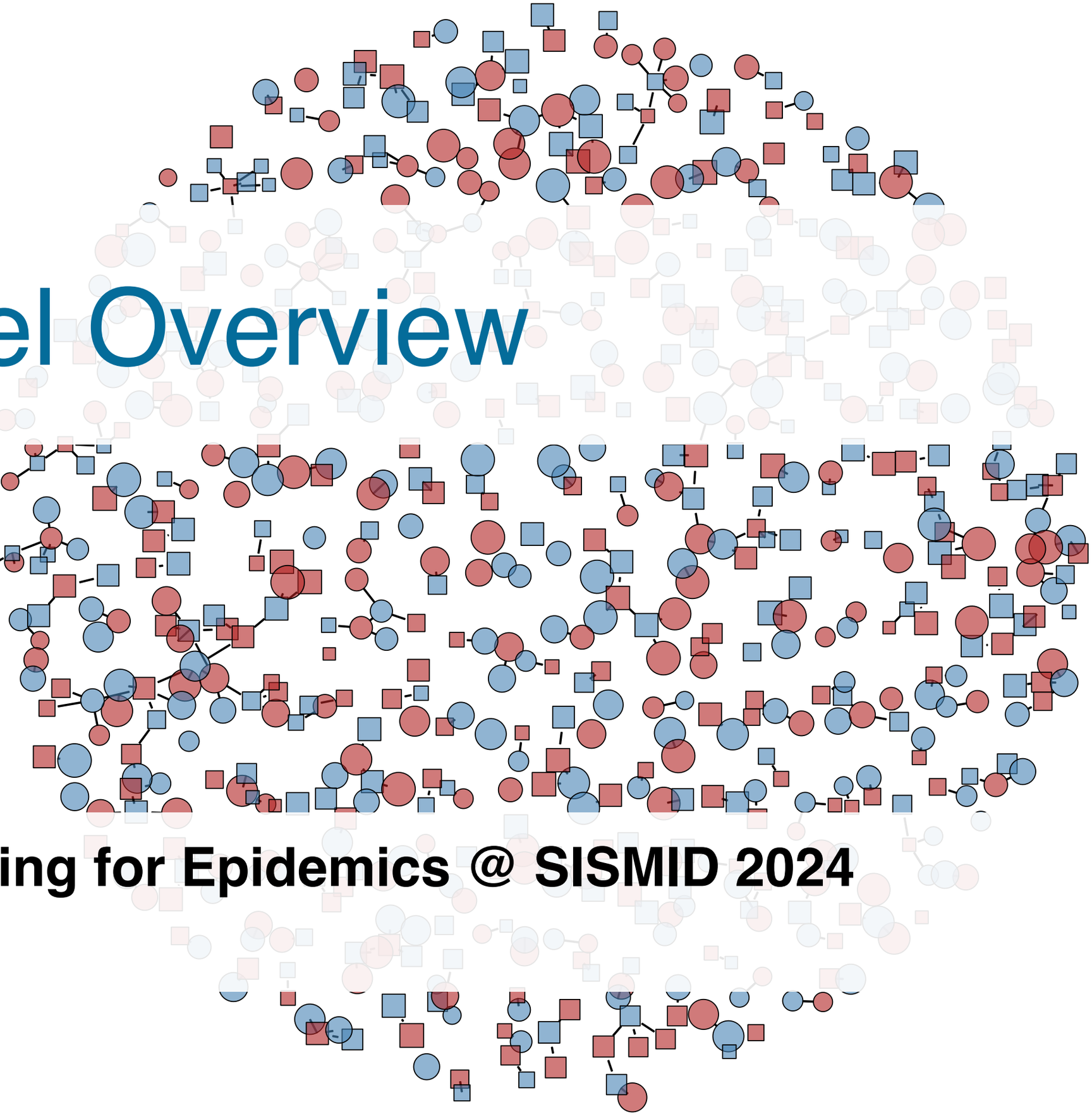
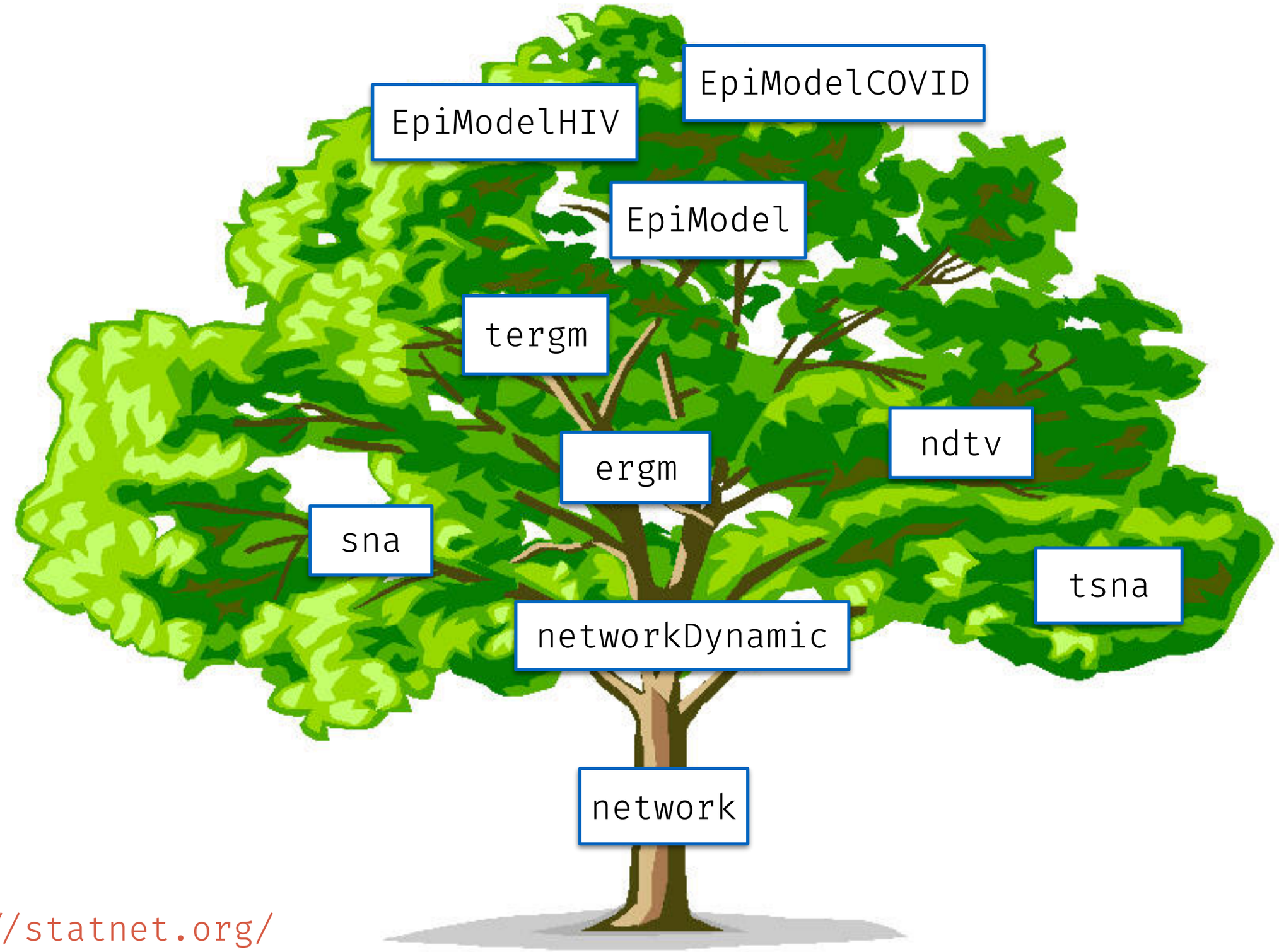
EpiModel Overview



Network Modeling for Epidemics @ SISMID 2024

Module 4

The Statnet/EpiModel Family Tree



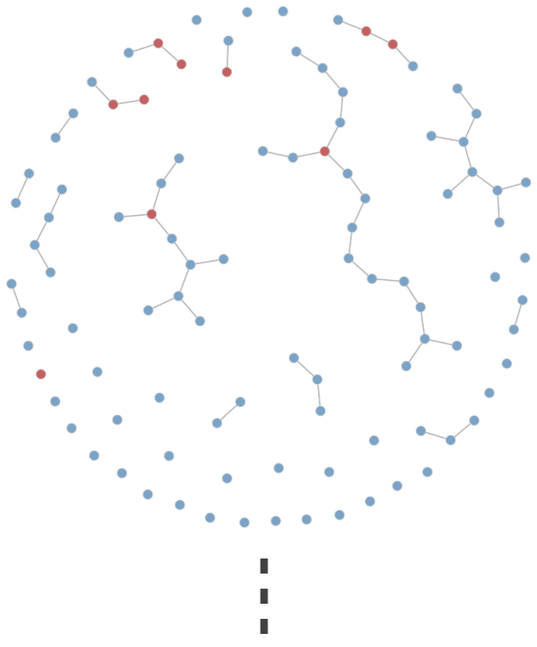
http://statnet.org/

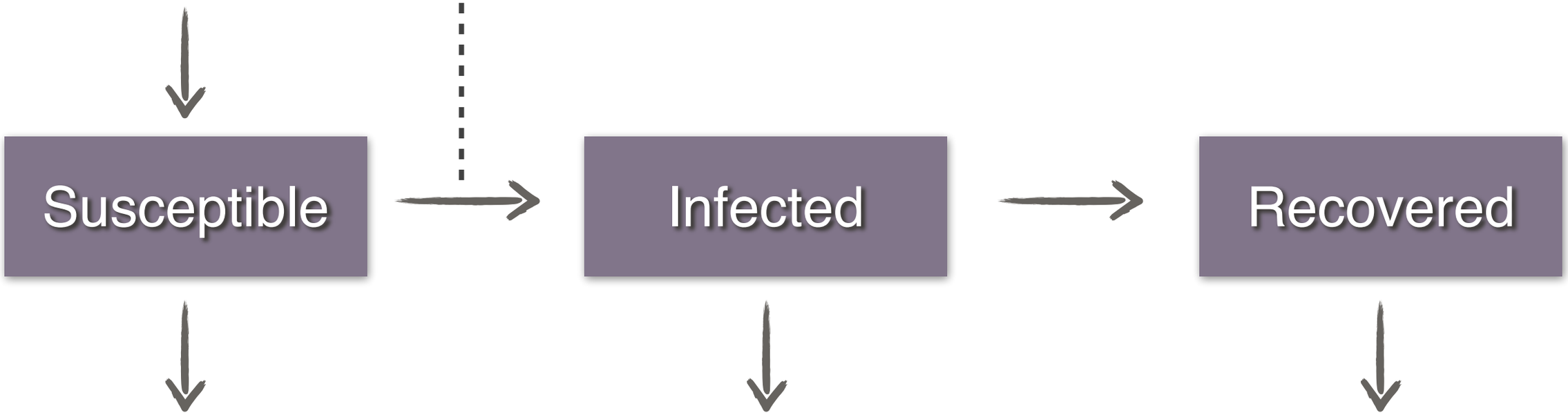
https://CRAN.R-project.org/package=statnet

Outline for EpiModel Modules

- Module 4, 5, & 7
  - Modeling epidemics + networks = modeling epidemics over networks
  - Core assumption: no feedback of epidemiology on networks
    - One important implication: closed populations
    - Still feedback: *network structure* $\Longrightarrow$ *epidemiology* and *incidence* $\Longrightarrow$ *prevalence*
  - Built-in **epidemiology** types (SI, SIR, SIS)
    - Working with nodal attributes, with heterogeneity in network structure and epidemiological parameters
- Module 8
  - Feedback: epidemiology $\Longrightarrow$ network structure
    - Vital dynamics, “sero-sorting” (edge formation based on changing nodal attributes)
  - Simple vaccine intervention
  - Built-in **epidemiology** types (SI, SIR, SIS), then getting started with extensions
- Module 9
  - Getting comfortable with extensions
  - Building a network-based extension model for COVID, step-by-step…

“Built-in Epidemiology”





Fixed

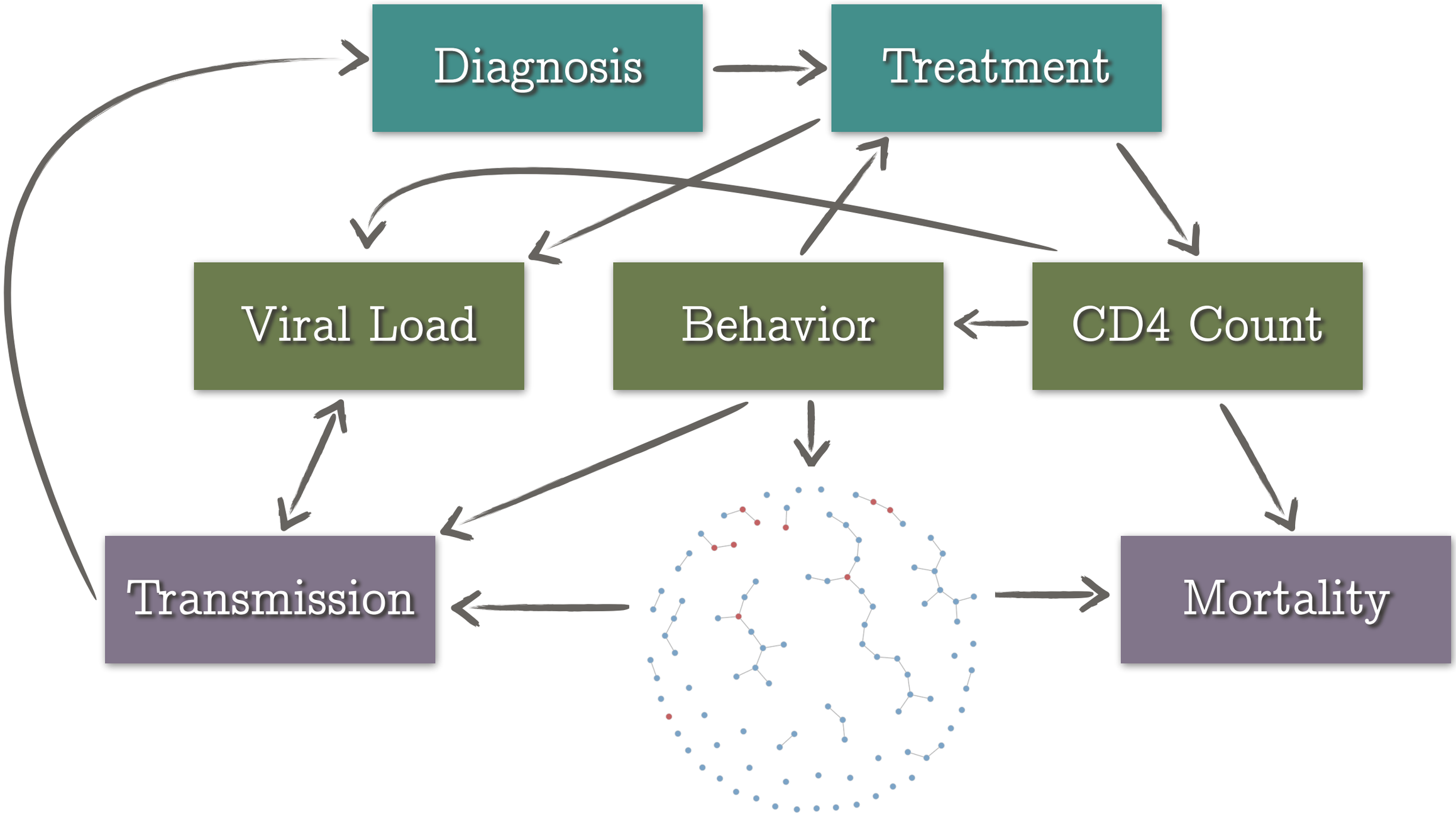
Basic structure of states and flows

Modifiable

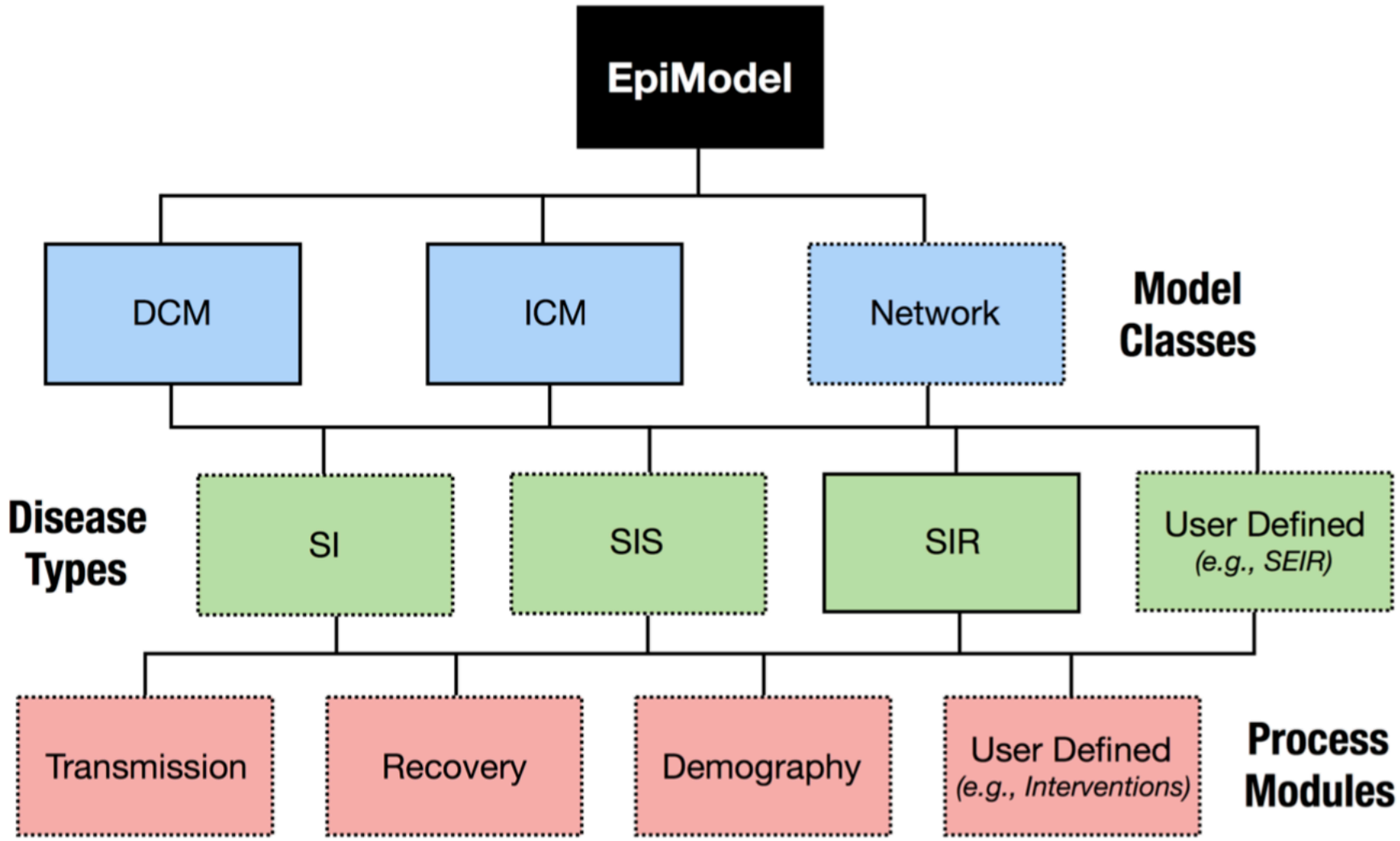
Epidemic parameters

Dynamic network structure

Complex Epidemic Models



EpiModel

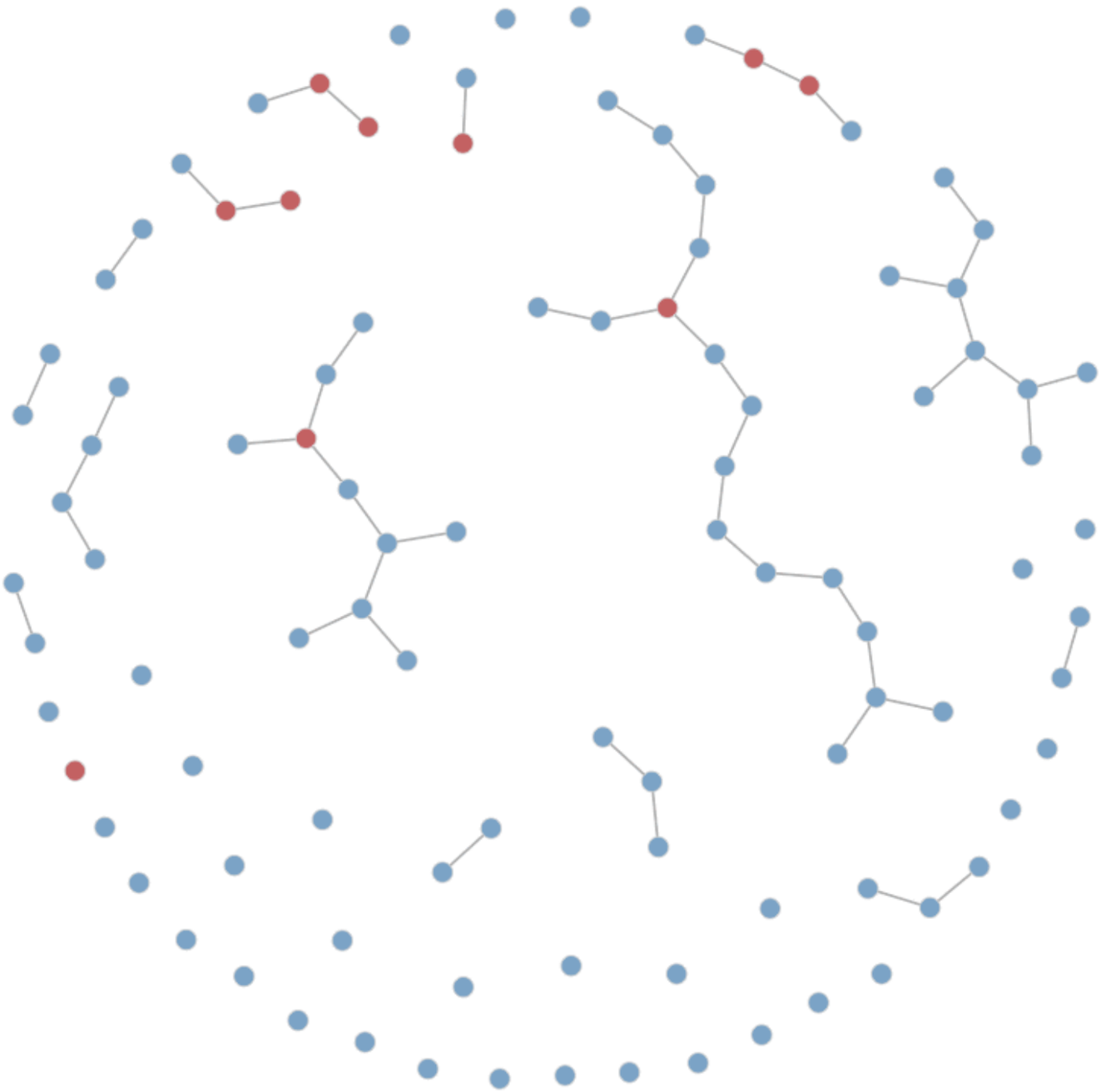


- EpiModel designed specifically to allow for both built-in ("toy models") and user-defined extensions ("research models")
- You have seen this for DCMs. Computer lab this week is focus on built-in network models. Extensions are more complicated…

```
sti_recov <- function(dat, at) {

  # Parameters
  rgc.dur.asympt <- dat$param$rgc.dur.asympt
  ugc.dur.asympt <- dat$param$ugc.dur.asympt
  gc.dur.tx <- dat$param$gc.dur.tx
  gc.dur.ntx <- dat$param$gc.dur.ntx

  rct.dur.asympt <- dat$param$rct.dur.asympt
  uct.dur.asympt <- dat$param$uct.dur.asympt
  ct.dur.tx <- dat$param$ct.dur.tx
  ct.dur.ntx <- dat$param$ct.dur.ntx


  # GC recovery
  idsRGC_asympt <- which(dat$attr$rGC == 1 & dat$attr$rGC.infTime < at &
                           dat$attr$rGC.sympt == 0)
  idsUGC_asympt <- which(dat$attr$uGC == 1 & dat$attr$uGC.infTime < at &
                           dat$attr$uGC.sympt == 0)
  idsRGC_tx <- which(dat$attr$rGC == 1 & dat$attr$rGC.infTime < at &
                       dat$attr$rGC.sympt == 1 & dat$attr$rGC.tx == 1)
  idsUGC_tx <- which(dat$attr$uGC == 1 & dat$attr$uGC.infTime < at &

  idsRGC_ntx <- which(dat$attr$rGC == 1 & dat$attr$rGC.infTime < at &

  idsUGC_ntx <- which(dat$attr$uGC == 1 & dat$attr$uGC.infTime < at &
                        dat$attr$uGC.sympt == 1 & dat$attr$uGC.tx == 0)

  recovRGC_asympt <- idsRGC_asympt[which(rbinom(length(idsRGC_asympt), 1,
                                                1/rgc.dur.asympt) == 1)]
  recovUGC_asympt <- idsUGC_asympt[which(rbinom(length(idsUGC_asympt), 1,
                                                1/ugc.dur.asympt) == 1)]

  recovRGC_tx <- idsRGC_tx[which(rbinom(length(idsRGC_tx), 1,
                                        1/gc.dur.tx) == 1)]
  recovUGC_tx <- idsUGC_tx[which(rbinom(length(idsUGC_tx), 1,
                                        1/gc.dur.tx) == 1)]

  if (!is.null(gc.dur.ntx)) {
    recovRGC_ntx <- idsRGC_ntx[which(rbinom(length(idsRGC_ntx), 1,
                                           1/gc.dur.ntx) == 1)]
    recovUGC_ntx <- idsUGC_ntx[which(rbinom(length(idsUGC_ntx), 1,
                                           1/gc.dur.ntx) == 1)]
  } else {
    recovRGC_ntx <- idsRGC_ntx[which(rbinom(length(idsRGC_ntx), 1,
                                           1/rgc.dur.asympt) == 1)]
    recovUGC_ntx <- idsUGC_ntx[which(rbinom(length(idsUGC_ntx), 1,
                                           1/ugc.dur.asympt) == 1)]
  }

  recovRGC <- c(recovRGC_asympt, recovRGC_tx, recovRGC_ntx)
  recovUGC <- c(recovUGC_asympt, recovUGC_tx, recovUGC_ntx)

  dat$attr$rGC[recovRGC] <- 0
  dat$attr$rGC.sympt[recovRGC] <- NA
  dat$attr$rGC.infTime[recovRGC] <- NA
  dat$attr$rGC.tx[recovRGC] <- NA

  dat$attr$uGC[recovUGC] <- 0
  dat$attr$uGC.sympt[recovUGC] <- NA
  dat$attr$uGC.infTime[recovUGC] <- NA
  dat$attr$uGC.tx[recovUGC] <- NA

  dat$attr$GC.cease[c(recovRGC, recovUGC)] <- NA

  # CT recovery
  idsRCT_asympt <- which(dat$attr$rCT == 1 & dat$attr$rCT.infTime < at &
                           dat$attr$rCT.sympt == 0)
  idsUCT_asympt <- which(dat$attr$uCT == 1 & dat$attr$uCT.infTime < at &
                           dat$attr$uCT.sympt == 0)
  idsRCT_tx <- which(dat$attr$rCT == 1 & dat$attr$rCT.infTime < at &
                       dat$attr$rCT.sympt == 1 & dat$attr$rCT.tx == 0)
  idsUCT_ntx <- which(dat$attr$uCT == 1 & dat$attr$uCT.infTime < at &
                        dat$attr$uCT.sympt == 1 & dat$attr$uCT.tx == 0)

  recovRCT_asympt <- idsRCT_asympt[which(rbinom(length(idsRCT_asympt),
                                                1, 1/rct.dur.asympt) == 1)]
  recovUCT_asympt <- idsUCT_asympt[which(rbinom(length(idsUCT_asympt),
                                                1, 1/uct.dur.asympt) == 1)]

  recovRCT_tx <- idsRCT_tx[which(rbinom(length(idsRCT_tx),
                                        1, 1/ct.dur.tx) == 1)]
  recovUCT_tx <- idsUCT_tx[which(rbinom(length(idsUCT_tx),
                                        1, 1/ct.dur.tx) == 1)]

  if (!is.null(ct.dur.ntx)) {
    recovRCT_ntx <- idsRCT_ntx[which(rbinom(length(idsRCT_ntx),
                                           1, 1/ct.dur.ntx) == 1)]
    recovUCT_ntx <- idsUCT_ntx[which(rbinom(length(idsUCT_ntx),
                                           1, 1/ct.dur.ntx) == 1)]
  } else {
    recovRCT_ntx <- idsRCT_ntx[which(rbinom(length(idsRCT_ntx),
                                           1, 1/rct.dur.asympt) == 1)]
    recovUCT_ntx <- idsUCT_ntx[which(rbinom(length(idsUCT_ntx),
                                           1, 1/uct.dur.asympt) == 1)]
  }
```

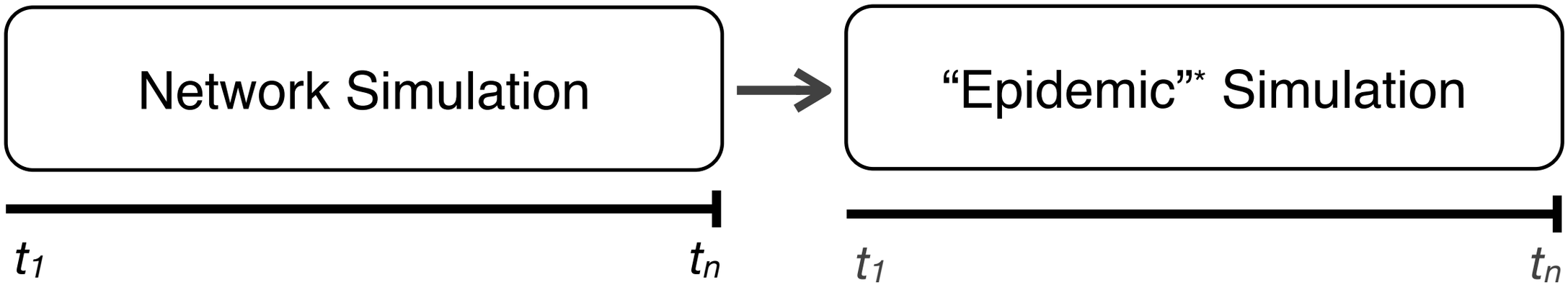
Model Extensions Require Some More Advanced Coding

Closed Population

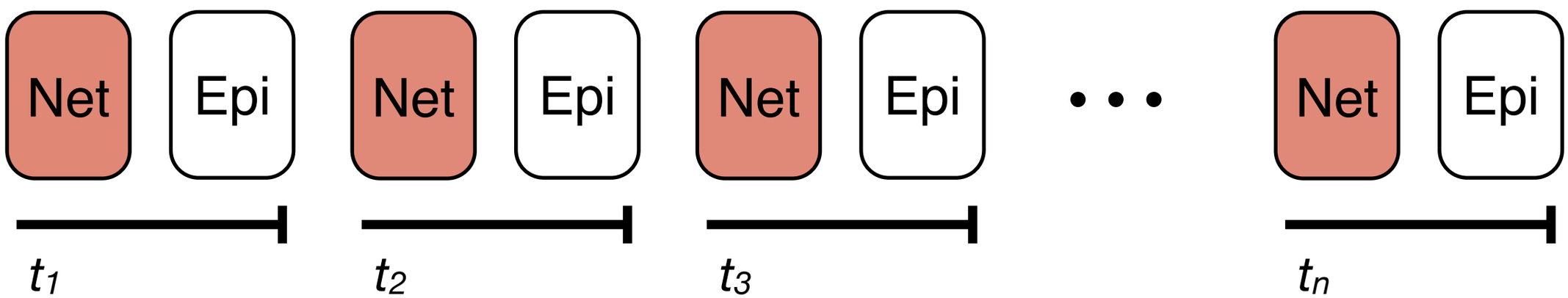


Model Feedback

Models without Feedback



Models with Feedback



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

EpiModel Workflow for Built-In 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 Built-In 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, …`