

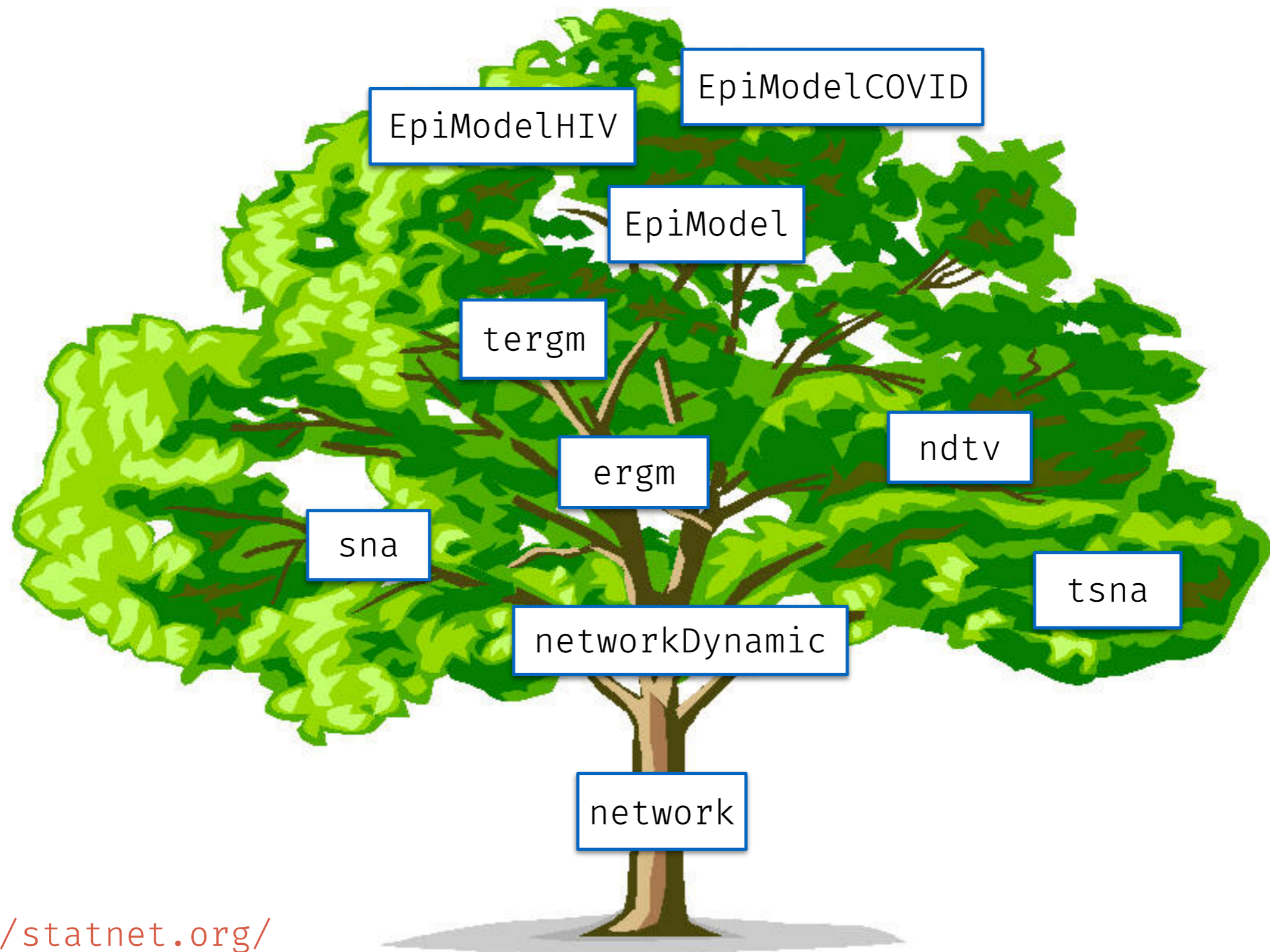
A complex network diagram with black and white nodes and edges, serving as a background for the top half of the slide. The nodes are represented by circles of varying sizes, and the edges are lines of varying thicknesses connecting them. The overall structure is dense and interconnected.

EpiModel Resources and Next Steps

Network Modeling for Epidemics @ SISMID 2024

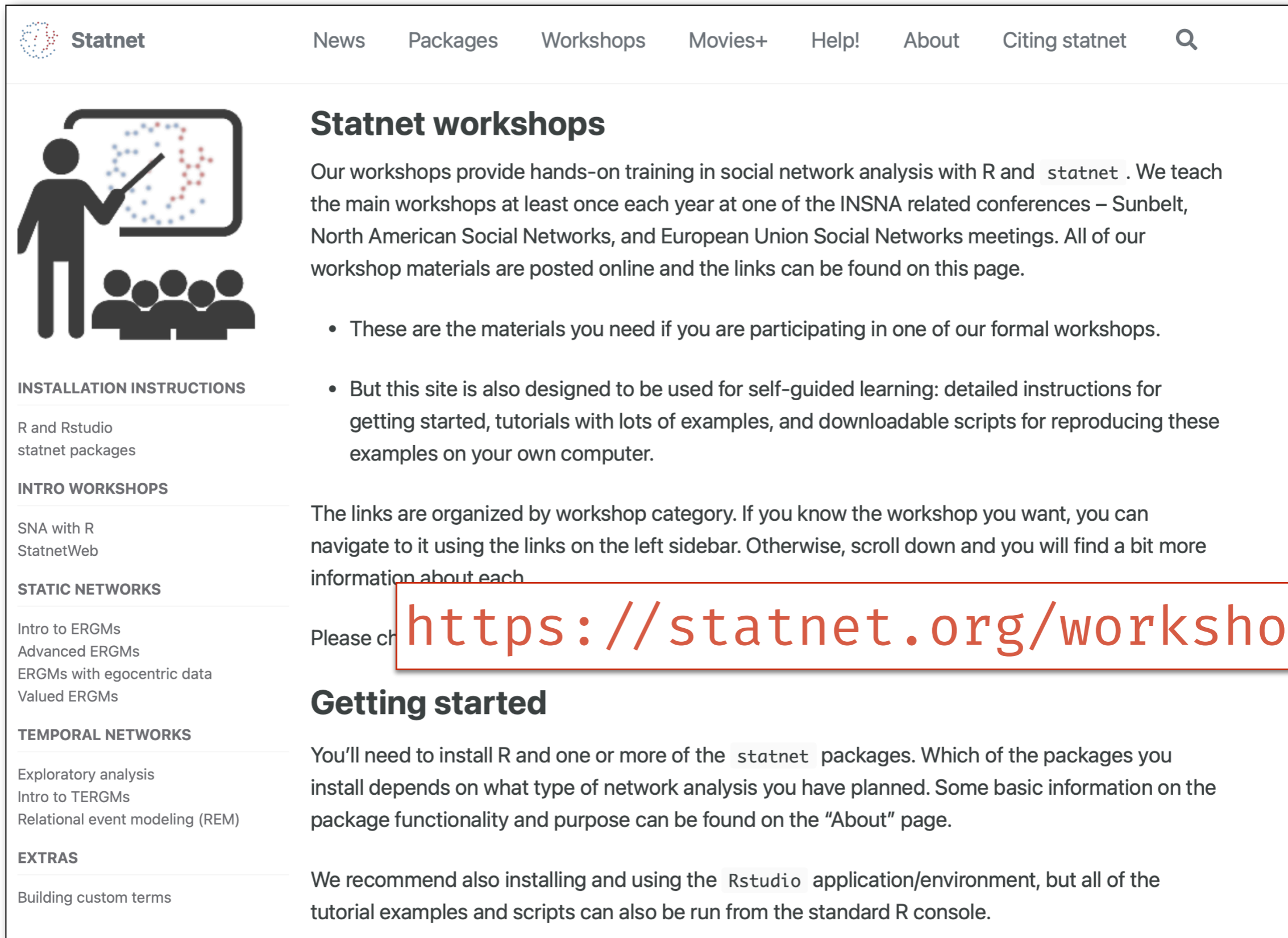
Module 10

The Statnet/EpiModel Family Tree



<http://statnet.org/>

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



The screenshot shows the Statnet website with a navigation bar at the top containing links for News, Packages, Workshops, Movies+, Help!, About, and Citing statnet, along with a search icon. A sidebar on the left lists various categories: INSTALLATION INSTRUCTIONS (R and Rstudio, statnet packages), INTRO WORKSHOPS (SNA with R, StatnetWeb), STATIC NETWORKS (Intro to ERGMs, Advanced ERGMs, ERGMs with egocentric data, Valued ERGMs), TEMPORAL NETWORKS (Exploratory analysis, Intro to TERGMs, Relational event modeling (REM)), and EXTRAS (Building custom terms). The main content area features an icon of a person presenting to an audience, followed by the heading "Statnet workshops". The text describes hands-on training in social network analysis with R and statnet, mentioning conferences like Sunbelt, North American Social Networks, and European Union Social Networks. A list of bullet points highlights that the materials are for formal workshops and self-guided learning. A large red box highlights the URL <https://statnet.org/workshops>. Below this, the "Getting started" section discusses installing R and statnet packages, and recommends using Rstudio.

Statnet workshops

Our workshops provide hands-on training in social network analysis with R and `statnet`. We teach the main workshops at least once each year at one of the INSNA related conferences – Sunbelt, North American Social Networks, and European Union Social Networks meetings. All of our workshop materials are posted online and the links can be found on this page.

- These are the materials you need if you are participating in one of our formal workshops.
- But this site is also designed to be used for self-guided learning: detailed instructions for getting started, tutorials with lots of examples, and downloadable scripts for reproducing these examples on your own computer.

The links are organized by workshop category. If you know the workshop you want, you can navigate to it using the links on the left sidebar. Otherwise, scroll down and you will find a bit more information about each

Please check

<https://statnet.org/workshops>

Getting started

You'll need to install R and one or more of the `statnet` packages. Which of the packages you install depends on what type of network analysis you have planned. Some basic information on the package functionality and purpose can be found on the "About" page.

We recommend also installing and using the `Rstudio` application/environment, but all of the tutorial examples and scripts can also be run from the standard R console.

Main EpiModel Website

EpiModel News [Package](#) [Learn](#) Help About ▾

EpiModel

Mathematical Modeling of Infectious Disease Dynamics

EpiModel is an R package that provides tools for simulating and analyzing mathematical models of infectious disease dynamics. Supported epidemic model classes include deterministic compartmental models, stochastic individual contact models, and stochastic network models. Disease types include SI, SIR, and SIS epidemics with and without demography, with utilities available for expansion to construct and simulate epidemic models of arbitrary complexity. The network model class is based on the statistical framework of temporal Exponential-family Random Graph Models (ERGMs) implemented in the [Statnet](#) suite of software for R.

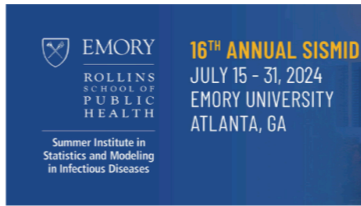
Current version of EpiModel available on CRAN is **Version 2.4.0**. For more information see [the latest release](#) and [package repository](#).

Recent news

Dec 15, 2023
The EpiModel Team

Network Modeling for Epidemics @ SIS MID 2024

Our Network Modeling for Epidemics (NME) summer course joins SIS MID starting 2024



Nov 17, 2023
The EpiModel Team

The new EpiModel website

Welcome to the new EpiModel website

<https://epimodel.org/>

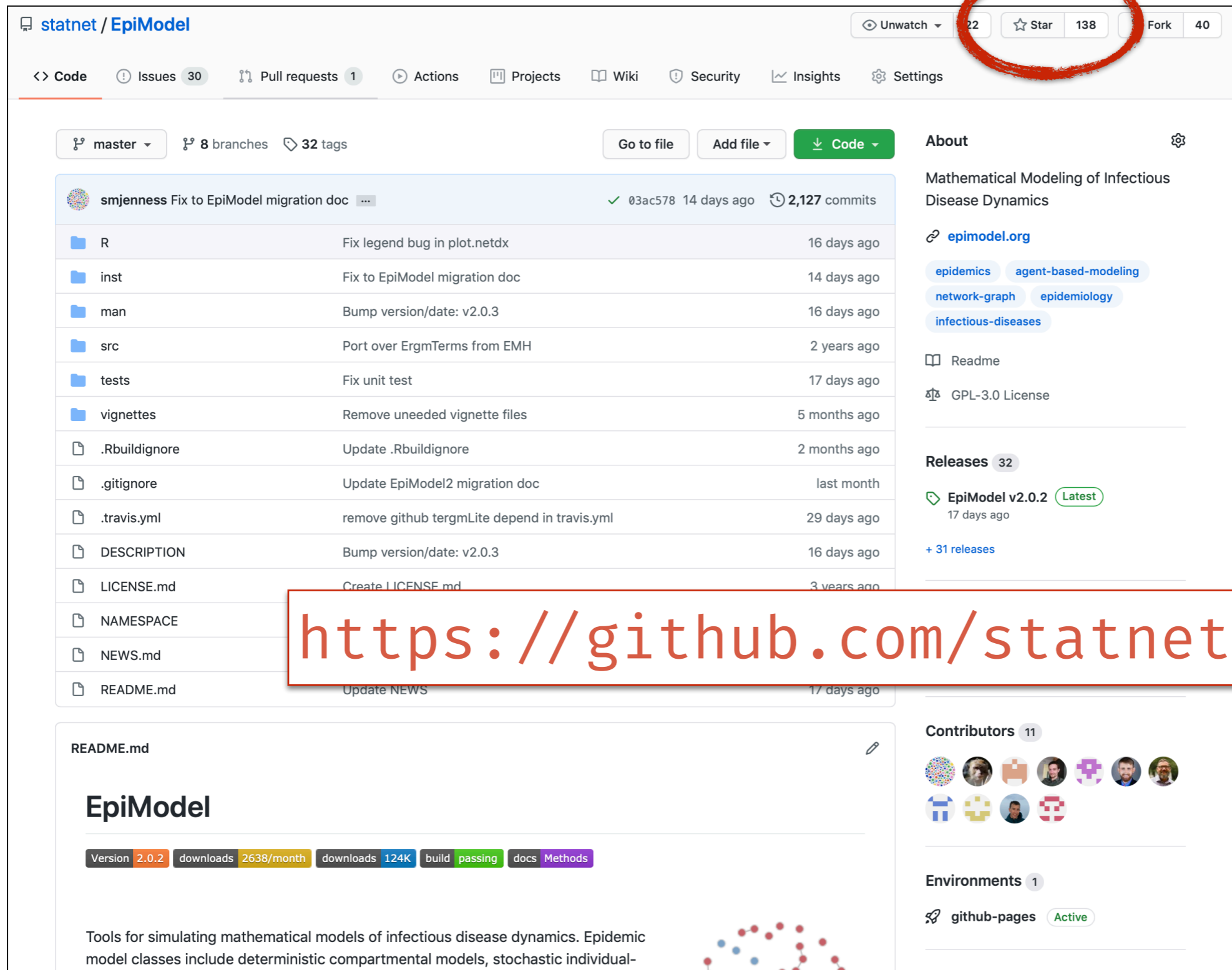
Jun 23, 2023
Samuel Jenness

EpiModel v2.4.0 Release

Version 2.4.0 of the core EpiModel package was published on CRAN

[More news...](#)

Github Repository



statnet / EpiModel

Unwatch 22 Star 138 Fork 40

Code Issues 30 Pull requests 1 Actions Projects Wiki Security Insights Settings

master 8 branches 32 tags

Go to file Add file Code

smjenness Fix to EpiModel migration doc 03ac578 14 days ago 2,127 commits

R	Fix legend bug in plot.netdx	16 days ago
inst	Fix to EpiModel migration doc	14 days ago
man	Bump version/date: v2.0.3	16 days ago
src	Port over ErgmTerms from EMH	2 years ago
tests	Fix unit test	17 days ago
vignettes	Remove unneeded vignette files	5 months ago
.Rbuildignore	Update .Rbuildignore	2 months ago
.gitignore	Update EpiModel2 migration doc	last month
.travis.yml	remove github tergmLite depend in travis.yml	29 days ago
DESCRIPTION	Bump version/date: v2.0.3	16 days ago
LICENSE.md	Create LICENSE.md	3 years ago
NAMESPACE		
NEWS.md		
README.md	Update NEWS	17 days ago

About

Mathematical Modeling of Infectious Disease Dynamics

epimodel.org

epidemics agent-based-modeling network-graph epidemiology infectious-diseases

Readme GPL-3.0 License

Releases 32

EpiModel v2.0.2 Latest 17 days ago + 31 releases

Contributors 11

Environments 1

github-pages Active

README.md

EpiModel

Version 2.0.2 downloads 2638/month downloads 124K build passing docs Methods

Tools for simulating mathematical models of infectious disease dynamics. Epidemic model classes include deterministic compartmental models, stochastic individual-

<https://github.com/statnet/EpiModel>

EpiModel Package Vignettes

EpiModel: Mathematical Modeling of Infectious Disease Dynamics

Tools for simulating mathematical models of infectious disease dynamics. Epidemic model classes include deterministic compartmental models, stochastic individual-contact models, and stochastic network models. Network models use the robust statistical methods of exponential-family random graph models (ERGMs) from the Statnet suite of software packages in R. Standard templates for epidemic modeling include SI, SIR, and SIS disease types. EpiModel features an API for extending these templates to address novel scientific research aims. Full methods for EpiModel are detailed in Jenness et al. (2018, <[doi:10.18637/jss.v084.i08](https://doi.org/10.18637/jss.v084.i08)>).

Version: 2.4.0
Depends: R (≥ 4.1), [deSolve](#) (≥ 1.21), [networkDynamic](#) (≥ 0.11.3), [tergm](#) (≥ 4.2.0), [statnet.common](#) (≥ 4.8.0)
Imports: graphics, grDevices, stats, utils, [doParallel](#), [ergm](#) (≥ 4.5.0), [ergm.ego](#) (≥ 1.1.0), [egor](#), [foreach](#), [network](#) (≥ 1.18.1), [RColorBrewer](#), [ape](#), [lazyeval](#), [ggplot2](#), [tibble](#), methods, [rlang](#), [dplyr](#), [coda](#), [networkLite](#) (≥ 1.0.5)
LinkingTo: [Rcpp](#), [ergm](#)
Suggests: [knitr](#), [ndtv](#), [rmarkdown](#), [shiny](#), [testthat](#), [tidyr](#)
Published: 2023-06-20
DOI: [10.32614/CRAN.package.EpiModel](https://doi.org/10.32614/CRAN.package.EpiModel)
Author: Samuel Jenness [cre, aut], Steven M. Goodreau [aut], Martina Morris [aut], Adrien Le Guillou [aut], Chad Klumb [aut], Skye Bender-deMoll [ctb]
Maintainer: Samuel Jenness <samuel.m.jenness@emory.edu>
BugReports: <https://github.com/EpiModel/EpiModel/issues>
License: [GPL-3](#)
URL: <http://www.epimodel.org/>
NeedsCompilation: yes
Citation: [EpiModel citation info](#)
Materials: [NEWS](#)
In views: [Epidemiology](#)
CRAN checks: [EpiModel results](#)

Documentation:

Reference manual: [EpiModel.pdf](#)
Vignettes: [EpiModel Introduction](#)
[Working with Custom Attributes and Summary Statistics](#)
[Working with Model Parameters](#)
[Working with Network Objects](#)

EpiModel Package Vignettes

Working with Model Parameters in EpiModel

EpiModel v2.4.0

2023-06-20

Introduction

In a model, *parameters* are the input variables used to define aspects of the system behavior. In the basic built-in SIS (Susceptible-Infected-Susceptible) model, these parameters could be the **act rate**, the **infection probability** and the **recovery rate**. In simple models, each of these parameters are single fixed values that do not change over the course of a simulation. In more complex models, we may want more flexibility in model parameterization.

Therefore, in this vignette, we demonstrate how to implement:

- Scenarios: sets of parameters to be changed for a simulation, either at the start or at a specific timestep.
- Random parameters: distributions of possible values rather than a single fixed value.
- Time-varying parameters and control settings: The scenarios functionality provides the most straightforward way to implement time-varying parameters, but more direct functionality is demonstrated here for advanced users seeking to implement time-varying parameters or control settings.

Scenarios

Scenarios can be defined as a single set of parameters to be used for a particular model run. For this example we will use a simple SIS model to demonstrate how scenarios work. First, we set up the model as we would normally.

```
set.seed(10)

nw <- network_initialize(n = 200)
est <- netest(nw,
  formation = ~edges, target.stats = 60,
  coef.diss = dissolution_coefs(~offset(edges), 10, 0),
  verbose = FALSE
)
#> Starting maximum pseudolikelihood estimation (MPLE):
#> Obtaining the responsible dyads.
#> Evaluating the predictor and response matrix.
#> Maximizing the pseudolikelihood.
#> Finished MPLE.

param <- param.net(inf.prob = 0.9, rec.rate = 0.01, act.rate = 2)
init <- init.net(i.num = 10)
control <- control.net(type = "SIS", nsims = 1, nsteps = 250, verbose = FALSE)
```

Scenario Definitions

To define the scenarios, we will make use of the `EpiModel::create_scenario_list` function. It takes a specially formatted `data.frame` as

Working with Network Objects in EpiModel

EpiModel v2.4.0

2023-06-20

Introduction

This vignette discusses mechanisms usable inside `EpiModel` network models with custom modules. More information about these in the “New Network Models with EpiModel” section of [the EpiModel tutorials](#).

Inside the simulation, the networks themselves are stored under `dat[["nw"]]`. Ultimately this vignette will describe multiple aspects of working with network objects.

Cumulative Edgelist

The cumulative edgelist refers to the historical list of edges in a network with the time step they start and stopped. Such a list allows to query current relationships (contacts, partnerships, etc.) as well as past ones.

Using the Cumulative Edgelist

The creation and update of the cumulative edgelist is done through the `EpiModel::update_cumulative_edgelist` function.

```
dat <- update_cumulative_edgelist(dat, network, truncate = Inf)
```

This function takes 3 arguments:

1. `dat`: the *Main List Object*.
2. `network`: the number of the network for which to create the cumulative edgelist (for multi-layer network simulations).
3. `truncate`: a number of time steps after which an inactive edge should be removed from the cumulative edgelist (this saves computer memory for large-scale simulations).

The function returns a modified version of `dat` that needs to be assigned back.

The following snippet will update the cumulative edgelist for all the networks used by a model and remove the edges that ended more than 100 steps ago.

```
for (n_network in seq_along(dat[["nw"]])) {
  dat <- update_cumulative_edgelist(dat, n_network, truncate = 100)
}
```

In a complete model, this code would need to be run at the end of the initialization module and at each time-step after the resimulation of the networks.

Accessing the Cumulative Edgelist

Cumulative edge-list refers to nodes with their Unique Ids. See `help("unique_id-tools", package = "EpiModel")` for more information.

For a Specific Network

Accessing the cumulative edge-list of a given network is done using the `EpiModel::get_cumulative_edgelist` function.

EpiModel Gallery

[EpiModel / EpiModel-Gallery](#) Unwatch 10 Star 34 Fork 14

<> Code Issues 8 Pull requests 1 Actions Projects Wiki Security Insights Settings

master 3 branches 1 tag Go to file Add file Code

smjenness Use renv 7439b2f 16 days ago 236 commits

2018-08-AddingAnExposedState	Removal of default functions/testing workflow.	last month
2018-08-ObservedNetworkData	Removal of default functions/testing workflow.	last month
2018-08-SlwithVitalDynamics	Removal of default functions/testing workflow.	last month
2018-08-TestAndTreatIntervention	Removal of default functions/testing workflow.	last month
2018-09-CompetingStrains	Removal of default functions/testing workflow.	last month
2018-09-SocialDiffusion	Removal of default functions/testing workflow.	last month
2018-10-SEIRwithAONVax	Removal of default functions/testing workflow.	last month
2018-11-Syphilis	Removal of default functions/testing workflow.	last month
2018-12-SEIRSwithLeakyVax	Removal of default functions/testing workflow.	last month
2019-03-HIV	Removal of default functions/testing workflow.	last month

DESCRIPTION Add DESCRIPTION file for Travis build 2 years ago

LICENSE Initial commit 2 years ago

README.md Update README.md 9 months ago

renv.lock Use renv 16 days ago

test.sh Count directories in test.sh 2 years ago

README.md

EpiModel-Gallery

About
Gallery of Network-Based Epidemic Model Templates for EpiModel
[epimodel.org](#)
Readme
MIT License

Releases 1
Gallery for EpiModel v1.x Latest on Jul 10

Packages
No packages published
[Publish your first package](#)

Languages
R 99.6% Shell 0.4%

<https://github.com/EpiModel/EpiModel-Gallery>

EpiModel Gallery

The screenshot shows a GitHub repository page for 'EpiModel / EpiModel-Gallery'. The repository is on the 'main' branch. The commit history table shows the following entries:

Name	Last commit message	Last commit date
..		
README.md	Updates to CompetingStrains example	3 years ago
model.R	Update extraction syntax	2 years ago
module-fx.R	Delinting entire gallery	2 years ago

The README.md file content is as follows:

Modeling Two Competing Strains in an SIS Epidemic

Description

In this example we build an SIS model that considers two strains of a pathogen that differ in their infectiousness and their recovery rates. New arguments include the infection probability for the second strain, the recovery rate for the second strain, and the proportion of the initial infections that entail the second strain. No entirely new modules are needed, but two of the built-in modules (`infection` and `recovery`) are edited:

Modules

The **strain initialization module** (function = `init_strain`) runs as the first module on time step 2 to set up the new strain attribute on the data object.

The **infection module** (function = `infection_2strains`) includes the following changes from the base EpiModel infection module (`infection.net`):

- Existing functionality to pass different transmission probabilities by direction across two modes is turned off, and warnings added if users invoke this functionality

EpiModel Gallery

The screenshot shows a GitHub repository page for 'EpiModel / EpiModel-Gallery'. The repository has 8 issues and various navigation options like Code, Pull requests, Discussions, etc. The 'Files' sidebar on the left shows a directory structure with folders for different dates and files like README.md, model.R, .Rbuildignore, .gitignore, .lintr, DESCRIPTION, LICENSE, and test.sh. The main content area shows the '2022-12-Multinets' directory, which contains a commit by 'smjennness' titled 'Update model.R'. Below the commit is a table of files:

Name	Last commit message	Last commit date
..		
README.md	update README for multinets example	2 years ago
model.R	Update model.R	last year

The README.md file content is displayed below, titled 'Epidemics with Multiple Networks'. It includes sections for 'Description', 'Modules', and 'Parameters'.

Epidemics with Multiple Networks

Description

This example shows how to use core EpiModel functionality to include multiple, interacting networks in a single epidemic model. The node set is required to be the same for all networks. The edge formation and dissolution models may vary from one network to the next, and the formation model for one network may depend on the edge states in the other networks, represented via edge-dependent nodal attributes. We give an example with two networks, including cross-network dependency. The two network models are fit successively and then passed jointly to `netsim`.

Modules

We use built-in modules only, to illustrate their capabilities.

Parameters

The cross-network dependency requires that we maintain the edge-dependent nodal attributes during the `netsim` run via an appropriately specified `dat.updates` argument to `control.net`.

Additionally, certain arguments to `control.net` may vary from one network to the next via the `multilayer` specification, and we illustrate this functionality here for the `nwstats.formula` argument.

- NME @ SISMID 2024 Resources:
 - We will keep Slack workspace open as long as SISMID organizers let us
 - Message us or your classmates there with any questions or comments
 - Feel free to email or Github issue us
 - NME SISMID website available indefinitely
 - Updated at least yearly
 - We plan to add additional materials from a larger course book (epimodel.git.io/epimodel-training)

EpiModelCOVID

EpiModelCOVID Public

Edit Pins Unwatch 3 Fork 3 Star 9

main 8 Branches 3 Tags

Go to file Add file Code

smjenness Merge pull request #35 from chad-klumb/init_nets 12e1bc7 · last year 179 Commits

.github	Update R-CMD-check.yaml	last year
R	Remove line overriding dat object class	last year
man	netsim_dat class documentation updates	last year
tests	update EpiModelCOVID for recent/pending EpiModel cha...	last year
.Rbuildignore	Update .Rbuildignore	2 years ago
.gitignore	Update .gitignore	3 years ago
.lintr	Add .lintr file	2 years ago
DESCRIPTION	Update dependencies	last year
NAMESPACE	update EpiModelCOVID for recent/pending EpiModel cha...	last year
README.md	Update README.md	3 years ago

About
Network-Based Epidemic Modeling of Transmission Dynamics for SARS-CoV-2

Readme Activity Custom properties 9 stars 3 watching 3 forks Report repository

Releases
3 tags Create a new release

Packages
No packages published

EpiModelCOVID

R-CMD-check passing

Modules for simulating SARS-CoV-2 transmission dynamics in different epidemiological settings, developed as an extension to our general network-based epidemic modeling platform, [EpiModel](#).

EpiModel and EpiModelCOVID use the statistical framework of temporal exponential-family random graph models to fit and simulate models of dynamic contact networks. These [statistical methods](#) have been developed and implemented as open-source software, building on the extensive efforts of the [Statnet](#) research group to build software tools for the representation, analysis, and visualization of complex network data.

These packages combine these Statnet methods with an individual-based epidemic modeling engine to simulate

Languages
R 100.0%

<https://github.com/EpiModel/EpiModelCOVID>

EpiModelHIV Public

Edit Pins Unwatch 11 Fork 13 Star 24

CombPrev 18 Branches 13 Tags

Go to file Add file Code

smjenness Final CombPrev version for AIDS paper 26ea27a · 4 years ago 480 Commits

R	Final CombPrev version for AIDS paper	4 years ago
inst	Add CombPrev branch of EpiModelHIV	4 years ago
man	Add CombPrev branch of EpiModelHIV	4 years ago
tests	Add CombPrev branch of EpiModelHIV	4 years ago
.Rbuildignore	Remove LICENSE.md from build	7 years ago
.gitignore	Update gitignore	7 years ago
.travis.yml	Add Travis integration to slack	7 years ago
DESCRIPTION	Add CombPrev branch of EpiModelHIV	4 years ago
LICENSE.md	Create LICENSE.md	7 years ago
NAMESPACE	Add CombPrev branch of EpiModelHIV	4 years ago

https://github.com/EpiModel/EpiModelHIV

EpiModelHIV

build unknown

Modules for simulating HIV/STI transmission dynamics among men who have sex with men and heterosexual populations, developed as an extension to our general network-based epidemic modeling platform, [EpiModel](#).

`EpiModel` and `EpiModelHIV` use the statistical framework of temporal exponential-family random graph models to fit and simulate models of dynamic networks. These [statistical methods](#) have been developed and implemented as open-source software, building on the extensive efforts of the [Statnet](#) research group to build software tools for the representation, analysis, and visualization of complex network data.

+ 10 releases

Packages

No packages published
[Publish your first package](#)

Contributors 5

Languages

ARTnet Dataset for HIV Modeling of US MSM

The screenshot displays the GitHub repository for ARTnet. At the top, the repository name 'ARTnet' is shown as public, with 10 stars, 5 forks, and 7 watchers. The main content area shows a file tree with folders like 'R', 'inst', 'man', and 'tests', and files like '.Rbuildignore', '.gitignore', and 'ARTnet.Rproj'. A merge pull request by AdrienLeGuillou is visible. The right sidebar contains 'About' information, 'Releases' (including the latest version v2.6.0), and 'Contributors' (8 people). The bottom section shows the 'README' file content.

ARTnet: Model Parameterization with the ARTnet Study Data

ARTnet is an anonymous cross-sectional web-based survey conducted from 2017 to 2019 of HIV-related risk behaviors, testing, and use of prevention services among men who have sex with men (MSM) in the United States. It recruited MSM who have completed the American Men's Internet Survey (AMIS) study, and therefore, the dataset contains variables merged from that study as well. Full access to the dataset from ARTnet will allow the researchers to conduct analyses and disseminate results using the data.

For further details on the ARTnet Study, you can read the descriptive paper ["Egocentric Sexual Networks of Men"](#)

<https://github.com/EpiModel/ARTnet>

EpiModelHPC

EpiModelHPC Public

Edit Pins Unwatch 11 Fork 2 Star 6

main 4 Branches 5 Tags

Go to file Add file Code

AdrienLeGuillou fix typos ✓ 6cab1b9 · 8 months ago 419 Commits

.github	add basic pkgdown config	9 months ago
R	fix typos	8 months ago
inst	delint	2 years ago
man	add get_scenarios_tibble_infos helper	8 months ago
tests	Merge branch 'main' into autocalib	last year
vignettes	fix typo in vignette	last year
.Rbuildignore	Add lintr	2 years ago
.gitignore	Move gitignore	2 years ago
.lintr	Add lintr	2 years ago
DESCRIPTION	add get_scenarios_tibble_infos helper	8 months ago
NAME		
README		
_pkgdown.yml	add basic pkgdown config	9 months ago

About

High-Performance Computing Extensions for EpiModel

epimodel.github.io/EpiModelHPC/

Readme Activity Custom properties 6 stars 11 watching 2 forks Report repository

Releases 5

EpiModelHPC v2.1.0 Latest on Jan 7, 2020 + 4 releases

Contributors 3

- AdrienLeGuillou Adrien Le Guillou
- smjenness Samuel Jenness
- andsv2 Shawnee M Anderson

Deployments 4

github-pages 8 months ago

README

EpiModelHPC

R-CMD-check passing

EpiModelHPC is an R package that provides extensions for simulating stochastic network models in EpiModel on high-performance computing (HPC) systems. Functionality provided to simulate models in parallel, with checkpointing functions to save and restore simulation work.

<https://github.com/EpiModel/EpiModelHPC>

Suggested Approach to Self-Learning

- Review the Journal of Statistical Software paper on EpiModel
- Review these SISMID course materials in more depth
 - Work through tutorials and lab examples we didn't do in class
- Consult the EpiModel Gallery for examples of EpiModel disease extensions for research
- Build a basic model of your disease with a simple network parameterization
 - Incrementally add complexity to both network and disease components
- Source and implement real-world network data into your model
- Consider full-scale implementation of research-level model
 - Get inspiration from extension packages like EpiModelHIV and CRAN package vignettes
- Ask for help!

We are here to help!

- A central mission of the EpiModel/Statnet platforms is to assist our users
 - Ask for help in a semi-public forum so others can learn from your questions
- We request that you cite EpiModel if you use it
 - Jenness SM, Goodreau SM and Morris M. EpiModel: An R Package for Mathematical Modeling of Infectious Disease over Networks. *Journal of Statistical Software*. 2018; 84(8): 1-47.
 - Send us an email to let us know, so we can add it to our bibliography
- Consider using an open-source, open-development model yourself

Thank you!

Remaining time is available for questions, project consultations, small group discussions...