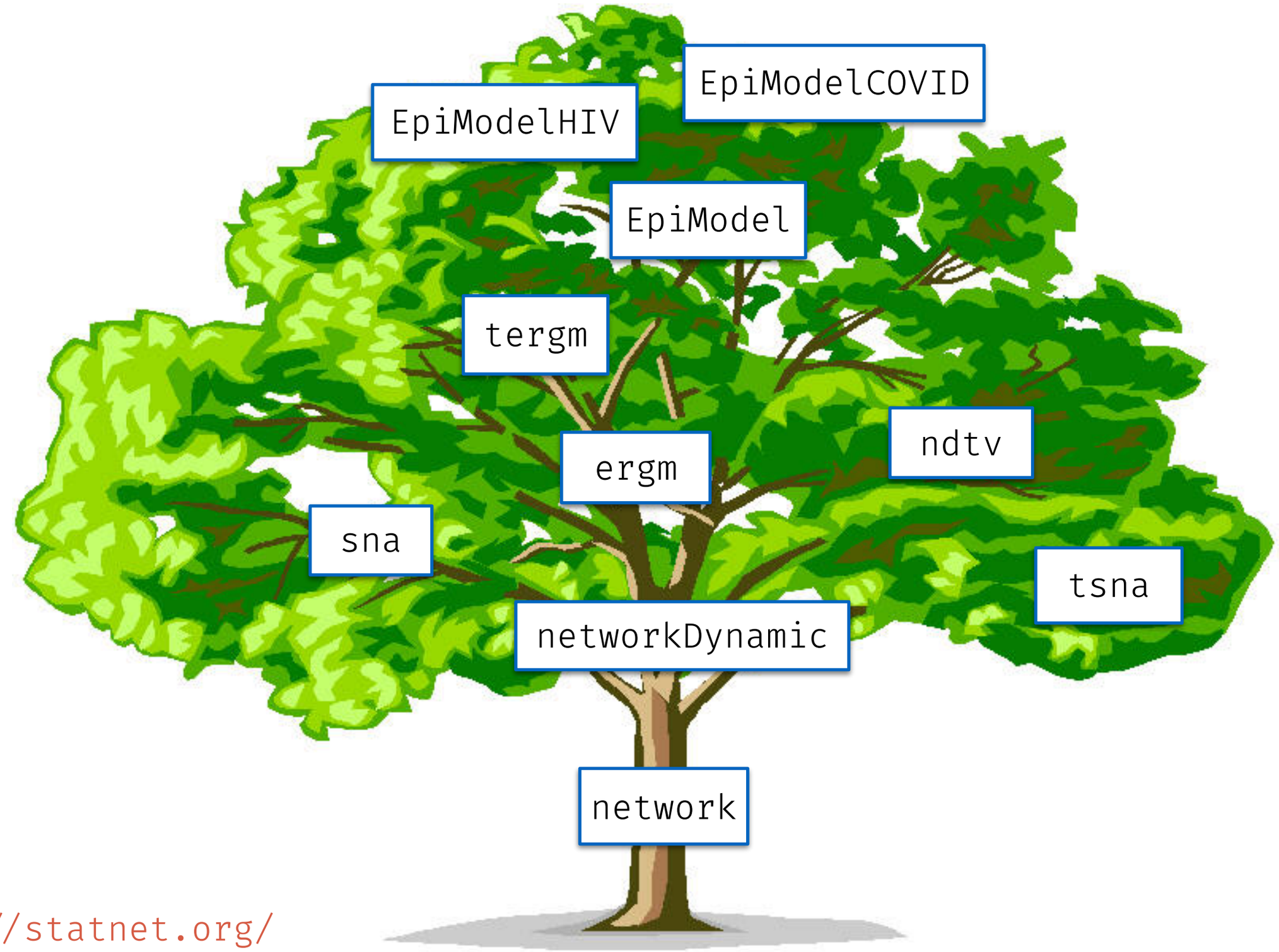
EpiModel Resources and Next Steps

Network Modeling for Epidemics 2025

The Statnet/EpiModel Family Tree



http://statnet.org/

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

Statnet Tutorials

Statnet News Packages Workshops Movies+ Help! About Citing statnet

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)

EXTRAS

Building custom terms

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 ch

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.

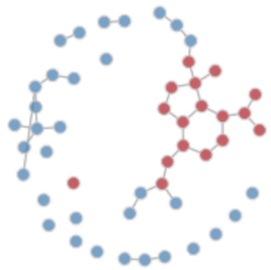
We recommend also installing and using the `Rstudio` application/environment, but all of the tutorial examples and scripts can also be run from the standard R console.

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 @ SISMID 2024

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

Nov 17, 2023
The EpiModel Team

The new EpiModel w

Welcome to the new EpiModel

https://epimodel.org/

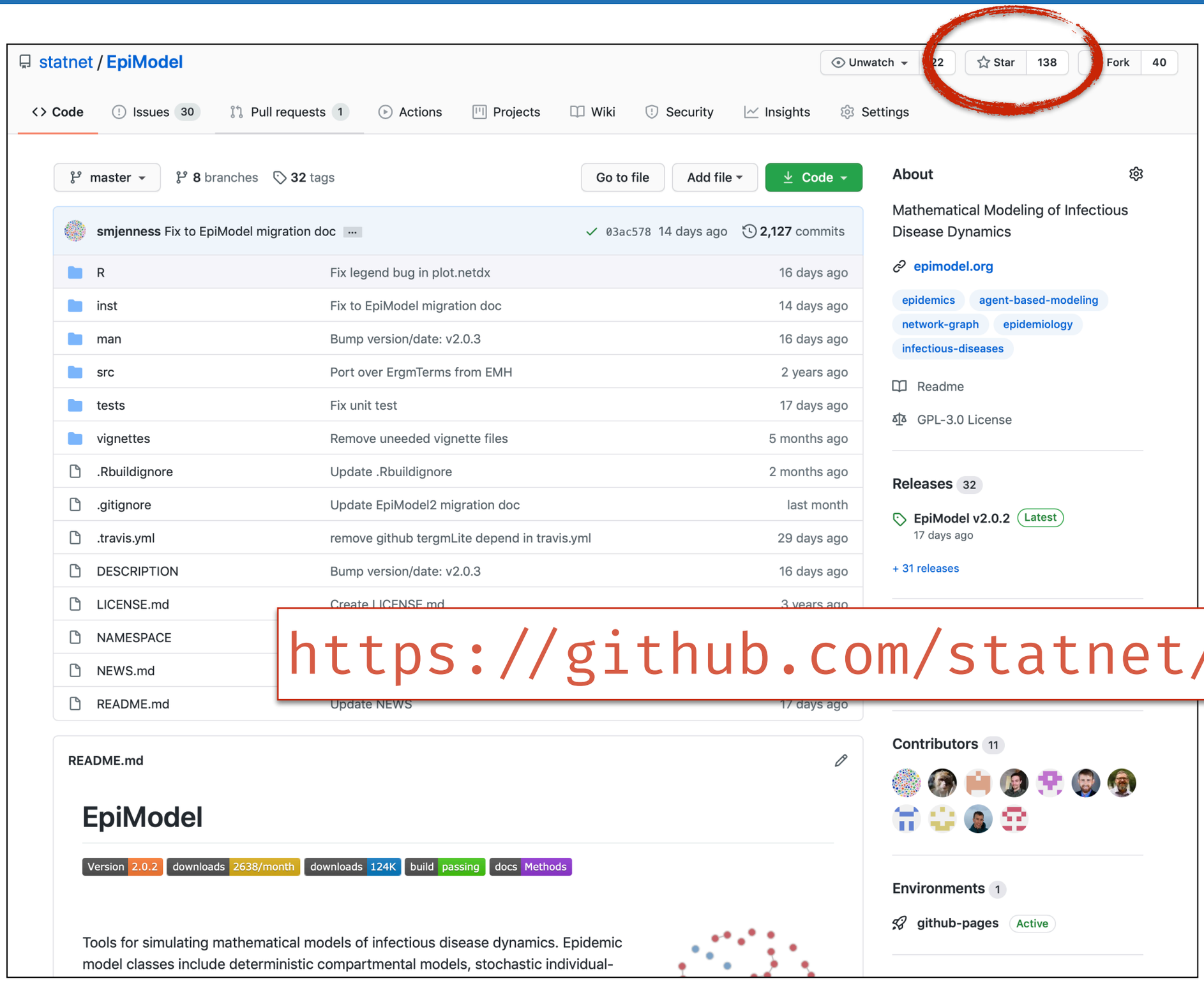
Jun 23, 2023
Samuel Jenness

EpiModel v2.4.0 Release

Version 2.4.0 of the core EpiModel package was published on CRAN

More news…

Github Repository



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>).

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
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 at 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**

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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-SIwithVitalDynamics	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
.Rbuildignore	Use renv	16 days ago
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

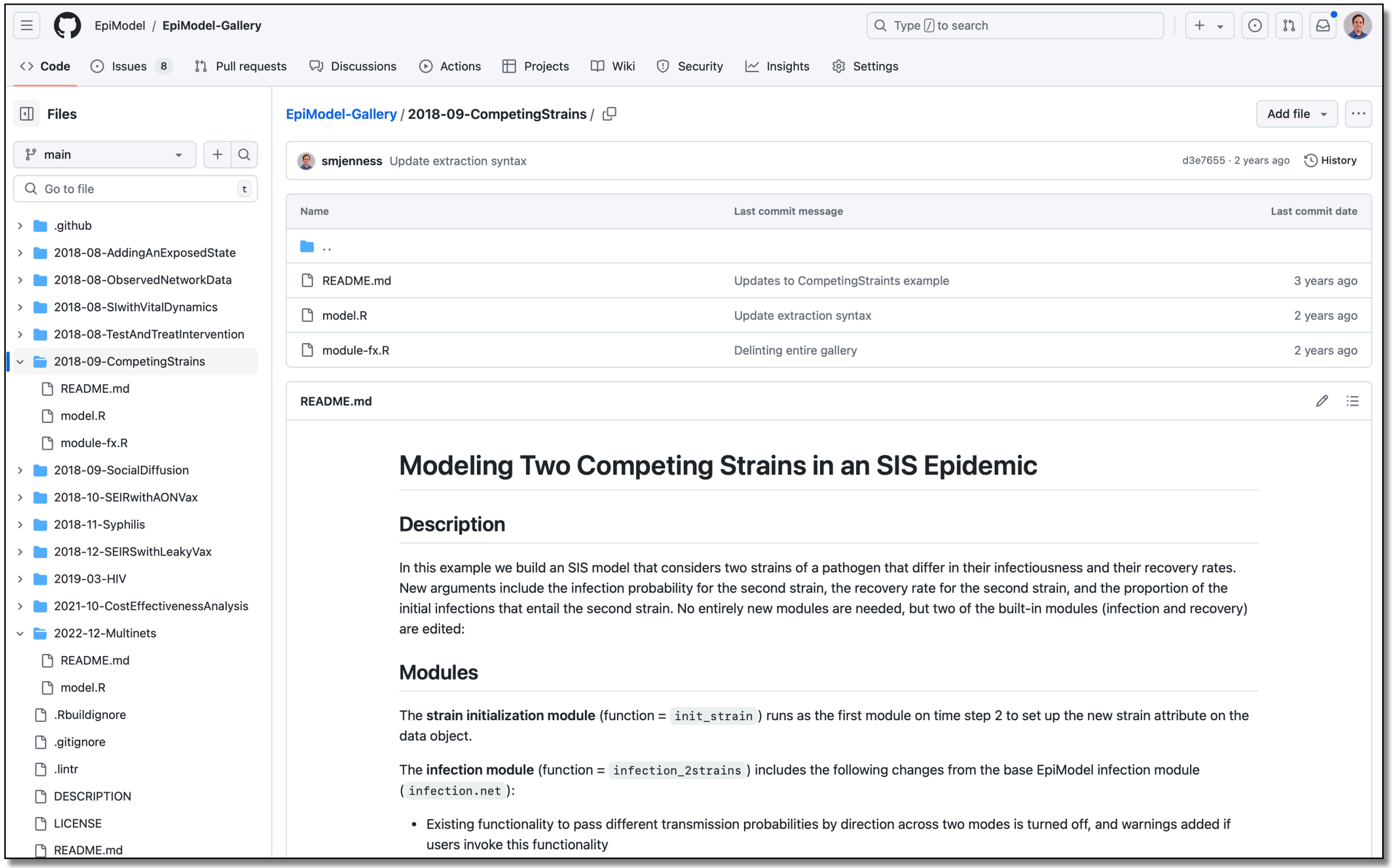
No packages published
Publish your first package

Languages

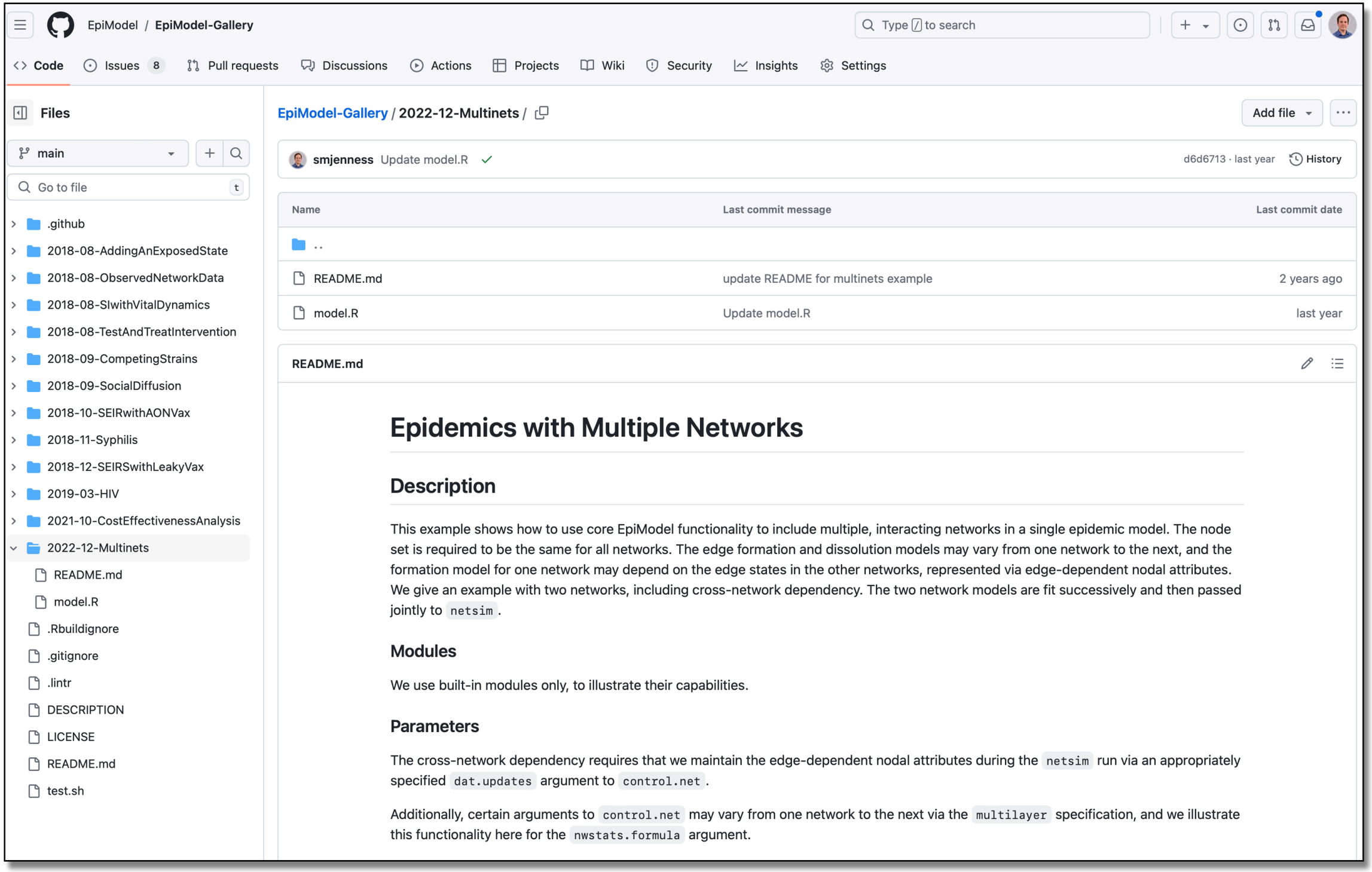
R 99.6% | Shell 0.4%

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

EpiModel Gallery



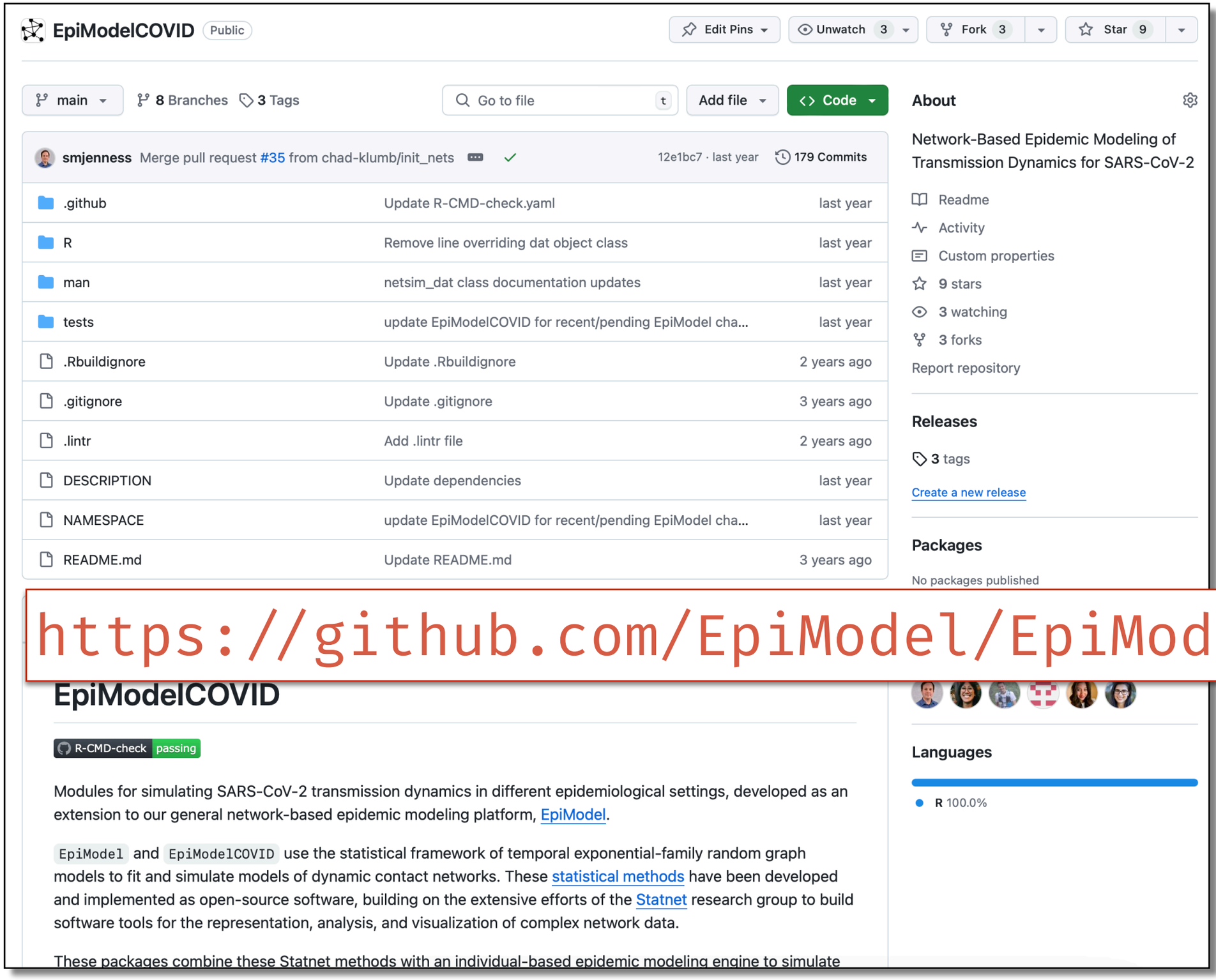
EpiModel Gallery



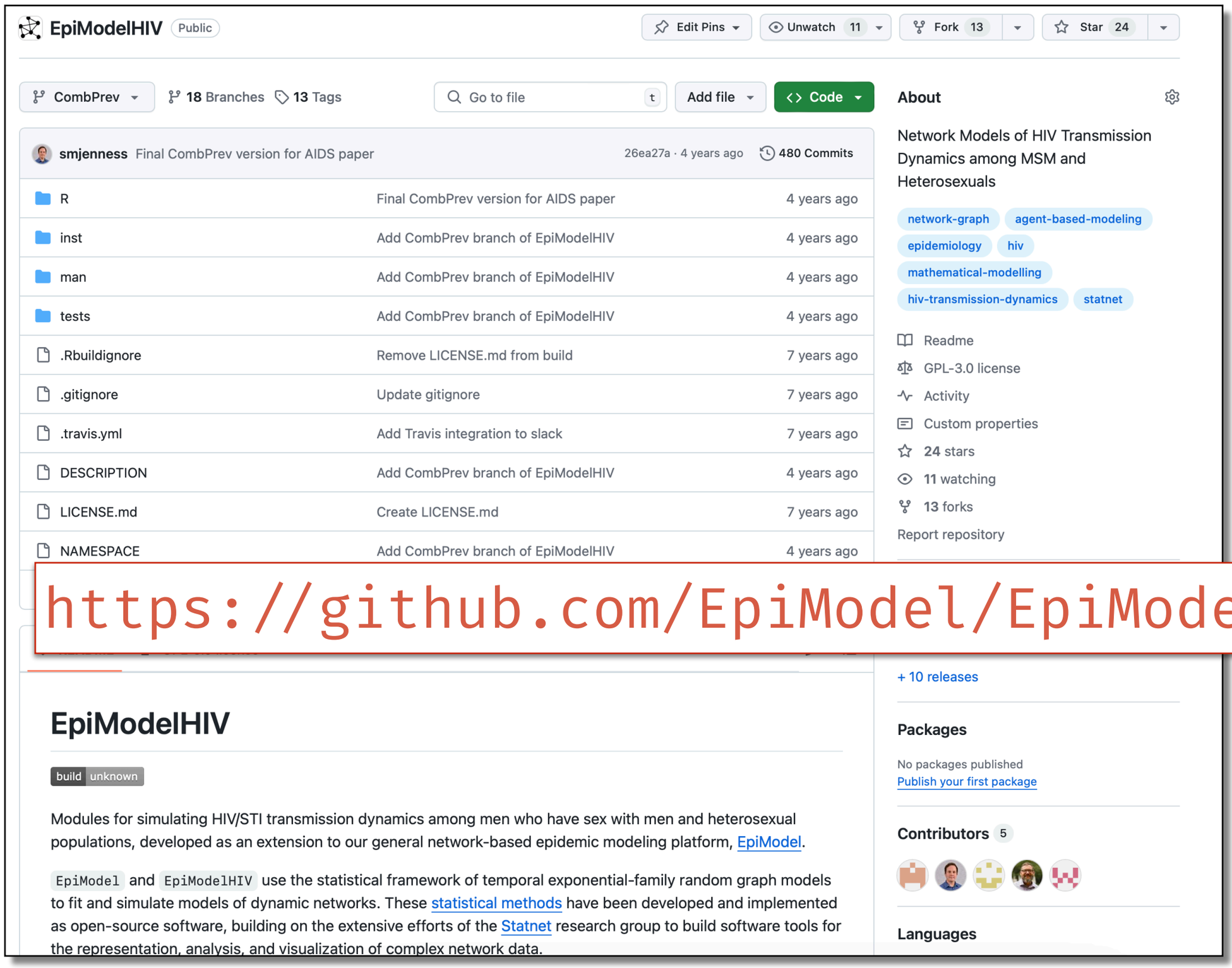
NME @ SISMID

- NME @ SISMID 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

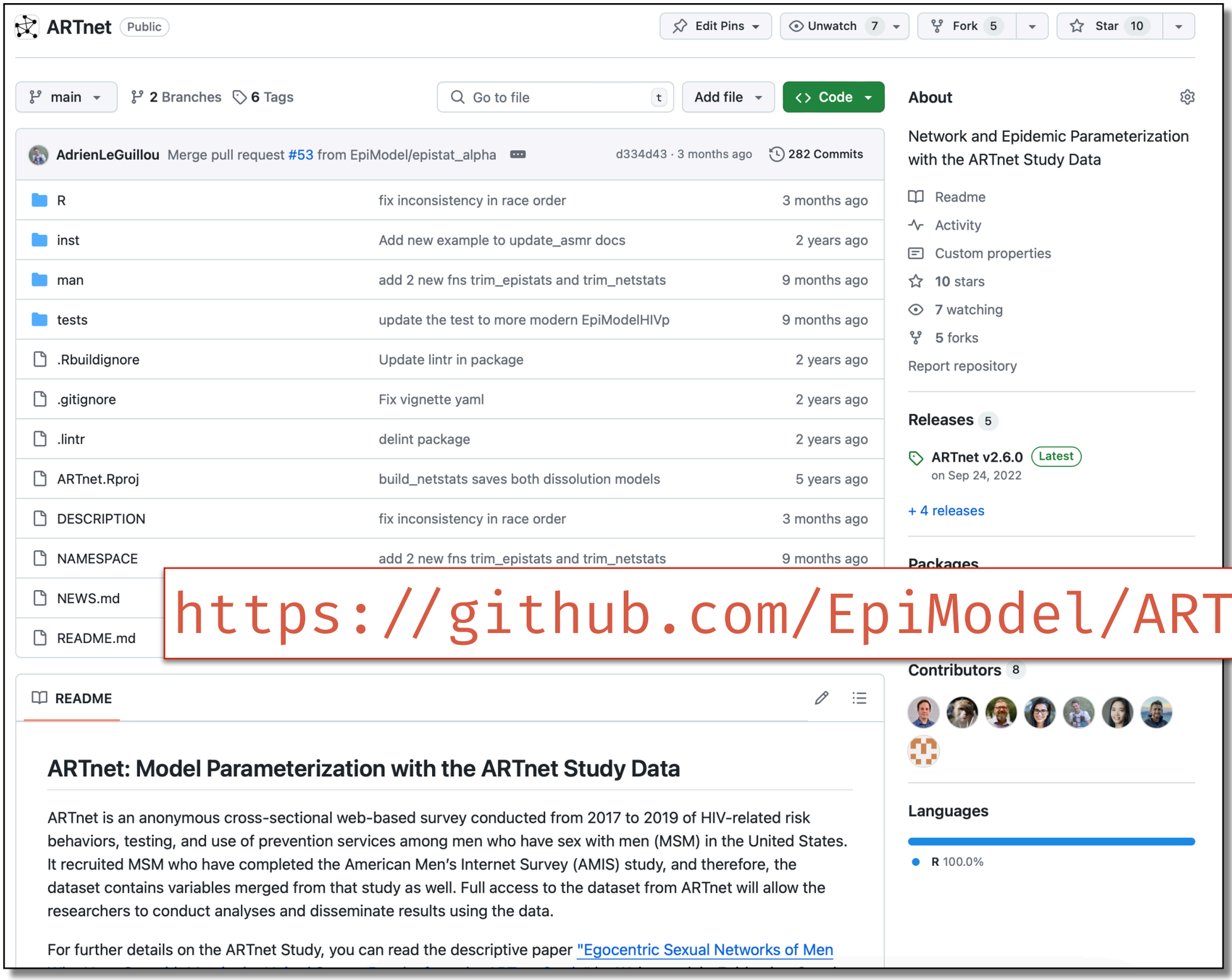


EpiModelHIV



https://github.com/EpiModel/EpiModelHIV

ARTnet Dataset for HIV Modeling of US MSM



EpiModelHPC

EpiModelHPC Public

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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		
READM		
_pkgdown.yml	add basic pkgdown config	9 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

About

High-Performance Computing Extensions for EpiModel

epimodel.github.io/EpiModelHPC/

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Releases 5

EpiModelHPC v2.1.0 Latest
on Jan 7, 2020

+ 4 releases

https://github.com/EpiModel/EpiModelHPC

Publish your first package

Contributors 3

AdrienLeGuillou Adrien Le Guillou
smjenness Samuel Jenness
andsv2 Shawnee M Anderson

Deployments 4

github-pages 8 months ago

Suggested Approach to Self-Learning

- Take NME-II, or…
- Review the Journal of Statistical Software paper on EpiModel
- Review these SISMID course materials in more depth
  - Work though 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 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…