



SIRE 2.0

Susceptibility, Infectivity and Recoverability Estimation

NOTE: This manual is currently under development and not all SIRE 2.0 features have been added yet.

Christopher M. Pooley^{1,2*}, Stephen C. Bishop[†], Andrea B. Doeschl-Wilson^{1&}, and Glenn Marion^{2&}

¹ The Roslin Institute, The University of Edinburgh, Midlothian, EH25 9RG, UK.

² Biomathematics and Statistics Scotland, James Clerk Maxwell Building, The King's Buildings, Peter Guthrie Tait Road, Edinburgh, EH9 3FD, UK

[†] Deceased

[&] These authors contributed equally to this work.

Table of Contents

1 Introduction	3
1.1 Downloading	3
1.2 Getting started	4
1.3 Loading and Saving	9
2 The Interface	Error! Bookmark not defined.

1 Introduction

Three key epidemiological host traits affect infectious disease spread: susceptibility (propensity to acquire infection), infectivity (propensity to transmit infection to others, once infected) and recoverability (propensity to recover quickly). SIRE is a desktop application for estimating factors affecting these traits from individual-based data.


SIRE takes as input any combination of information about infection times, recovery times, disease status measurements, disease diagnostic test results, genotypes of SNPs or any other fixed effects, details of which individuals belong to which contact groups and any prior specifications. The output from SIRE consists of posterior trace plots for model parameters θ , distributions, visualisation of infection and recovery times ξ , dynamic population estimates and summary statistics (means and 95% credible intervals) as well as MCMC diagnostic statistics.

1.1 Downloading

SIRE is freely available to download from www.mkodb.roslin.ed.ac.uk/EAT/SIRE.html.

Depending on your platform, the following instructions should be followed:

- **Windows** – The file SIRE_v1.0_windows.zip is first downloaded and unzipped. SIRE is then simply run by clicking on the SIRE.exe icon.
- **Linux** – The file SIRE_v1.0_linux.tar.gz is first downloaded. This can be extracted by using the terminal command “**tar -zxvf SIRE_v1.0_linux.tar.gz**”. **The code can then simply be executed using ./SIRE.**
- **Macintosh** – The file SIRE_v1.0_Mac.zip is first downloaded and unzipped. SIRE is then simply run by clicking on the SIRE.app icon.




[Home](#)
[Description](#)
[Model](#)
[Data](#)
[Prior](#)
[Inference](#)

About

SIRE stands for 'Susceptibility Infectivity and Recoverability Estimation'.
The aim of this software is to facilitate estimation of these epidemiological traits from individual-based data.
To start, create a new model, load an existing SIRE file or try one of the examples below.

Examples



EX 1: Known infection and recovery times (DS1)

EX 2: Staggered contact group timings (DS1)

EX 3: Known recovery times (DS2)

EX 4: Disease transmission experiment (DS2)

EX 5: Known infection times (DS3)

EX 6: Periodic disease status checks (DS4)

EX 7: Disease diagnostic test results (DS4)

EX 8: Disease diagnostic test results II (DS4)

EX 9: Time censoring end of epidemics (DS5)

EX 10: Time censoring beginning of epidemics (DS5)

EX 11: Known infection and recovery times (DS1)

EX 12: Staggered contact group timings (DS1)

EX 13: Known recovery times (DS2)

Load

New Model

© SIRE 2019

Figure 1 – *The home screen.*

2 The interface

2.1 Getting started

Figure 1 shows the first screen you see when SIRE is loaded. From this three options can be pursued: a new analysis can be started (A), a previous analysis can be loaded (B) or one of the illustrative examples can be investigated at (C). New users are encouraged to try the latter option and spend some minutes exploring the software to get a feel for how it works. The examples (C) are described in detail in section 3 below.

This manual follows the order of the menu items on the main menu (D), which is the order in which analysis would be made

SIRE

[Load](#) [Save](#)

Description

A

- This example assumes that the infection and recovery times for all individuals are known (DS 1).
- Data was generated using a modified Doob-Gillespie algorithm for $N_{\text{group}}=50$ contact groups each containing $G_{\text{size}}=20$ individuals.
- Epidemics were initiated with a single infected individual at time $t=0$ and simulated until $t=60$ (example dataset 1).
- The following parameters were used: $\beta=0.015$, $\gamma=0.1$, $k=5$, $a_g=0.4$, $a_f=0.3$, $a_r=-0.4$, $\Delta_g=0.4$, $\Delta_f=0.1$, $\Delta_r=-0.3$, $b_{g0}=0.2$, $b_{f0}=0.3$, $b_{r0}=-0.2$ with A allele frequency $p=0.3$.
- The model does not contain group effects or residual variation in traits.

B

[Edit](#) [Next >>](#)

© SIRE 2019

Figure 2 – Data and analysis *description*.

2.2 Analysis description

As shown in Fig. 2, SIRE allows users to provide a brief description of the data and analysis (A). This is not only useful to keep track for personal use, but also makes it easier for other to understand what has been done.

The description can simply be edited by clicking on (B). Note, bullet points are automatically generated for each carriage return.

SIRE

> Home

> Description

> **Model**

> Data

> Prior

> Inference

Model

Load Save

Select model type

☒ S → I → R ☐ S → I (A)

Include residual individual-based variation in traits?

☐ Yes ☒ No (B)

Include random group effect?

☐ Yes ☒ No (C)

Next >>

© SIRE 2019

Figure 3 – Selecting model options.

2.3 The model

Here we specify the model used for analysis, which is dependent on the nature of the disease, the conditions under which individuals are kept and prior assumptions regarding individual based variation in traits.

For the SIR model individuals are classified as being either susceptible to infection (S), infected and infectious (I), or recovered/removed/dead (R). The time-dependent force of infection for a susceptible individual j (*i.e.* the probability per unit time of becoming infected) is given by $\lambda_j(t)$. For those individuals which do become infected, the distribution in the duration of the disease is assumed to be gamma distributed with individual-based mean w_m and shape parameter k .

In some circumstances individuals do not recover from disease (*e.g.* bovine tuberculosis), so the recovery dynamics become redundant. This possibility can be selected by choosing the SI model in Fig. 3(A).


In most standard analyses individual-based variation is ignored. However in reality it may play an important role in determining disease dynamic behaviour. For this reason SIRE allows either option to be selected

Data Sources

[> Home](#)[> Description](#)[> Model](#)

v Data

[> Sources](#)[> Individuals](#)[> Prior](#)[> Inference](#)

Type	From	To		
 Contact Group	---	---	Data	×
SNP	---	---	Data	×
Fixed Effect	---	---	Data	×
Infection Times	0	36.5098	Data	×
Recovery Times	3.41891	53.197	Data	×



+ Contact Group
+ Disease Status

+ SNP
+ Diag. Test

+ Fixed Effect
+ Infection Times

+ Recovery Times

[Next >>](#)

Load

Save

Add contact group data

Please edit entries if needed and press 'Done' when complete.

ID	Contact group	SNP				Type
ind0	Gr 1	AB				Seed
ind1	Gr 1	AA				Conta
ind2	Gr 1	AA				Conta
ind3	Gr 1	AB				Conta
ind4	Gr 1	AB				Conta
ind5	Gr 1	AA				Conta
ind6	Gr 1	AA				Conta
ind7	Gr 1	AB	26.4476	32.8291	1	Conta
ind8	Gr 1	AA	17.6246	37.3628	1	Conta
ind9	Gr 1	AB	26.1643	30.9336	1	Conta
ind10	Gr 1	AB	36.5098	42.7773	1	Conta
ind11	Gr 1	AB	18.5259	25.1732	0	Conta
ind12	Gr 1	BB	23.4827	38.6574	1	Conta
ind13	Gr 1	AA	18.2189	24.1706	0	Conta
ind14	Gr 1	AB	6.14483	11.5008	0	Conta
ind15	Gr 1	AA	25.2372	53.197	0	Conta
ind16	Gr 1	BB	13.0307	19.0811	0	Conta
ind17	Gr 1	BB	12.6646	22.5914	1	Conta
ind18	Gr 1	AA	22.9859	41.9323	1	Conta
ind19	Gr 1	AA	13.185	19.415	0	Conta
ind20	Gr 2	AB	0	14.3063	0	Seed

Name: fix0

fix0

Search

Replace

Sort (A-Z)

Sort (0-9)

Delete rows

Rows:1000 # Cols:7

Back

Cancel

Done

© SIRE 2019

The downloaded folder contains the subdirectory “Datasets”.

3.1

Parameter	Description
β	Population average contact rate.
γ	Population average recovery rate.
k	Shape parameter that characterises the gamma distributed infection duration.
λ_j	Force of infection (probability per unit time for individual j to become infected).
w_j	Mean recovery time for individual j .
g_j, f_j, r_j	Fractional deviation in susceptibility, infectivity and recoverability of individual j .
$g_j^{\text{SNP}}, f_j^{\text{SNP}}, r_j^{\text{SNP}}$	SNP-based contribution to g_j, f_j, r_j .
a_g, a_f, a_r	SNP effects, <i>i.e.</i> change in g_j, f_j, r_j coming from an A allele compared to a B allele.
$\Delta_g, \Delta_f, \Delta_r$	Scaled dominance factors (1 when A is completely dominant over B).
X	The design matrix for fixed effects.
b_g, b_f, b_r	Vectors of fixed effects for the three traits.
$\epsilon_g, \epsilon_f, \epsilon_r$	Residual contributions to g, f, r (coming from sources other than the SNP).
Σ	Covariance matrix of residual contributions.
G_z	Group effects (accounts for differences in transmission rates in different groups).
σ_G	Standard deviation in group effects.
θ	Model parameters.
ξ	Event data (infection and recovery times).

$H_{\text{seed}}, H_{\text{cont}}$	Proportion of homozygotes (<i>i.e.</i> AA or BB) in the seeders and contacts.
$\chi_{\text{seed}}, \chi_{\text{cont}}$	Homozygote balance (<i>i.e.</i> the proportion of AA individuals minus the proportion of BB individuals) in the seeders and contacts.
N_{group}	Number of contact groups.
N_{seed}	Number of seeders (initially infected individuals) in each contact group.
N_{cont}	Number of contacts (initially susceptible individuals) in each contact group.
G_{size}	Total number of individuals per group $G_{\text{size}} = N_{\text{seed}} + N_{\text{cont}}$.
N_{total}	Total number of individuals $N_{\text{total}} = N_{\text{group}} \times G_{\text{size}}$ in the experiment.
N_i	Total number of observed infection events in the experiment.
ϕ	The average fraction of contacts that become infected.
h	The proportion of infections that occur during initialisation of contact groups.
M	Observed Fisher information matrix.

Table 1. A description of key quantities used in the paper.

1.3 Loading and Saving

SIRE permits users to load and save analysis in a special “.sire” format which save the data along with everything required for analysis. This is useful not only because it allows for analysis options This

Exporting

Posterior distribution graphs can be exported from SIRE and also files containing posterior samples of θ and ξ for further analysis using other tools. The user guide for SIRE is available in the electronic supplementary material and on the website.