

# Full Pipeline

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## Overview

Create simulated epidemic data and send to SIRE 2.0. Eventually intend to replace simulated data with Turbot data.

R functions based on Richard Bailey's originals. SIRE 2.0 modified from Chris Pooley's original.

## Load source files

```
setwd("~/Dropbox/Roslin/pipeline")

# source("parameters.R")
source("pedigree_grm-old.R")
source("pedigree_grm.R")
source("make_traits.R")
source("episim3.R")
source("episim3-new.R")
source("group_assignment.R")
source("discrete_time.R")
source("data_table_to_tsv_string.R")
```

## Parameters

Population numbers

```
# No. of sires, dams per sire, and offspring per pair, and groups
nsire <- 10
dpsire <- 5
oppair <- 2
ngroups <- 2

# Derived population numbers
ndam = nsire * dpsire
nparent = nsire + nsire * dpsire
nprogeny = nsire * dpsire * oppair
nind = nprogeny

# TODO: I think it should be this, but we'll keep it as is for the moment
nind = nparent + nprogeny
```

```
# TODO: what if this isn't an integer?
group_size = nprogeny / ngroups
```

Traits

```
# Names
traitnames <- c("susceptibility", "infectivity", "recoverability")
# No. of traits to simulate.
ntraits <- length(traitnames)
# Trait means
tmeans <- rep(0, ntraits)
# Trait additive genetic variance
tVA <- c(0.5, 0.1, 0.1)
# Trait non-additive (environmental) variance
# with no association to the pedigree
tVE <- c(0.3, 0.3, 0.3)
# Trait non-additive correlation matrix
trhoE <- diag(ntraits)
# Trait additive genetic correlation matrix.
# In this case correlations are zero.
trhoG <- diag(ntraits)
```

Infection and recoverability, targeting  $R_0 = 2.5$ ?

```
PairwiseBeta <- 0.1
RRgamma <- 0.2
```

MCMC settings

```
nsample <- 5000
burnin <- 500
```

Additional options

```
trim_parents <- FALSE
DEBUG <- FALSE
```

This will be a list for passing to functions

```
pars <- list(nsire = nsire, ndam = ndam, nprogeny = nprogeny, nind = nind, ngroups = ngroups,
            traitnames = traitnames, ntraits = ntraits, tmeans = tmeans,
            tVA = tVA, tVE = tVE, trhoE = trhoE, trhoG = trhoG,
            PairwiseBeta = PairwiseBeta, RRgamma = RRgamma,
            nsample = nsample, burnin = burnin,
            trim_parents = trim_parents, DEBUG = DEBUG)

# Quickly summarise what we've got
cat(with(pars, paste0(
  "Generating data with:\n",
  nsire, " sires, ",
  ndam, " dams, ",
```

```
nprogeny, " progeny, ("  
nind, " individuals)", "  
ngroups, " groups\n",  
"R0 = ", PairwiseBeta / RRgamma, "?\n"  
)))
```

```
## Generating data with:  
## 10 sires, 50 dams, 100 progeny, (160 individuals), 2 groups  
## R0 = 0.5?
```