

Community Genetics Simulations

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Estimated time to completion: 56 stats in 16.6333333 minutes for r1 3.367408 stats/minute
160000 stats / 3.367408 stats/minute = 47514.29 minutes 47514.29 / 60 minutes =
791.9048 hours 791.9048 hours / 24 = 32.99603 days

Current status:

1. Communities are made and backed up (on Hoth)

2. Null communities are made and backed up (on Hoth)
3. getStats for r00, r0, c0, r1 are running (on Hoth with nest and cscore running separately from mods).

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afternoon

Taking a look at the r00 stats:

```
> library(bipartite)
> library(ComGenR)
> asym11 <- read.csv('~/Desktop/asym11')
> asym11[asym11!=0] <- 1
> obs.nest <- nested(asym11)
> obs.mods <- computeModules(asym11,steps=10000)
> obs.mods <- slot(obs.mods,'likelihood')
> obs.cs <- cscore(asym11)
> #names
> com.n <- readLines('../results/com_names.txt')
> com.n <- unlist(strsplit(com.n,split=' '))
> com.type <- substr(com.n,4,7)
> com.ge <- substr(com.n,8,8)
> ##nestedness
> nest <- readLines('../results/nestr00.txt')
> nest <- as.numeric(unlist(strsplit(nest,split=' ')))
```

```

> hist(nest,xlim=c(0,100))
> abline(v=obs.nest)
> ##modularity
> mods <- readLines('../results/modsr00.txt')
> mods <- as.numeric(unlist(strsplit(mods,split=' ')))
> hist(mods)
> abline(v=obs.mods)
> ##co-occurrence
> cs <- readLines('../results/csr00.txt')
> cs <- as.numeric(unlist(strsplit(cs,split=' ')))
> hist(cs,xlim=c(40,110))
> abline(v=obs.cs)
>

```

morning

Streamline the workflow for this. See github Issue 8.

Waiting for null communities to finish before starting c0 and r1 stats. However, r00 stats are finished and r0 stats ended incomplete.

Backing up *cg_ssimulationsfolderonhothtocg_sim_backup27Feb2014.zip*

r00 null communities finished r0 null communities still running (screen -r cgsim)
c0 null communities still running (screen -r mkNull -p 0) r1 null communities still running (screen -r mkNull -p 1)

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Debugs run. Running simulation with:

- 5 genotypes
- 5 reps each
- 8 genetic scenarios
- 10 iterations per scenario
- 1000 null communities
- Also using a modularity step limit of 10,000
- File totals
 - $\text{coms} = 8 * 10 * 2 = 160$
 - $\text{null} = 160 * 1000 = 160000$
 - $\text{total} = 160000 * 4 = 640000$

Setting up on server:

1. Run *cgs_{init}.shClosescreen*
2. Run *cgs_{tats}.sh*

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New analysis structure for manuscript:

1. Genotype effect on network structure

2. Genotype effect on co-occurrence patterns
3. Selection effect on network structure

Modeling and simulation process

1. These are handled by mkComs.R
 - Generate communities with even species total abundances
 - Generate communities with asymptotic total abundances using gpm from even communities
2. This is being handled by mkNull.R
 - Generate null communities for r00, r0, c1, r1 models
3. Get network and co-occurrence statistics:
 - (a) Get nestedness
 - (b) Get modularity (this will need to be handled by a shell script)
 - (c) Get co-occurrence ses
4. Conduct selection:
 - (a) directional
 - (b) stabilizing
 - (c) disruptive

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Transferred files from research folder. Three script files:

1. `een.R` = nestedness and co-occurrence patterns
2. `eensym.Randeenasym.R` = *coupledsimulationsexaminingspeciesremoval*

Outputs are sent to results and data contains files for coupled simulations.