SINS

Simulating INdividuals in Space

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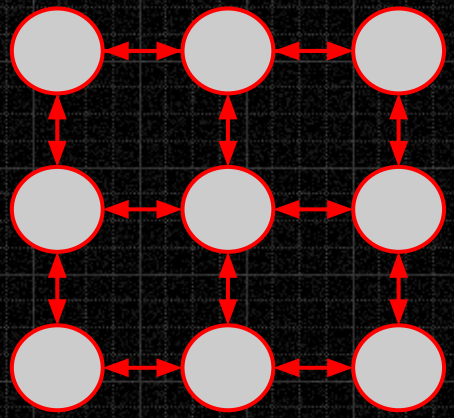
Instituto Gulbenkian de Ciência // 15.03.2017

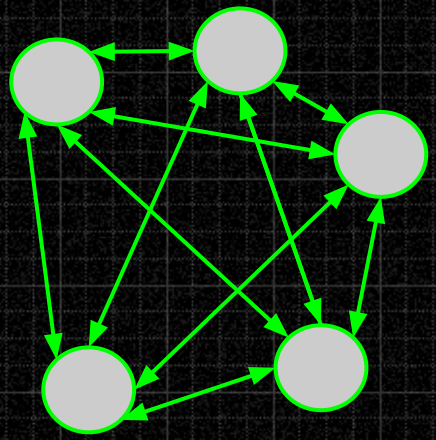
INSTITUTO GULBENKIAN DE CIÊNCIA

A look into (a few) Population Genetics Models

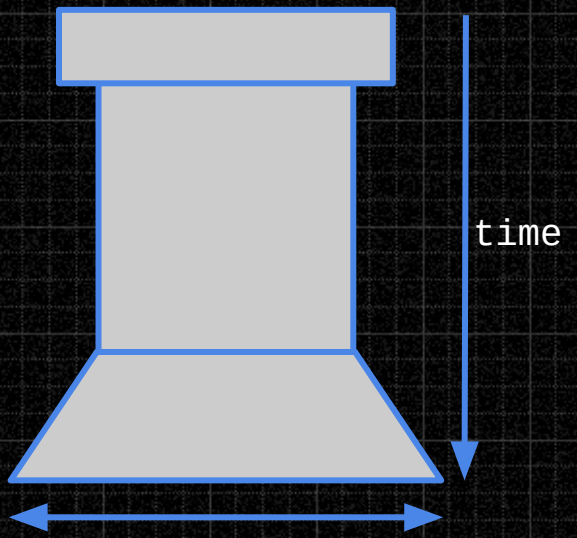
Stepping-stone model



N-island model



Population Size Change model



Structured models

Spatially explicit model

Non spatially explicit models

Population genetics inference typically assumes simple non-structured models

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Simulating INdividuals in Space

Forward in time simulation (past → present → future)

Explicit diploid individuals with a given sex

Independent neutral markers (no selection, no recombination)
- Sequences, microsatellites and SNPs
- Sexual chromosomes and mtDNA data

Population ecology and behavior
- Short and Long distance Migration (w/ sex-biased migration)
- Growth-rate
- Reproductive Success
- Admixture
- Competition
- Expansion/Colonization

Dynamic demographic and environmental events
- Carrying capacity
- Friction

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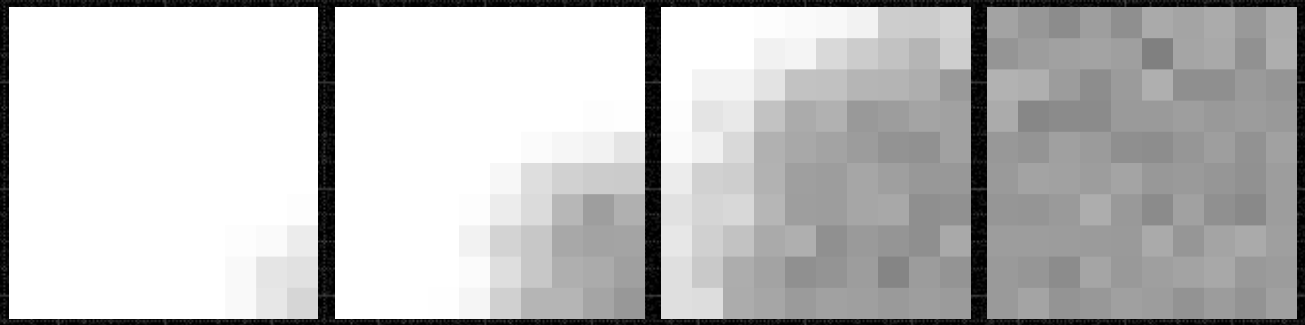
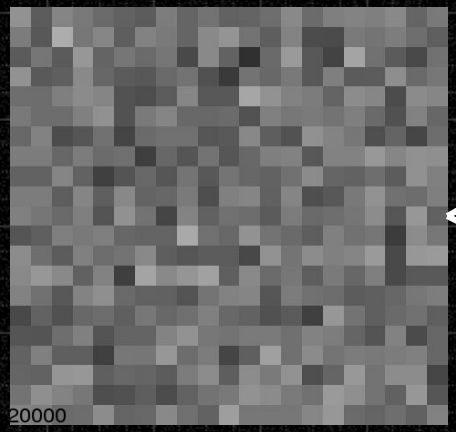
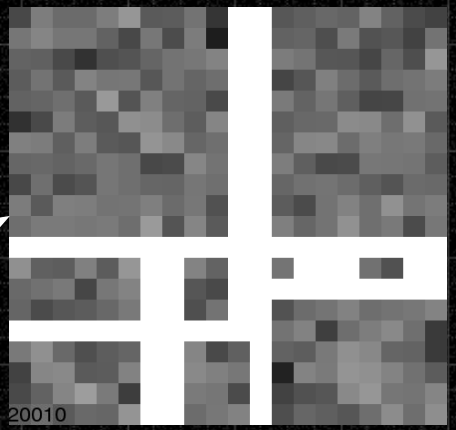
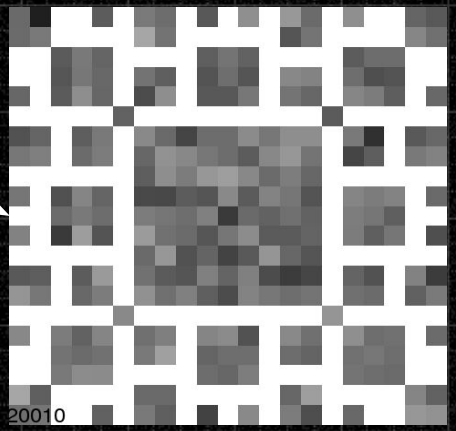


time



fragmentation



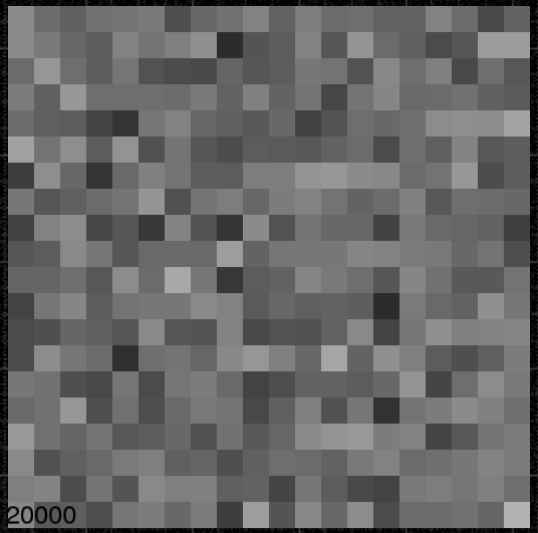


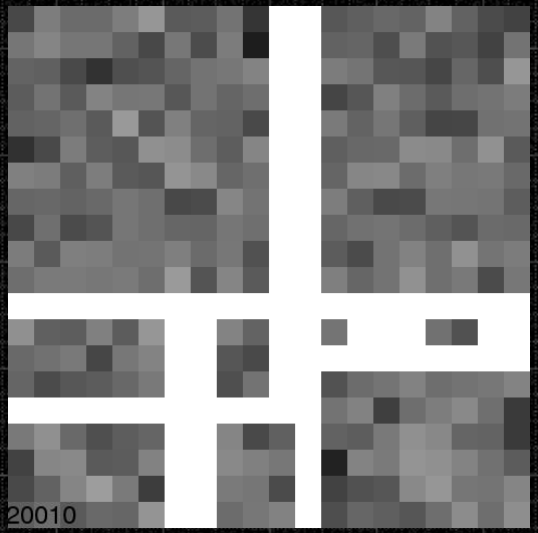
SINS - Technical details

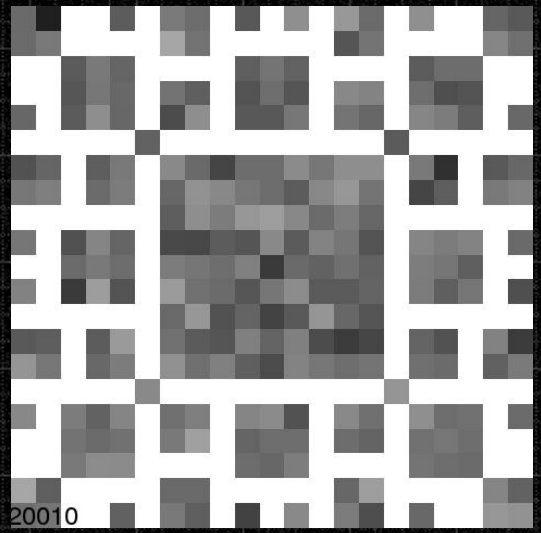
Carrying capacity ($0 \leq K < ?$)

Carrying capacity defines the (soft) maximum population size of a deme.

K is used to define the population at t + 1
Population size at t = 0 is defined by the user





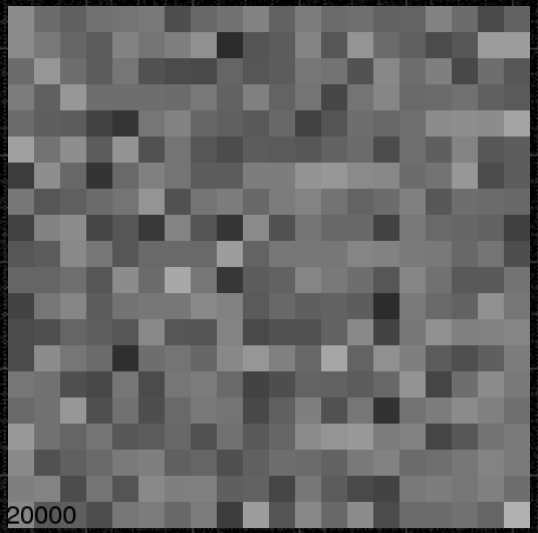


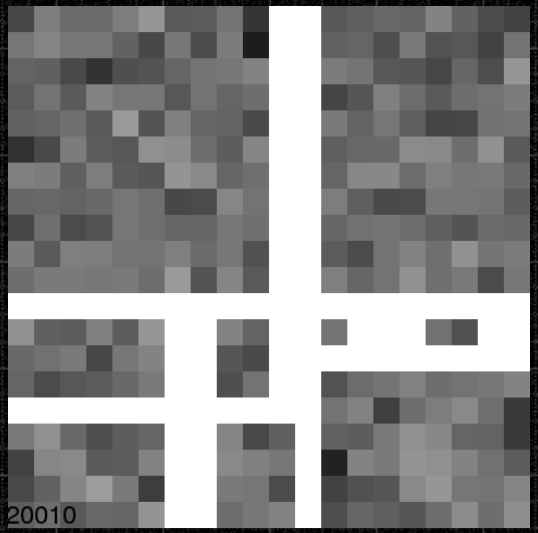
SINS - Technical details

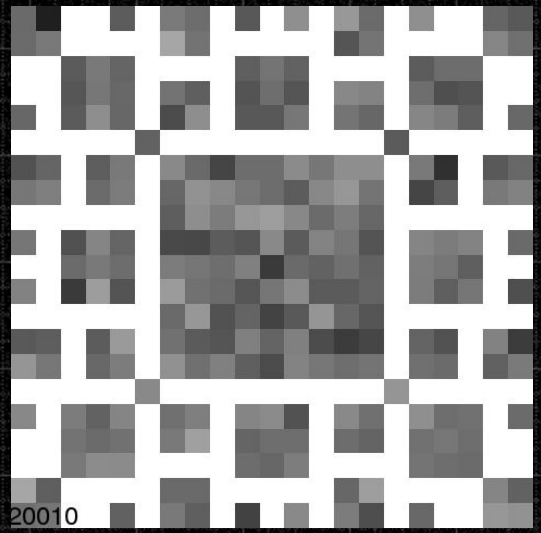
Friction ($0 \leq F \leq 1$)

Friction defines the difficulty to move to a deme.

F is used to define how migrants will be distributed among the neighbouring demes



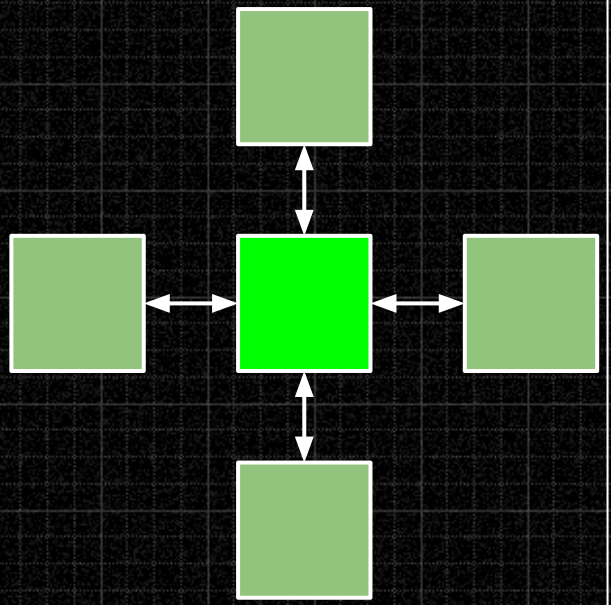




Migration

Migration can only take place in four different direction at most as in a typical 2D stepping stone model

- Number of migrants
- Sex-biased migration



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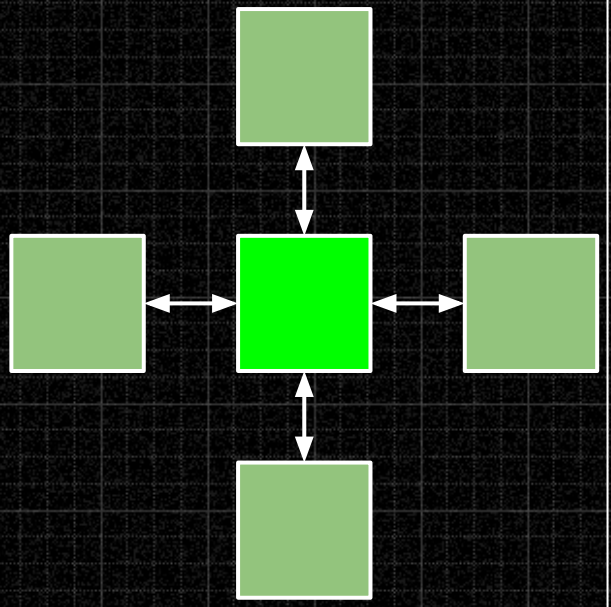
Migration - Number of migrants (M)

The number of migrants that each deme will have is deterministic and calculated as:

$$M = N_t m \frac{n_d}{4}$$



M = number of migrants

N_t = number of individuals in the deme at time t

n_d = number of receiving demes

m = migration rate

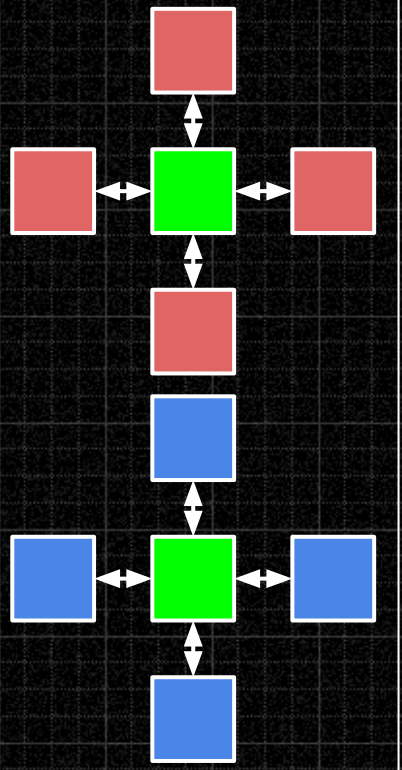
Migration - Sex-biased migration

After we calculate the number of migrants for each direction we apply a sex-ratio parameter (mSR) to determine how males and females will migrate

mSR > 0.5 females migrate more than males

$$mSR = \frac{m_f}{m_m + m_f}$$

mSR < 0.5 males migrate more than females



mSR = sex-biased migration ratio]0,1[

m_f = female migration rate

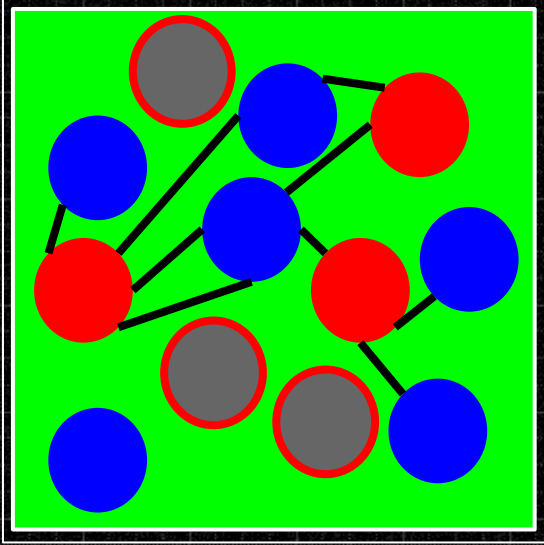
m_m = male migration rate

SINS - Technical details

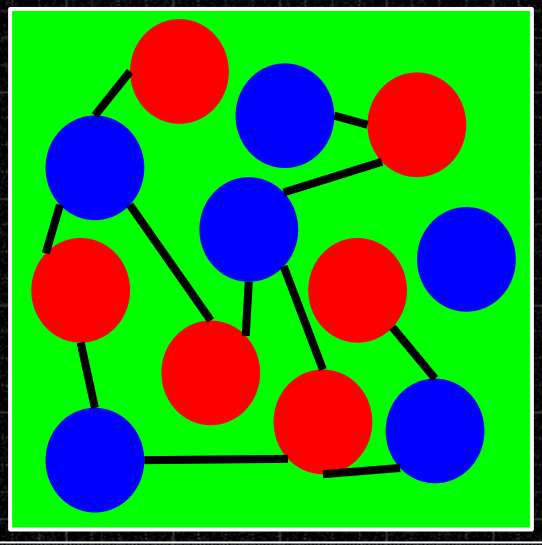
Reproductive Success ($0 < RS \leq 1$)

Populations can have a complex social structure. We don’t simulate this complex social structure (yet) but we can do an approximation by limiting the reproductive success of each sex.

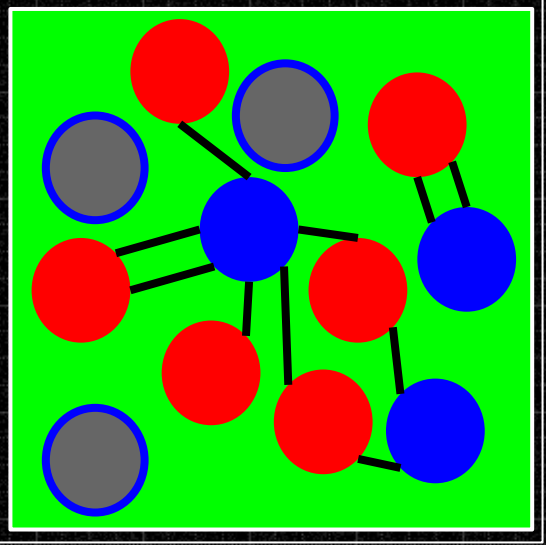
♀RS↘



♀RS = ♂RS



♂RS↘



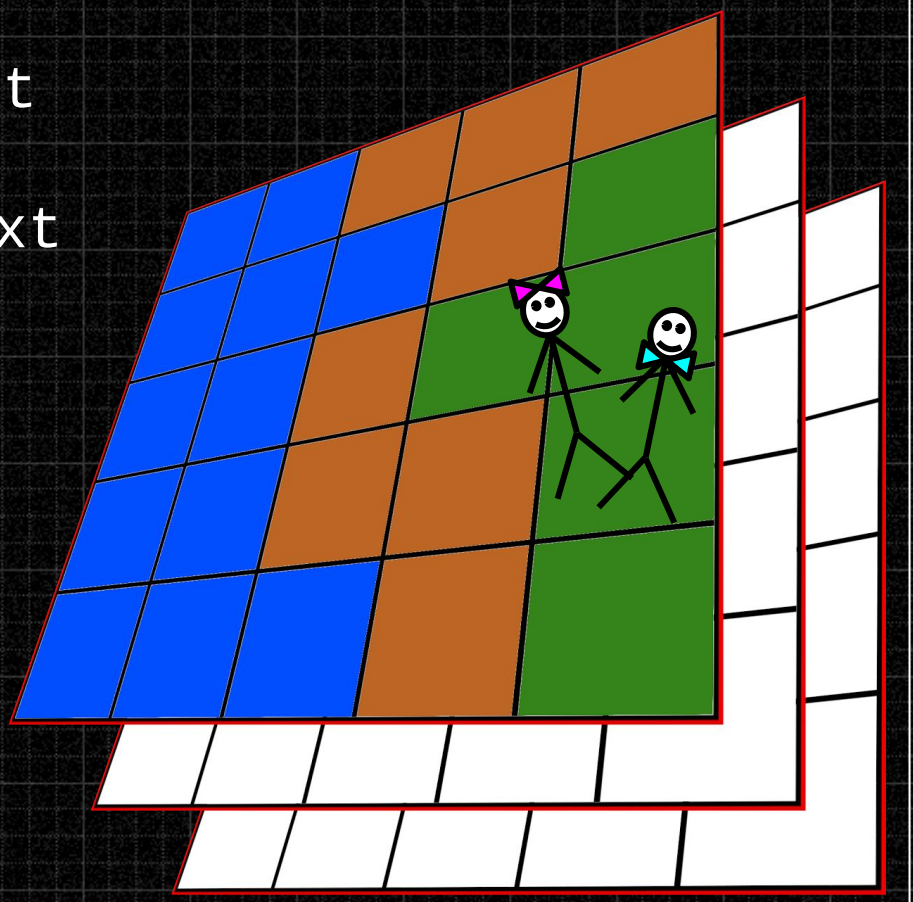
SINS

Folder and file structure

SINS_Sim

- Input/
  - world.txt
  - output_preferences.txt
  - environment/
    - layer0[CC/F]Init.txt
  - genetics/layer0/
    - genotype.txt (...)
  - layer_parameters/
    - layer0.txt
    - layer0_init.txt
  - sampling_preferences/
    - sampling_conf.txt
    - subset_map.txt

Name of layer:
layer0



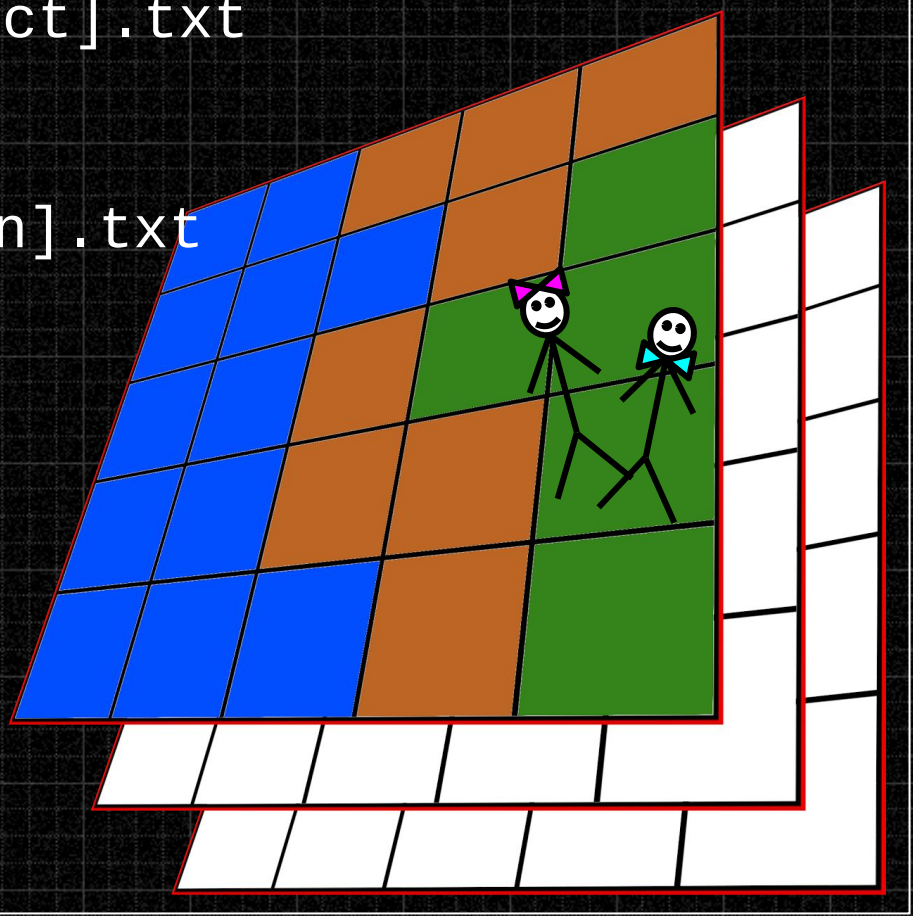
SINS

Folder and file structure

SINS_Sampler

- Input/
  - config_[name of project].txt
  - generations.txt
  - SamplingGenFiles/
    - sampling[generation].txt

Name of layer:
layer0



SINS

Class Exercise

1. In the “To_Participant/DAY_3_2017/” folder:
   a. Copy “SINS_Classes_Exercise” to your Desktop or working directory
2. Open a Command Line Interface and “move” to “SINS_Classes_Exercise” in your working directory
3. Run the “build_SINS_input.sh” script in your “SINS_Classes_Exercise” folder by typing:
   a. “./build_SINS_input.sh [name of your project]”
4. Inside your “SINS_Classes_Exercise” folder, explore the “SINS_Sim/input” and “SINS_Sampler/input” folder.
   a. Change the inputs accordingly
5. Inside your “SINS_Classes_Exercise” folder, run

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