

Mendel Genetic Counseling

Installation Instructions
using the Julia REPL

Before the Workshop

- It is important to install Julia
- Install Open Mendel modules:
 - SnpArrays.jl
 - MendelSearch.jl
 - MendelBase.jl
 - MendelGeneticCounseling.jl#ASHG2019
- And test Open Mendel with a small test example

Notebook or REPL?

- The Open Mendel team prefers to use Jupyter notebooks whenever possible, primarily because they make reproducibility easier. However you might find it easier to run Julia by just clicking on the Julia Icon.
- This presentation is designed to assist users who can't or don't want to use the Julia- jupyter notebooks combination.

Step 1: Install Julia and Open Julia

- Go to the Julia download site, <https://julialang.org/downloads/> and download the latest stable release of julia (version 1.2.0 on 9/19/2019).
- Once Julia is downloaded click on the julia icon to open the REPL

```

janets — julia — 80x24
Last login: Wed Sep 18 18:56:25 on ttys001
hg-js-mbp:~ janets$ exec '/Applications/Julia-1.2.app/Contents/Resources/julia/bin/julia'

      _
     (_)
    _(_)
   _(_)
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/_/

Documentation: https://docs.julialang.org
Type "?" for help, "]"? for Pkg help.
Version 1.2.0 (2019-08-20)
Official https://julialang.org/ release

julia> 
```

Step 2: Installing MendelGeneticCounseling

- Use the package manager in Julia.
- Invoke by typing "]" at the Julia prompt
- Then add **in order** the modules: SnpArrays.jl, MendelSearch.jl, MendelBase.jl and MendelGeneticCounseling.jl#ASHG2019
- Then give the command: build SpecialFunctions

```
pkg> add https://github.com/OpenMendel/SnpArrays.jl
```

```
pkg> add https://github.com/OpenMendel/MendelSearch.jl
```

```
pkg> add https://github.com/OpenMendel/MendelBase.jl
```

```
pkg>add https://github.com/OpenMendel/MendelGeneticCounseling.jl#ASHG2019
```

```
pkg> build SpecialFunctions
```

- To exit the package manager press the delete key

Step 3: Check for Input files

- Check for the working directory contains your files

julia> pwd()

- change to the appropriate directory if needed

- On Mac:

julia> cd("/Users/janets/GeneticCounseling/SmallSample")

- On PC:

julia> cd("C:\\Users\\janets\\GeneticCounseling\\SmallSample")

- Then check for the input files by typing

julia> readdir()

"ControlSmallParametric.txt"

"HeterozygousRisk.txt"

"LocusSmall.txt"

"PedSmall.csv"

"PhenoSmall.txt"

"SampleOutput"

Run MendelGeneticCounseling

- First compile MendelGeneticCounseling

julia> using MendelGeneticCounseling

- Then run the test problem by typing:

julia> GeneticCounseling("ControlSmallParametric.txt")

- Result:

The risk = 0.03892.

Report Any Difficulties

- Please report any problems on the open mendel github site or by email jsinshel@g.ucla.edu as soon as you have them (don't wait until the week of the workshop because we probably won't be able to help you).
- Be sure to provide as much information as you can on the commands you tried and the error messages you received. Also give us an email address that you check on a regular basis so the Open Mendel team can help you solve any problems.