

Mendel Genetic Counseling

Installation Instructions
using the Julia Icon (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 Commands within the Icon?

- The Open Mendel team prefers to use Jupyter notebooks whenever possible. See for example MendelGeneticCounselingTutorial.ipynb at https://github.com/OpenMendel/GeneticCounseling_ASHG2019. We prefer them 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 notebook option.

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 Icon

```

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
- Add **in order** the modules: SnpArrays.jl, MendelSearch.jl, MendelBase.jl and MendelGeneticCounseling.jl#ASHG2019

```
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
```

- Then give the command: build SpecialFunctions

```
pkg> build SpecialFunctions
```

- To exit the package manager press the delete key

Step 3: Check for Input files

- Check that working directory contains your files

```
julia> pwd()
```

```
julia> readdir()
```

- If the files aren't there change to the appropriate directory :

```
julia> cd("/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"
```

Step 4: Run MendelGenetiCounseling

- First compile MendelGeneticCounseling
julia> using MendelGeneticCounseling
- Then run the test problem by typing:
julia> GeneticCounseling("ControlSmallParametric.txt")
- Result:
The risk = 0.03892.

If you Decide you want to use the Jupyter Notebooks

- To use Jupyter notebooks within Julia you want to install IJulia within the package manager

] add IJulia

- then leave the package manager by hitting the delete key
- To run IJulia

julia>using IJulia

julia>notebook()

- When finished type “control C”

Step 5: Report Any Difficulties

- We've tried hard to test the installation and implementation of MendelGeneticCounseling on both Mac and PCs but you may have problems we haven't encountered before.
- So please report any problems on the open mendel github site or by email jsinshei@g.ucla.edu as soon as you have them (don't wait until the week of the workshop because we might not be able to help you in time).
- 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.