



JWAS:
Just another
Whole-genome
Analysis
Software

Hao Cheng, Rohan Fernando, Dorian Garrick

JWAS

Julia for Whole-genome Analysis Software

Bayesian Regression

- MCMC
- Bayesian Alphabet

Basic Analysis

- Linear Mixed Models
- Multivariate Analysis

Genomic Data

- Genomic Prediction
- Genome-wide Association Studies

Julia

Linear Mixed Models

Multivariate

Univariate

Missing Phenotypes

Whole-genome Data

Bayesian Alphabet

Pedigree

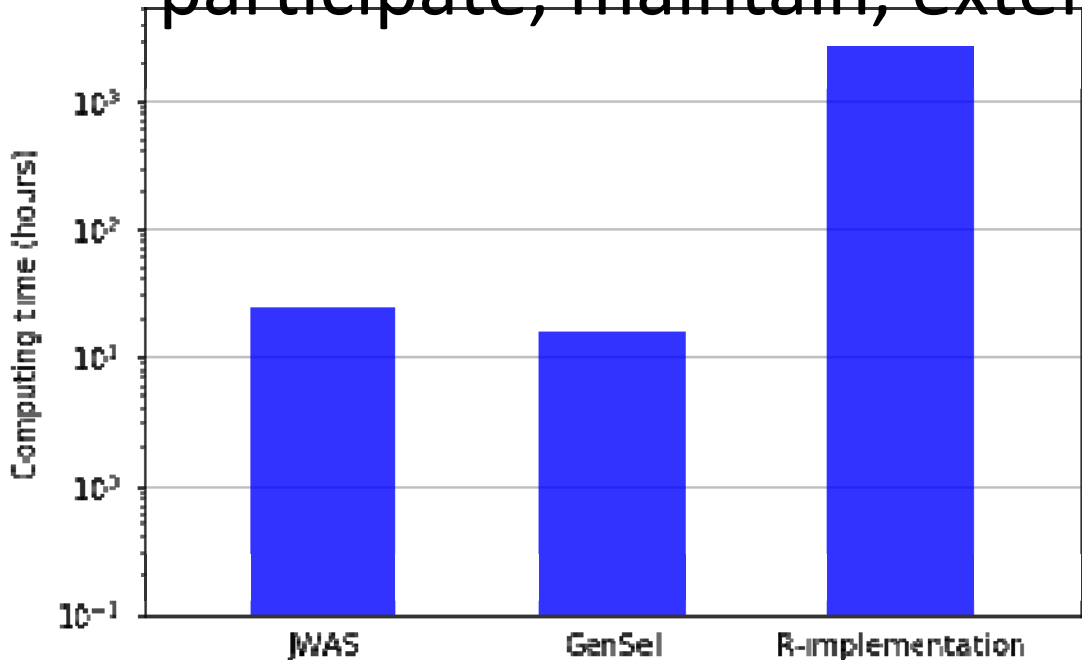
Incomplete Genomic Data

1. complete
2. routine
3. “reproducible”



Julia

• participate, maintain, extend



Jupyter JWAS Last Checkpoint: 3 minutes ago (autosaved) Logout

File Edit View Insert Cell Kernel Widgets Help Trusted Julia 0.5.2

user interface of JWAS

- In cell 2 below, the JWAS package is loaded, as well as the DataFrames package for reading text files.

```
In [2]: 1 using JWAS, DataFrames
```

- In cell 3 below, the data and pedigree information is loaded on line 1-2. The first several rows of data is shown on line 3.

```
In [3]: 1 data = readtable("phenotypes.txt")
2 pedigree = get_pedigree("pedigree.txt");
3 head(data)
```

Finished!

```
Out[3]:
```

	animal	trait1	trait2	age	sex	litter	dam
1	O1	150.0	13.0	3	M	b	D1
2	O3	40.0	5.0	4	F	a	D1

- In cell 4 below, the non-genomic part of the model equation for a 2-trait analysis is defined.
 - The effects fitted for trait 1 are the intercept, sex, direct genetic effects and maternal genetic effects.
 - The effects fitted for trait 2 are the intercept, sex, age, the interaction between sex and age and direct genetic effects.

```
In [4]: 1 model_equations = "trait1 = intercept + sex + litter + animal + dam
2 trait2 = intercept + sex + age + age*sex + animal";
```

- In cell 5 below, the model is built given the model equation in cell 3 and residual variance R. By default, all effects in model are fixed and factors. On line 2, the effect age is defined as covariates. On line 3, the effect litter is defined as random with variance G1. On line 4, direct genetic effects and maternal genetic effects are fitted as animal and dam with variance G2 and numerator relationship matrix from pedigree. (Codes to define G1,G2, G3, R are skipped for demonstration purpose)

```
In [5]: 1 model = build_model(model_equations,R)
2 set_covariate(model,"age")
3 set_random(model,"litter",G1)
4 set_random(model,"animal dam", pedigree,G2)
```

- In cell 6 below, genomic part of the model is defined with genotypes file and variance G3. The format of genotypes file is:


```
O1,1,2,0,1,0
O3,0,0,2,0,1
```

```
In [6]: 1 add_genotype(model,"genotypes.txt",G3)
```

- In cell 7 below, a multi-trait BayesC analysis is performed with model and data defined in cell 1 to 5.

```
In [7]: 1 runMCMC(model,data,methods="BayesC")
```

More information is available [here](#). For help on JWAS, type ?JWAS and press enter.

Bayesian Linear Mixed Models (BLMM)

BLMM	Marker Effect Model		Breeding Value Model
incomplete Genomic Data	Non-Mixture Priors	RR-BLUP ^{ss mt} BayesA ^{ss mt} ...	Genomic BLUP ^{ss mt}
	Mixture Priors	BayesB ^{ss mt} BayesC π ^{ss mt} BayesR ^{ss mt} ...	

user interface of JWAS

- In **cell 2** below, the JWAS package is loaded, as well as the DataFrames package for reading text files.

```
In [2]: 1 using JWAS, DataFrames
```

- In **cell 3** below, the data and pedigree information is loaded on line 1-2. The first several rows of data is shown on line 3.

```
In [3]: 1 data      = readtable("phenotypes.txt")  
2 pedigree = get_pedigree("pedigree.txt");  
3 head(data)
```

Finished!

```
Out[3]:
```

	animal	trait1	trait2	age	sex	litter	dam
1	O1	150.0	13.0	3	M	b	D1
2	O3	40.0	5.0	4	F	a	D1

Out [3]:

	animal	trait1	trait2	age	sex	litter	dam
1	O1	150.0	13.0	3	M	b	D1
2	O3	40.0	5.0	4	F	a	D1

- In **cell 4** below, the non-genomic part of the model equation for a 2-trait analysis is defined.
 - The effects fitted for trait 1 are the intercept, sex, direct genetic effects and maternal genetic effects .
 - The effects fitted for trait 2 are the intercept, sex, age, the interaction between sex and age and direct genetic effects.

In [4]:

```
1 model_equations = "trait1 = intercept + sex + litter + animal + dam  
2                   trait2 = intercept + sex + age + age*sex + animal";
```

In [4]:

```
1 model_equations = "trait1 = intercept + sex + litter + animal + dam  
2                   trait2 = intercept + sex + age + age*sex + animal";
```

- In **cell 5** below, the model is built given the model equation in cell 3 and residual variance **R**. *By default, all effects in model are fixed and factors.* On line 2, the effect **age** is defined as covariates. On line 3, the effect **litter** is defined as random with variance **G1**. On line 4, direct genetic effects and maternal genetic effects are fitted as **animal** and **dam** with variance **G2** and numerator relationship matrix from **pedigree**. (Codes to define G1,G2, G3, R are skipped for demonstration purpose)

In [5]:

```
1 model = build_model(model_equations,R)  
2 set_covariate(model,"age")  
3 set_random(model,"litter",G1)  
4 set_random(model,"animal dam", pedigree,G2)
```

- In **cell 6** below, genoimc part of the model is defined with genotypes file and variance **G3**. The format of genotypes file is:

```
O1,1,2,0,1,0  
O3,0,0,2,0,1
```

```
In [6]: 1 add_genotype(model, "genotypes.txt", G3)
```

- In **cell 7** below, a multi-trait BayesC analysis is performed with **model** and **data** defined in cell 1 to 5.

```
In [7]: 1 runMCMC(model, data, methods="BayesC")
```

More information is available [here](#). For help on JWAS, type ?JWAS and press enter.

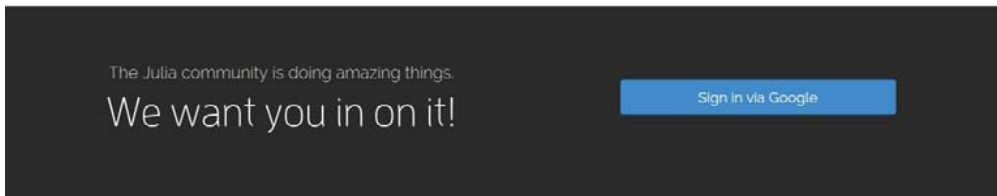
Future plan

BLMM	Marker Effect Model		Breeding Value Model
incomplete Genomic Data	Non-Mixture Priors	RR-BLUP ^{ss mt} BayesA ^{ss mt} ...	Genomic BLUP ^{ss mt}
	Mixture Priors	BayesB ^{ss mt} BayesC π ^{ss mt} BayesR ^{ss mt} ...	



JuliaBox beta

Run Julia from the Browser. No setup.



IJulia

Create IJulia Notebooks and share them.



Console

Use in-browser terminal emulator to fully control your Docker instance.



Google Drive

Collaborate with others. Sync notebooks and data via Google Drive.



Sync & Share

Setup folders to sync with remote git repositories.

reworkhow / JWAS.jl

Unwatch 4 Unstar 7 Fork 9

Code Issues 3 Pull requests 0 Projects 0 Wiki Insights Settings

Julia for Whole-genome Analyses Software

364 commits 1 branch 7 releases 3 contributors GPL-2.0

Branch: master New pull request Create new file Upload files Find file Clone or download

reworkhow update documentation 12 hours ago

docs update documentation 12 hours ago

src add H matrix for GBLUP 3 days ago

test allow MTBayeB to work as MTBayesA 10 months ago

.gitignore GBLUP now work a year ago

.travis.yml change require julia for travis 12 days ago

LICENSE Update and rename LICENSE.md to LICENSE 3 years ago

README.md Create README.md 8 months ago

REQUIRE update REQUIRE 12 days ago

workshops



Questions?

- <http://QTL.rocks>
- My group is Recruiting!

Software

open-source software tools for statistical genetics

- [JWAS](#)
Julia implementation of Whole-genome Analyses Software using Univariate and Multivariate Bayesian Mixed Effects Model
- [XSim](#)
Simulation of Descendants from Ancestors with Sequence Data
- [PedModule](#)
Pedigree-based Mixed Effects Models
- [SSBR](#)
Bayesian regression analyses combining information from genotyped and non-genotyped individuals

Books

interactive Jupyter notebooks for statistical genetics



Subscribe

subscribe to updates from QTL.rocks,
[subscribe to QTL.rocks](#)

workshops

[workshops about statistical genetics](#)

More

QTL.rocks is created and maintained by [Hao Cheng](#)