



JWAS: **J**ust another **W**hole-genome **A**nalysis **S**oftware

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

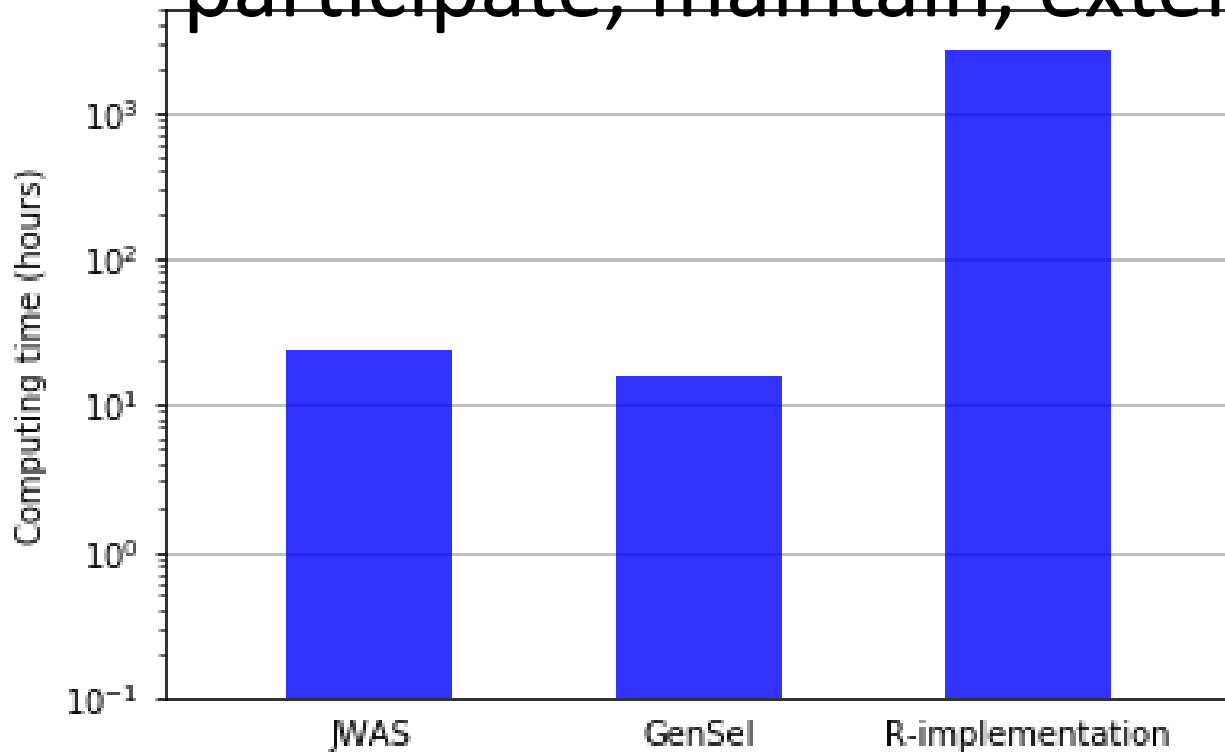
Pedigree

Incomplete Genomic Data

1. complete
2. routine
3. “reproducible”



- participate, maintain, extend



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

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Code

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} ...	

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03,0,0,2,0,1
```

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

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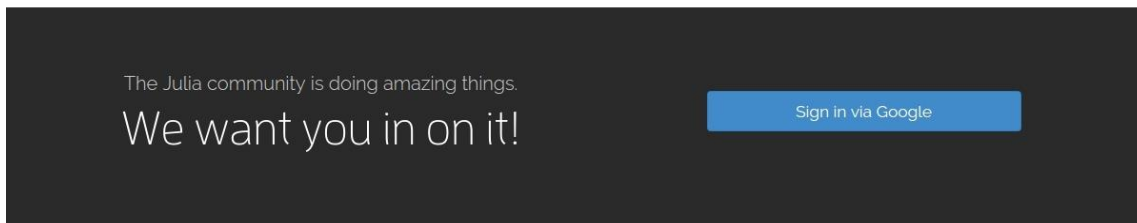
Future plan

BLMM	Marker Effect Model		Breeding Value Model
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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

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Julia for Whole-genome Analyses Software

364 commits 1 branch 7 releases 3 contributors GPL-2.0

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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!



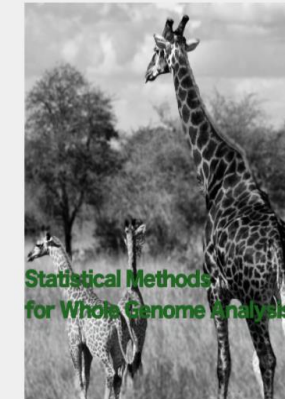
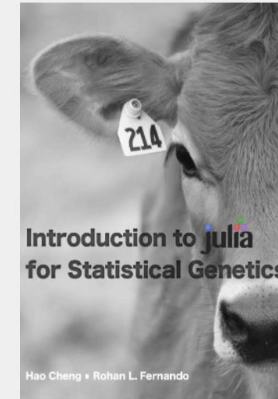
Software

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

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