Load your modules in Julia (packages in R)

```
begin
using CSV # module for reading and writing CSV files
using Plots # module for plotting
using StatsPlots
using DataFrames # ... working with data frames
using Random # ... random numbers
using Turing # Module for Bayesian statistics in Julia
using RCall # Module to run R code in Julia.
end
```

2. Get your data.

In this example, we will follow Richard McElreath's example on the partial census of the Dobe are !Kung San. These data was complaed b Nancy Howell in the late 1960s. The !Kung San are the most famus foragin hyman population of the 20^{th} century.

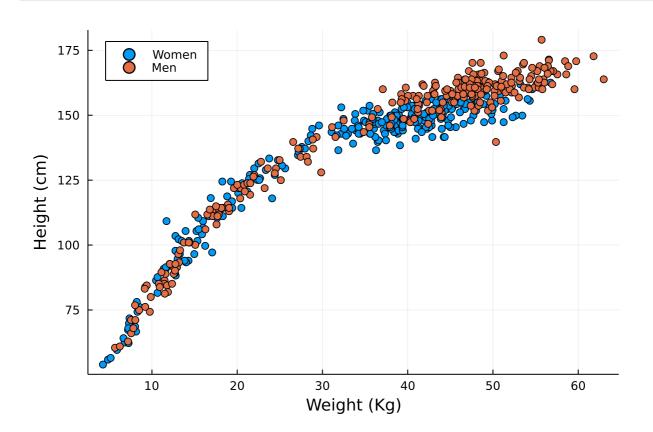


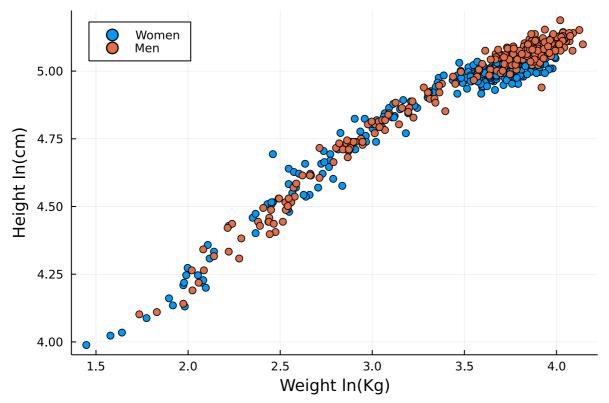
	Column1	height	weight	age	male	
1	1	151.765	47.8256	63.0	1	
2	2	139.7	36.4858	63.0	0	
3	3	136.525	31.8648	65.0	0	
4	4	156.845	53.0419	41.0	1	
5	5	145.415	41.2769	51.0	0	
6	6	163.83	62.9926	35.0	1	
7	7	149.225	38.2435	32.0	0	
8	8	168.91	55.48	27.0	1	
9	9	147.955	34.8699	19.0	0	
10	10	165.1	54.4877	54.0	1	
more						
544	544	158.75	52.5316	68.0	1	

```
begin
data = CSV.read("Howell1.csv", DataFrame; delim = ",");
#data = filter!(x -> x.age >= 18, data);
end
```

```
Men = filter(x -> x.male == 1, data);
```

```
• Women = filter(x -> x.male == 0, data);
```





```
begin
scatter(log.(Women.weight), log.(Women.height), lab= "Women", legend = :topleft)
scatter!(log.(Men.weight), log.(Men.height), lab= "Men")
xlabel!("Weight ln(Kg)")
ylabel!("Height ln(cm)")
```

The model

We want to model the relationship between weight and height and test whether this relationship is different between men and women.

Our model:

$$x_i = weight_i - \overline{weight}$$

,

$$Y \approx Normal(\mu, \sigma)$$

,

$$\mu_i = lpha + eta_w x_i + eta_m Male_i + eta_{mxw} Male_i x_i$$
 $lpha pprox Normal(0, 10)$

,

$$\beta_w \approx Normal(0, 10)$$

,

$$\beta_m \approx Normal(0, 10)$$

,

$$\beta_{mxw} \approx Normal(0, 10)$$

Define our model

In Julia, we basically make a function that looks almost exactly as in our writing model definition

Kung_San (generic function with 1 method)

```
@model function Kung_San(height, weight, male)

x = weight .- log(45) # define our continuous predictor

σ ~ truncated(Cauchy(0, 10), 0, Inf) # priors for error

α ~ Normal(4.93, 10) # priors for intercept

β_w ~ Normal(0, 10) # prior for weight effect (slope)

β_m ~ Normal(0, 10) # prior for sex effect (slope)

β_wm ~ Normal(0, 10) # prior for the interaction effects

μ = α .+ β_w .* x .+ β_m .* male .+ β_wm .* (x.*male) # linar model

height .~ Normal.(μ, σ) # likelihood

end
```

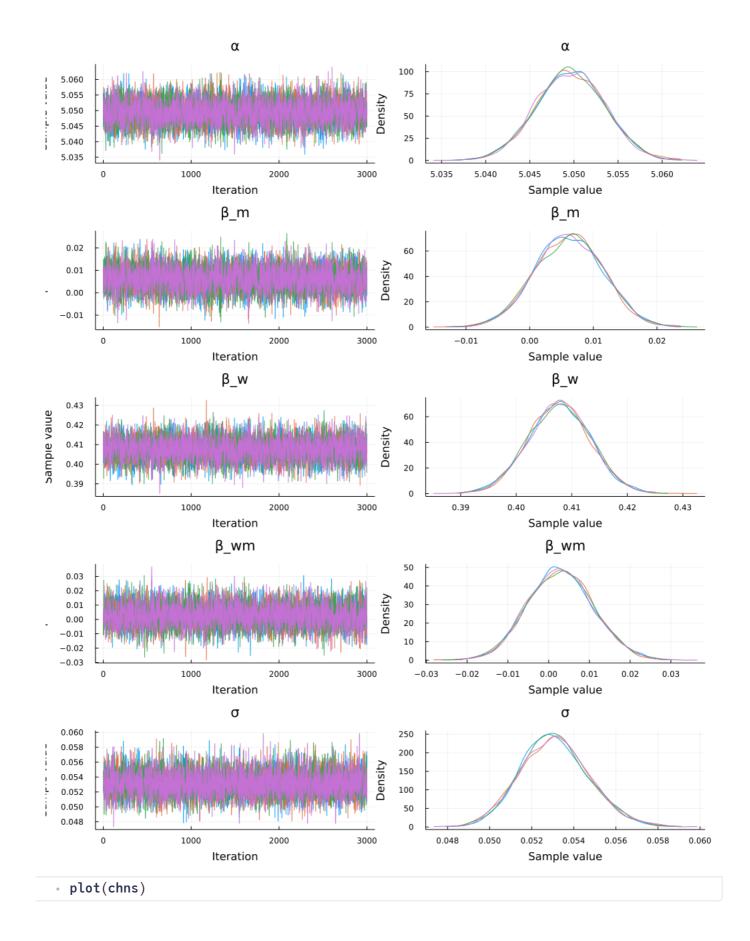
Create a model, with your data.

```
My_model = Kung_San(log.(data.height), log.(data.weight), data.male);
```

Now, we run the model, and collect our posterior samples.

```
# Run the model
# Multiple threads 4
# 3000 samples
chns = sample(My_model, NUTS(), MCMCThreads(), 3000, 4);
```

Now, we check if the MCC chains converged



Check your summary statistics

[parameters	mean	std	naive_se	mcse	ess	rhat
1	:α	5.04962	0.00387235	3.53495e-5	5.01242e-5	7361.59	0.999982
2	:β_m	0.00618889	0.0053693	4.90148e-5	7.28096e-5	7091.96	1.00007
3	:β_W	0.407733	0.00559922	5.11137e-5	7.0735e-5	6773.15	0.99996
4	:β_wm	0.00294581	0.00802802	7.32855e-5	0.000106298	6862.81	1.00002
5	: σ	0.0531063	0.00164275	1.49962e-5	1.68475e-5	9234.18	0.999735

```
describe(chns)
```

Let's test our hypothesis

Research hypothesis: the relationship between height and weight is stronger in males.

```
poste = DataFrame(chns);

p_link (generic function with 1 method)

*# model from the posteriors
function p_link(weight, male, α, β_w, β_m, β_wm) # weight in Kg, Male==1 female==0,

**

x = log.(weight) .- log.(45)

p = α .+ β_w .* x .+ β_m .* male .+ β_wm .* (x.*male)

return exp.(p)
end
**
```

Get summary statistics such as complementary intervals (CI)

```
function HDI(samples; credible_mass=0.95)
      # Computes highest density interval from a sample of representative values,
     # estimated as the shortest credible interval
     # Takes Arguments posterior_samples (samples from posterior) and credible mass
 (normally .95)
     # Originally from https://stackoverflow.com/questions/22284502/highest-
 posterior-density-region-and-central-credible-region
     # Adapted to Julialang
     sorted_points = sort(samples)
     ciIdxInc = Int(ceil(credible_mass * length(sorted_points)))
     nCIs = length(sorted_points) - ciIdxInc
     ciWidth = repeat([0.0],nCIs)
     for i in range(1, stop=nCIs)
         ciWidth[i] = sorted_points[i + ciIdxInc] - sorted_points[i]
     end
     HDImin = sorted_points[findfirst(isequal(minimum(ciWidth)),ciWidth)]
     HDImax = sorted_points[findfirst(isequal(minimum(ciWidth)),ciWidth)+ciIdxInc]
     return([HDImin, HDImax])
end
```

What is the predicted height of a 58.0 Kg woman of the !Kung San population

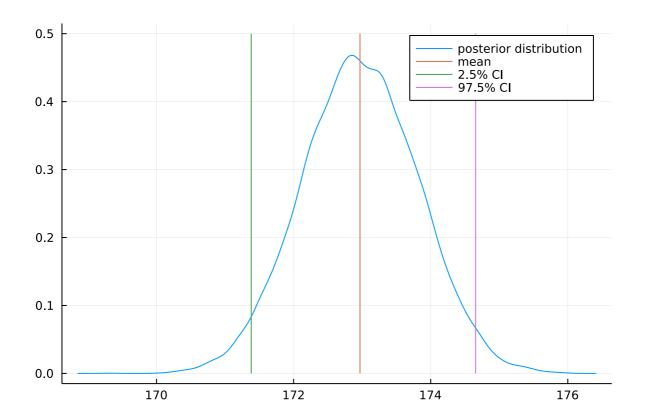


We use our new predicted function to estimate the most likely size range of a 58.0 Kg women.

prediction_W_58kg =

[172.067, 172.103, 174.075, 173.892, 173.696, 174.298, 172.823, 173.291, 173.391, 172.44]

prediction_W_58kg = p_link(58.0, 0, poste.α, poste.β_w, poste.β_m, poste.β_wm)



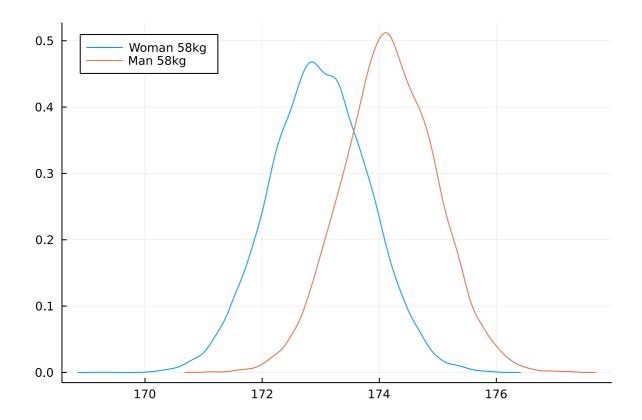
Time to test a research hypothesis (not a statistical hypothesis):

A man that weights 58 Kg is smaller than a woman of the same size

```
prediction_M_58kg =
```

[173.651, 173.66, 174.197, 174.043, 176.632, 173.758, 174.808, 173.213, 174.092, 172.988

```
prediction_M_58kg = p_link(58.0, 1, poste.α, poste.β_w, poste.β_m, poste.β_wm)
```

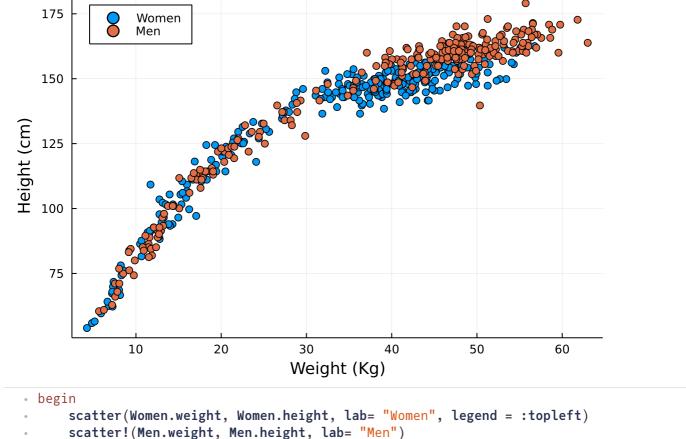


```
85.175
```

```
    # formal test
    100 * sum(prediction_M_58kg .- prediction_W_58kg .> 0) / length(prediction_M_58kg)
```

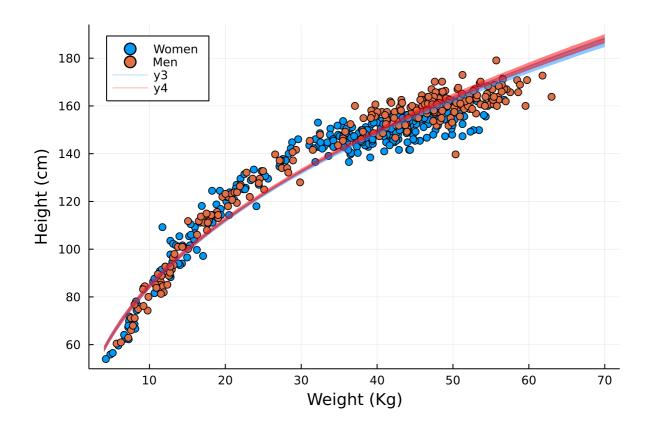
Our model predictions show that a 58 Kg man is much taller than a 58 Kg woman with a 100%

Are men always taller than women?



```
begin
scatter(Women.weight, Women.height, lab= "Women", legend = :topleft)
scatter!(Men.weight, Men.height, lab= "Men")
xlabel!("Weight (Kg)")
ylabel!("Height (cm)")
end
```

This plot shows that men are generally taller, but some women are taller than some men. **So, what** is the probability that a woman is taller than a man when we control for their weight?



79.2114465408805

100*sum(Matrix(raw_m .- raw_w)[:] .> 0) / length(Matrix(raw_m .- raw_w)[:])