



Introduction Experimental Design and to Bayesian statistics

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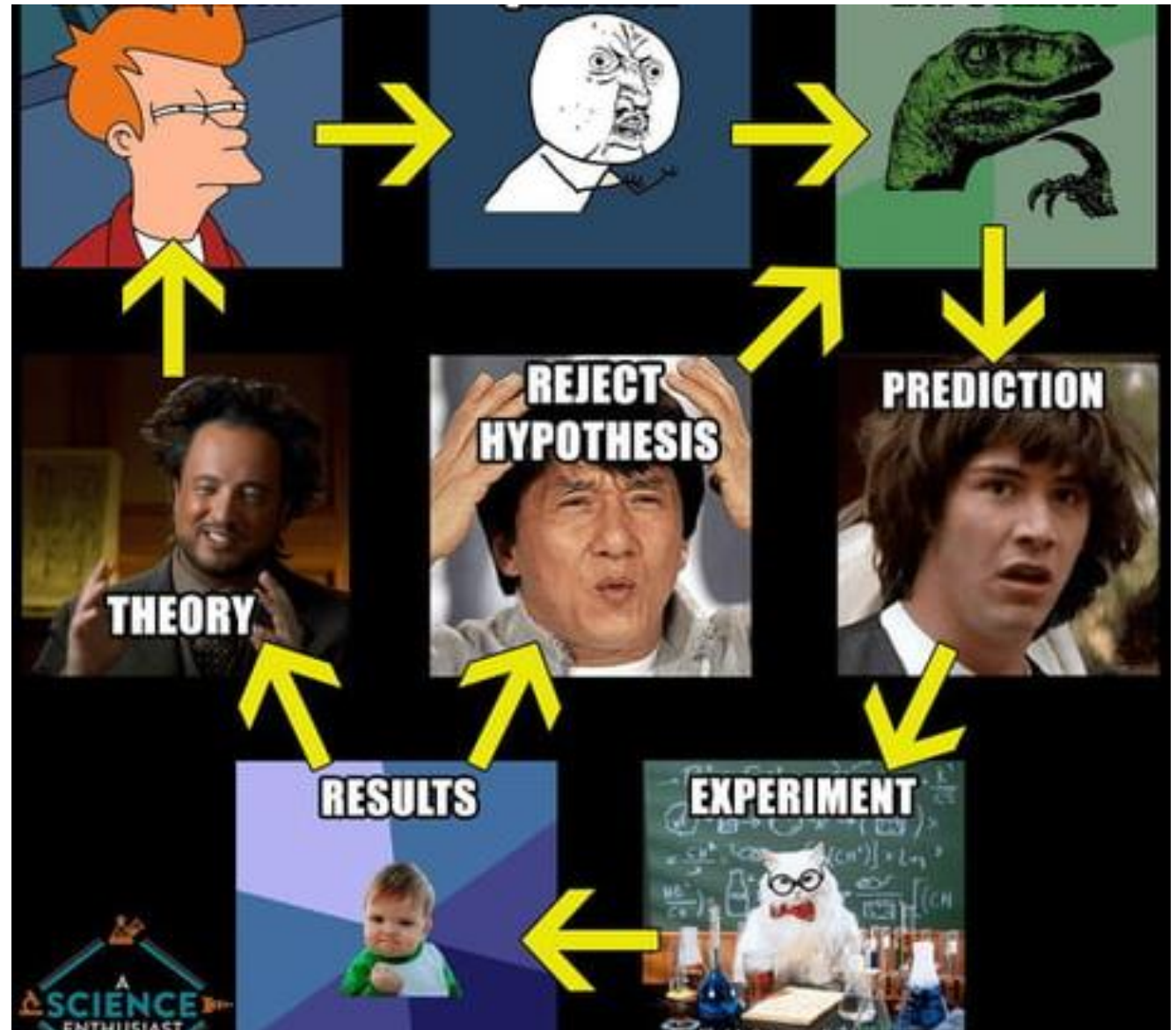
Animal Evolutionary Ecology Group

Three spined stickleback mating behavior



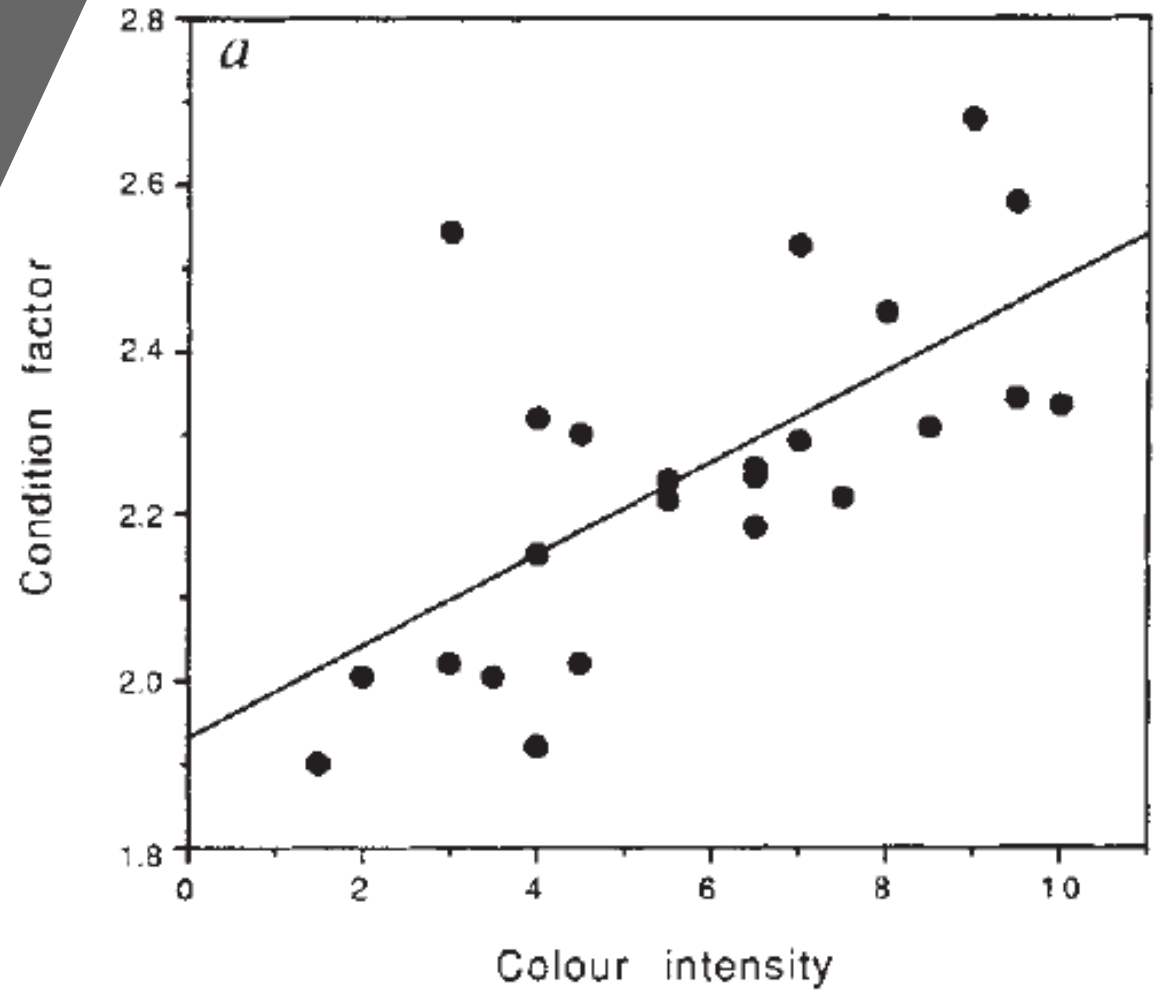
Discuss with your colleagues?

- What did you see?
- Which fish is the male?
- Which fish is the female?
- Why do they have different colorations?
- What is the role of color?
- Do parasites play a role in this behavior?
- How could you investigate if parasites are involved?



Observation and correlations

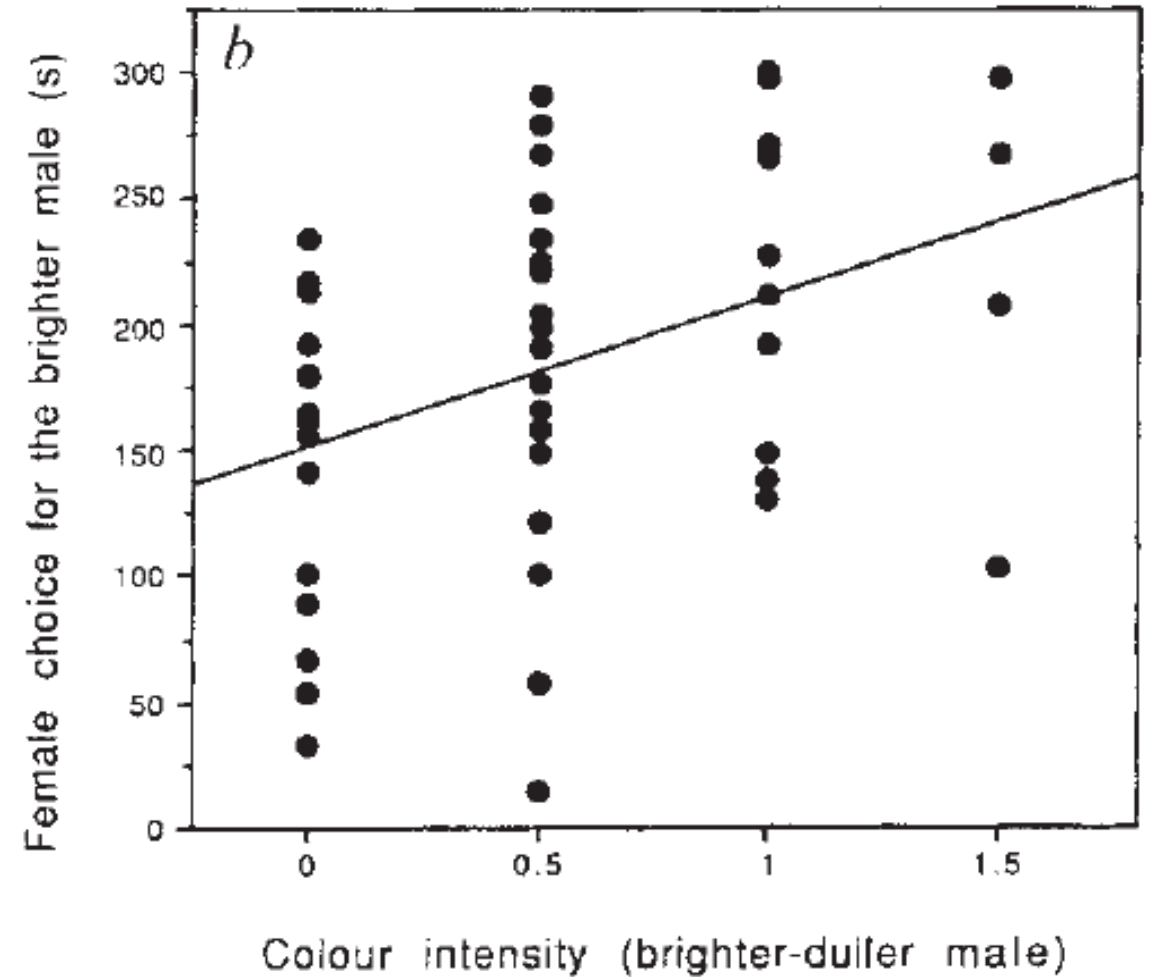
Males with more intense red coloration are in better condition



Observation and correlations

Males with more intense red coloration are in better condition

Females chose to mate with males that have more intense colorations

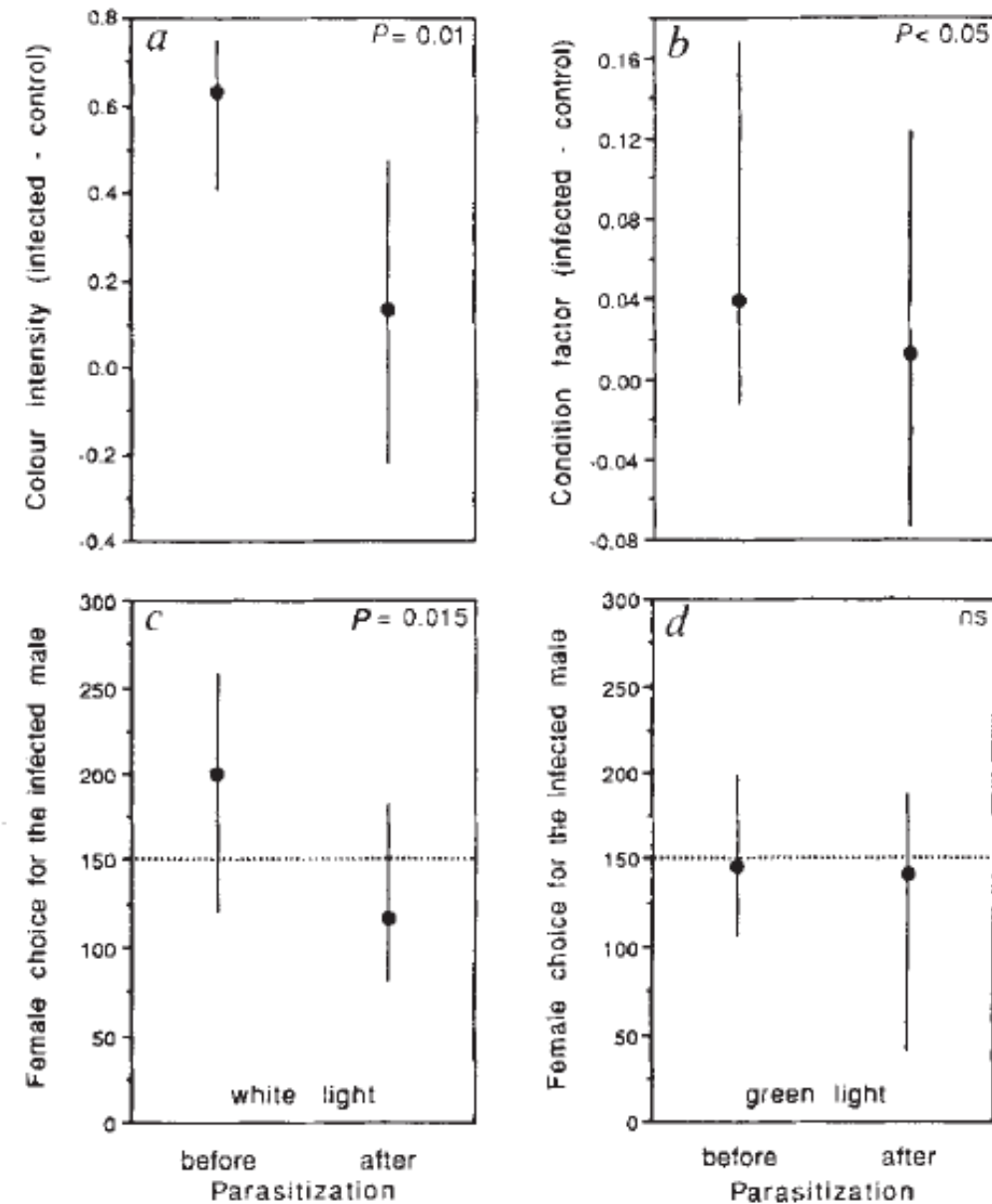


What are experiments and why to do them?

- tests under controlled conditions
- Elements of experiments:
 - Hypothesis
 - Define experimental treatments and controls
 - Replication
- to demonstrate a known truth
- Test hypothesis
- Evaluate the efficacy of something previously untried

Experimentation (parasite x light)

Color seems to be an honest signal
of male's condition and ability to
fight parasite infections



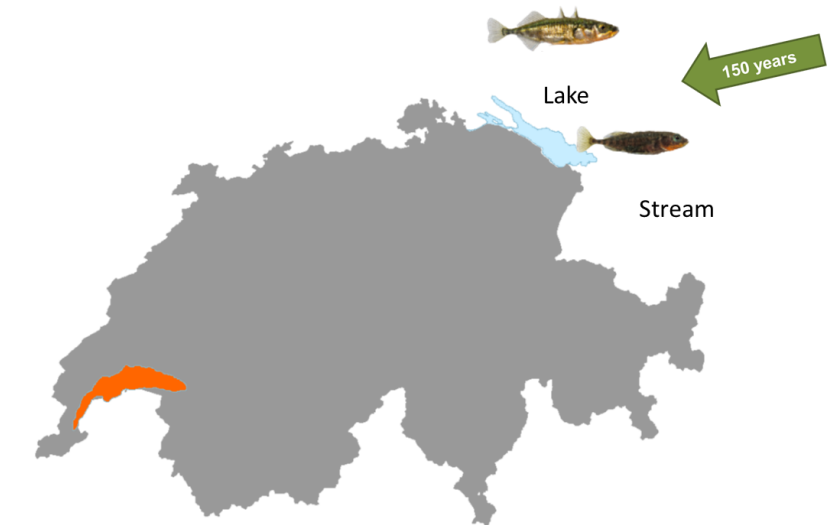
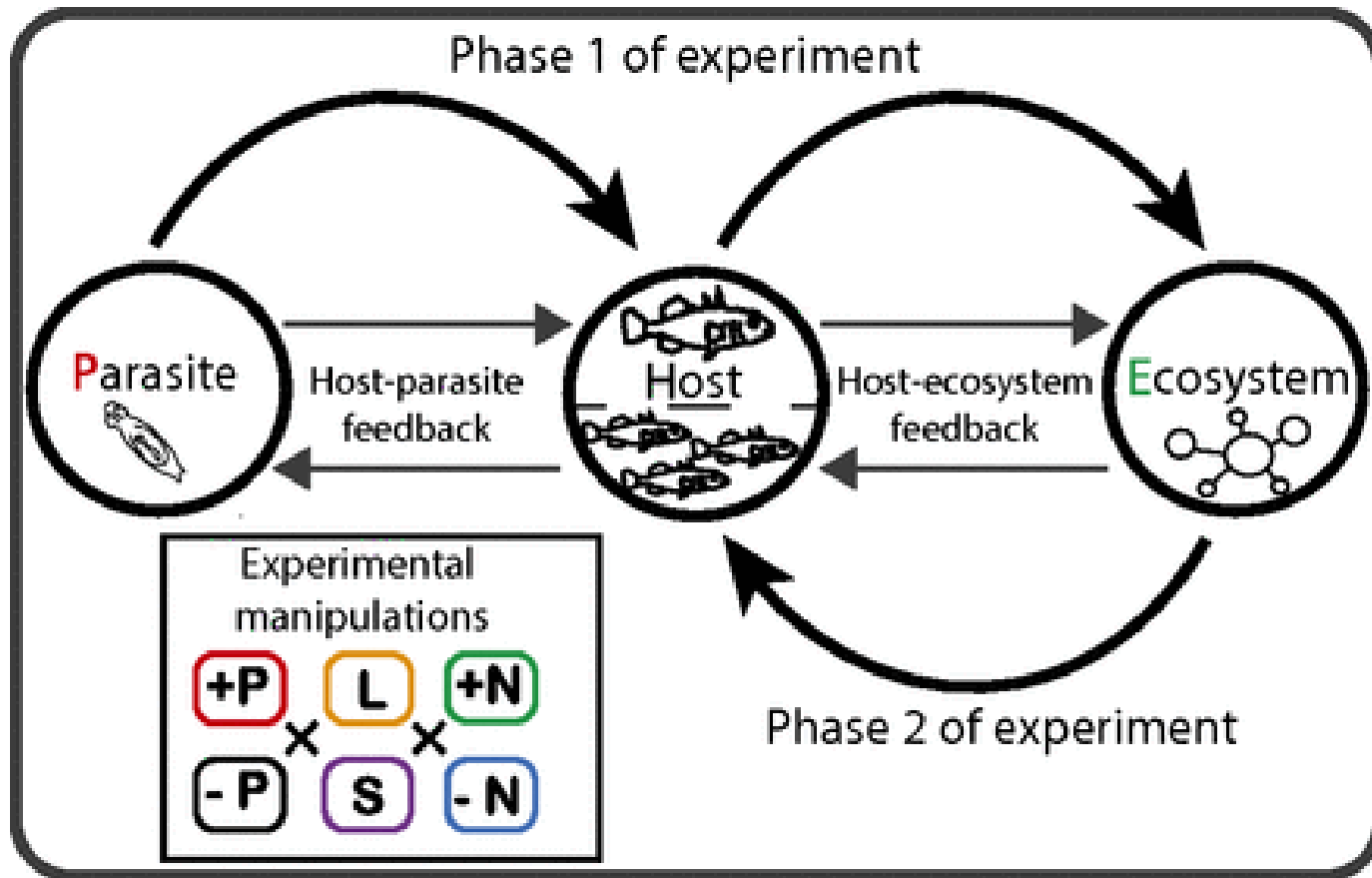


Experiments with host and parasites



Randomized factorial
experiment

What are the effects of parasites and nutrient loading in host-environment interactions?



Experimental treatments

(Host ecotype x Parasite x Nutrients)

Main effects:

Host ecotype: Lake vs Stream

Parasite exposure: G+ vs G-

Nutrient addition: High vs Low

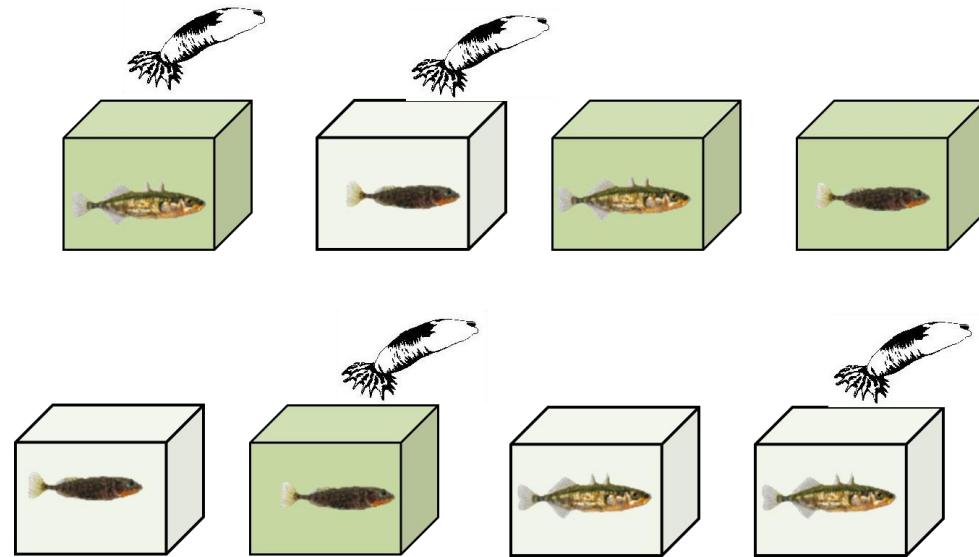
Interactive effects:

Two way: LakeG+ vs StreamG-

Two way: LakeHigh vs StreamHigh

Three way: $2 \times 2 \times 2 = 8$ treatments

LakeHighG+ vs StreamLowG-



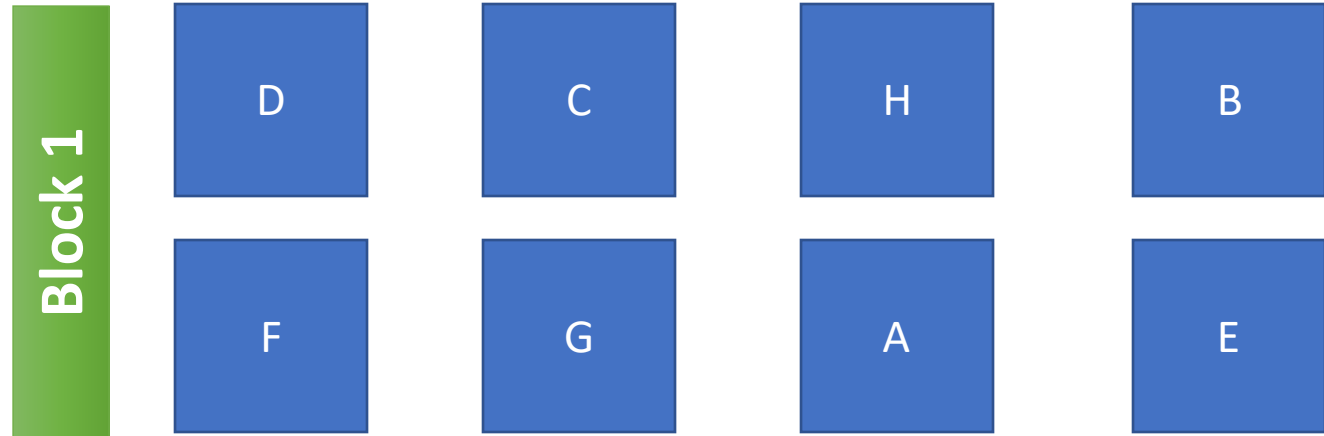
Avoiding **confounding** effects:

- What would happen if we used only stream parasites?

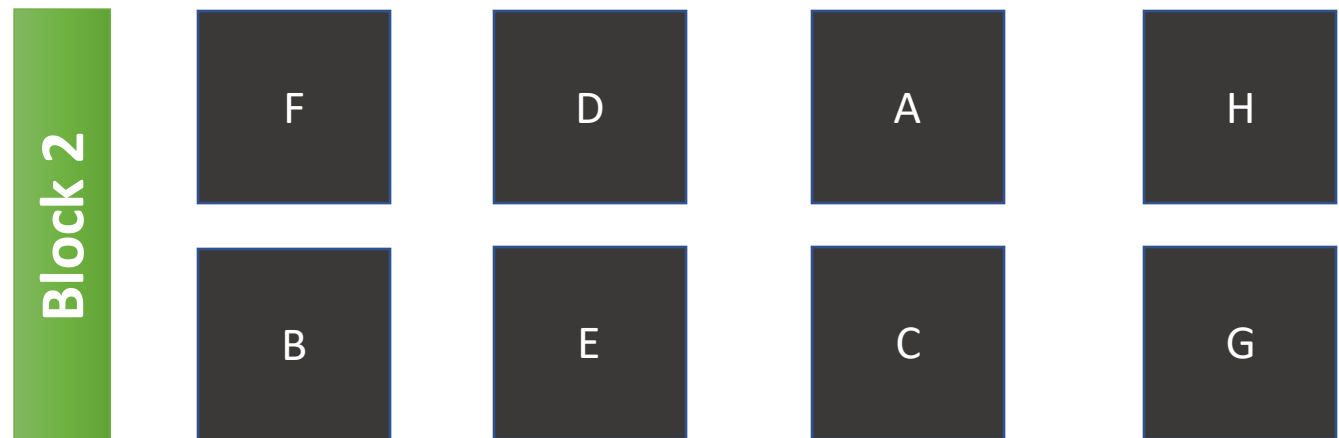
Replication (independence and heterogeneity)

(5 blocks and 40 tanks)

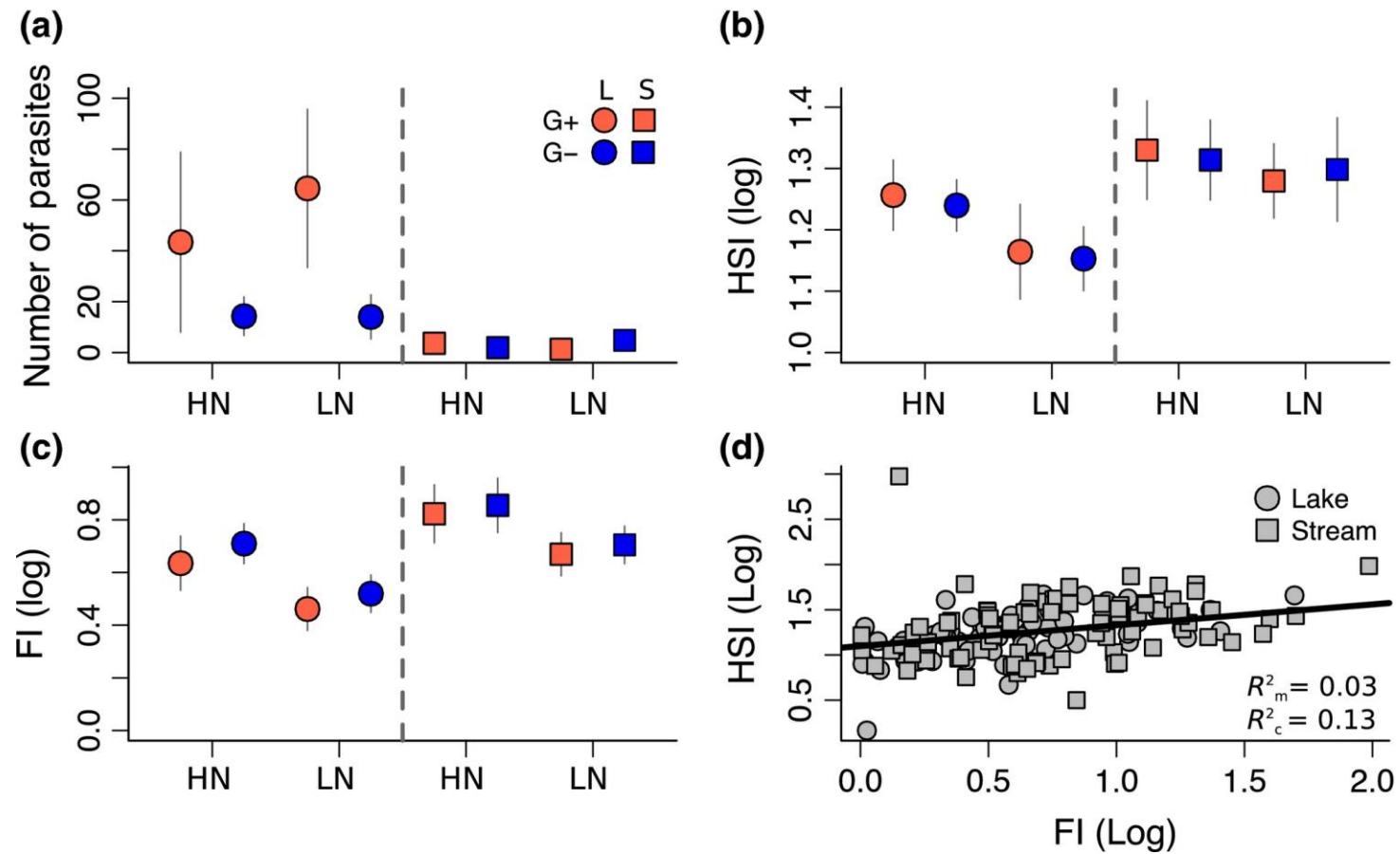
Lake	No Exposure (G-)	Exposure (G+)
High N	A = 6 fish	B= 6 fish
Low N	C= 6 fish	D= 6 fish



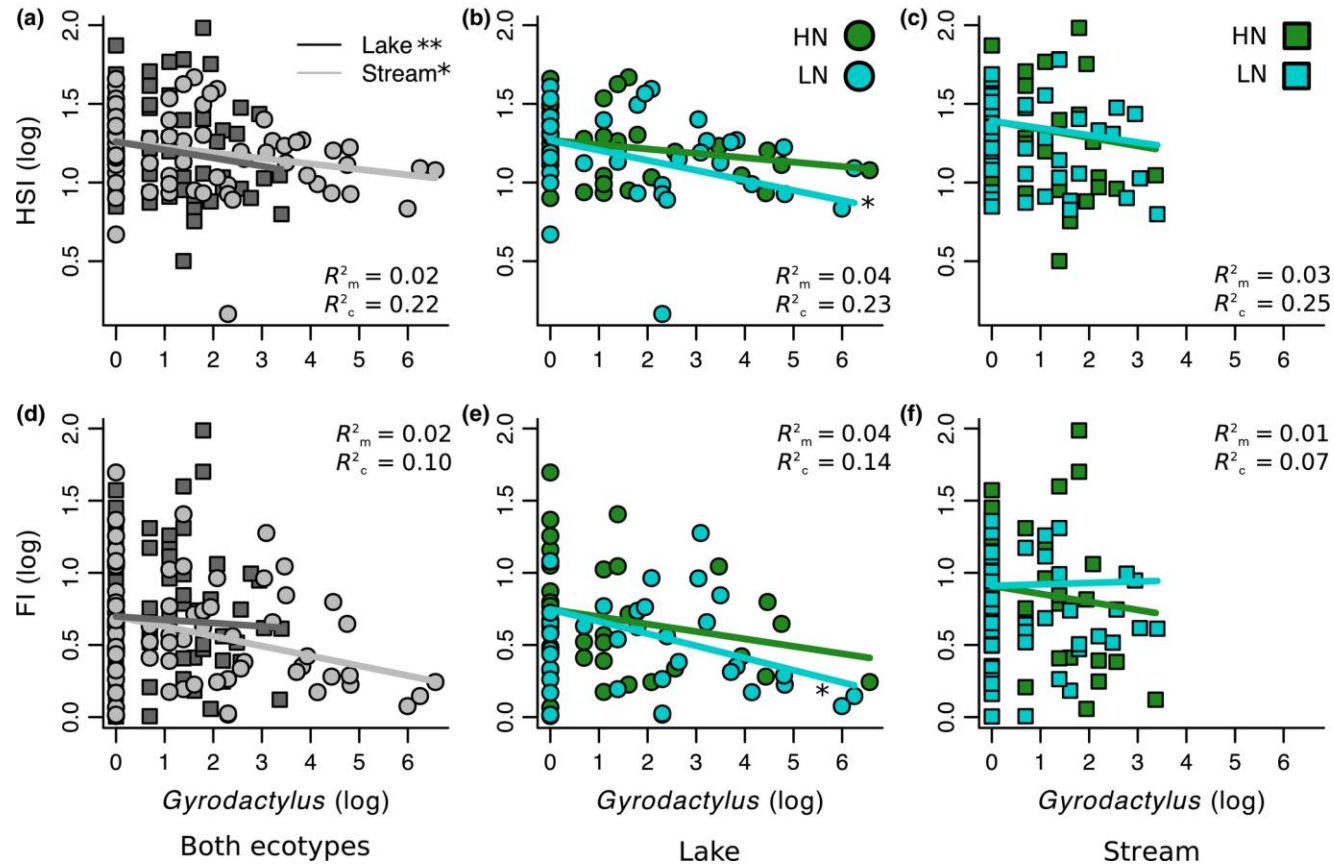
Stream	No Exposure (G-)	Exposure (G+)
High N	E= 6 fish	F= 6 fish
Low N	G= 6 fish	H= 6 fish

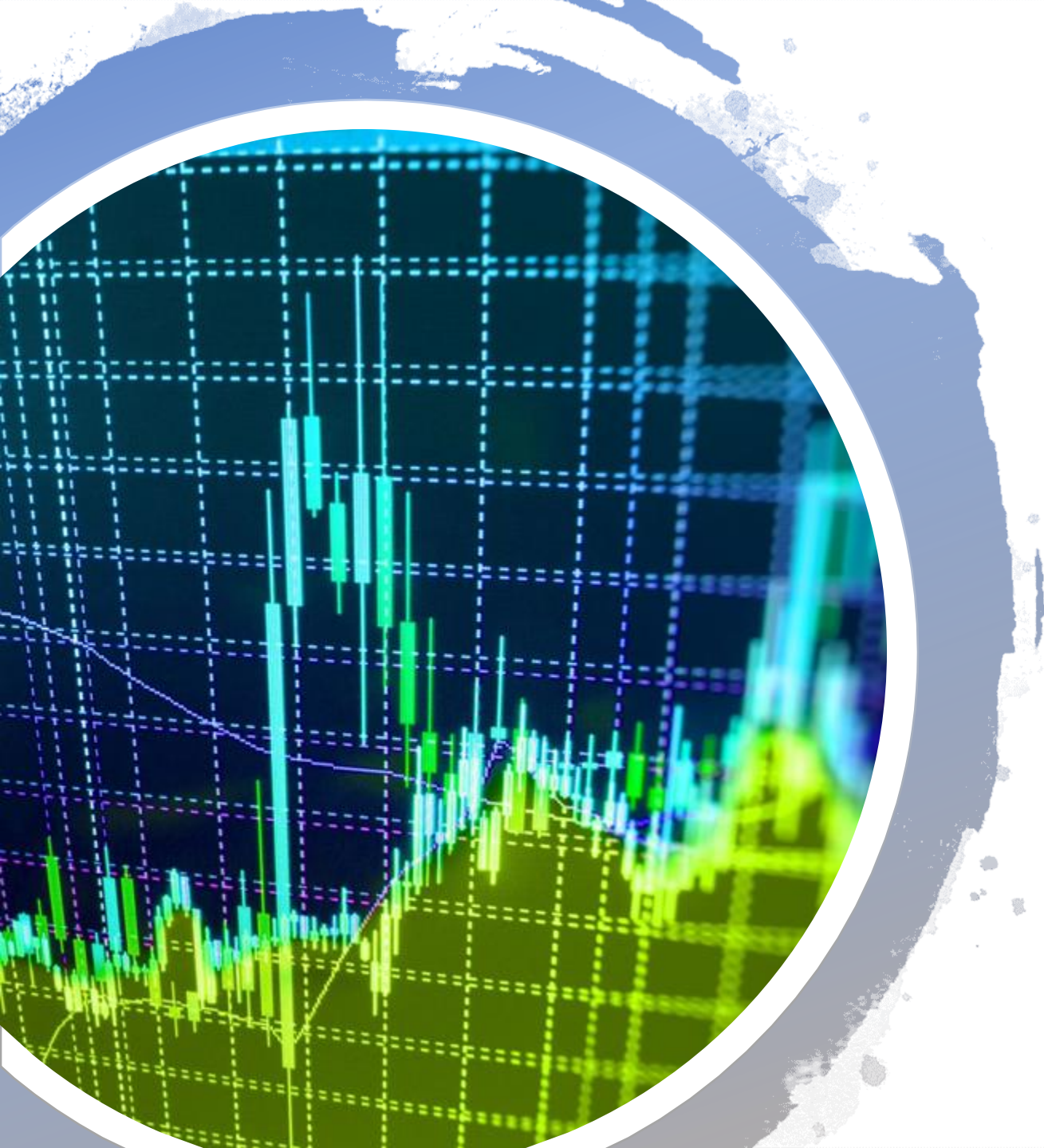


Effects of treatments on parasite load, fish condition, and diet

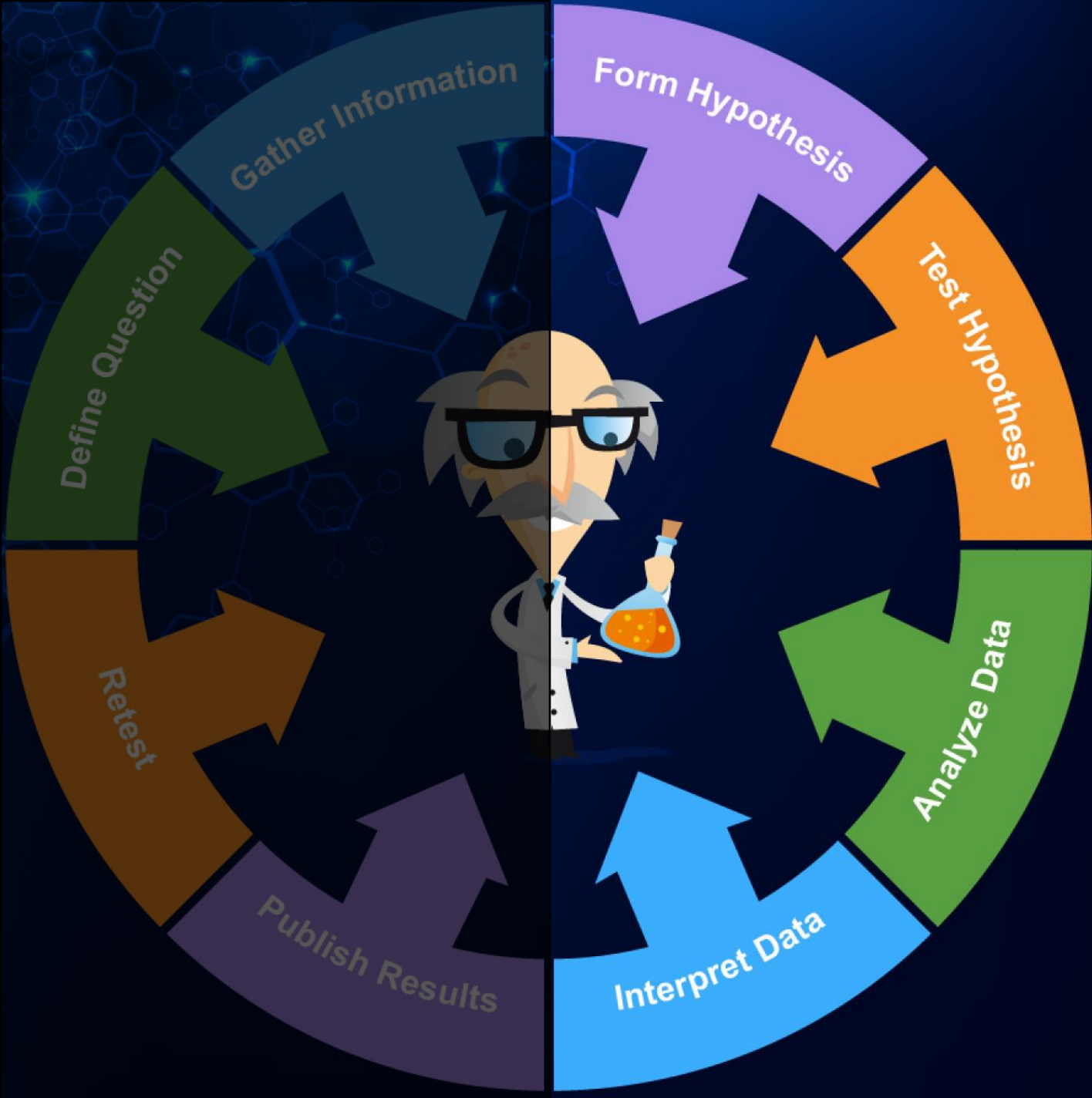


Effects of treatments of parasite load on fish condition and diet





Why to learn and do statistics?

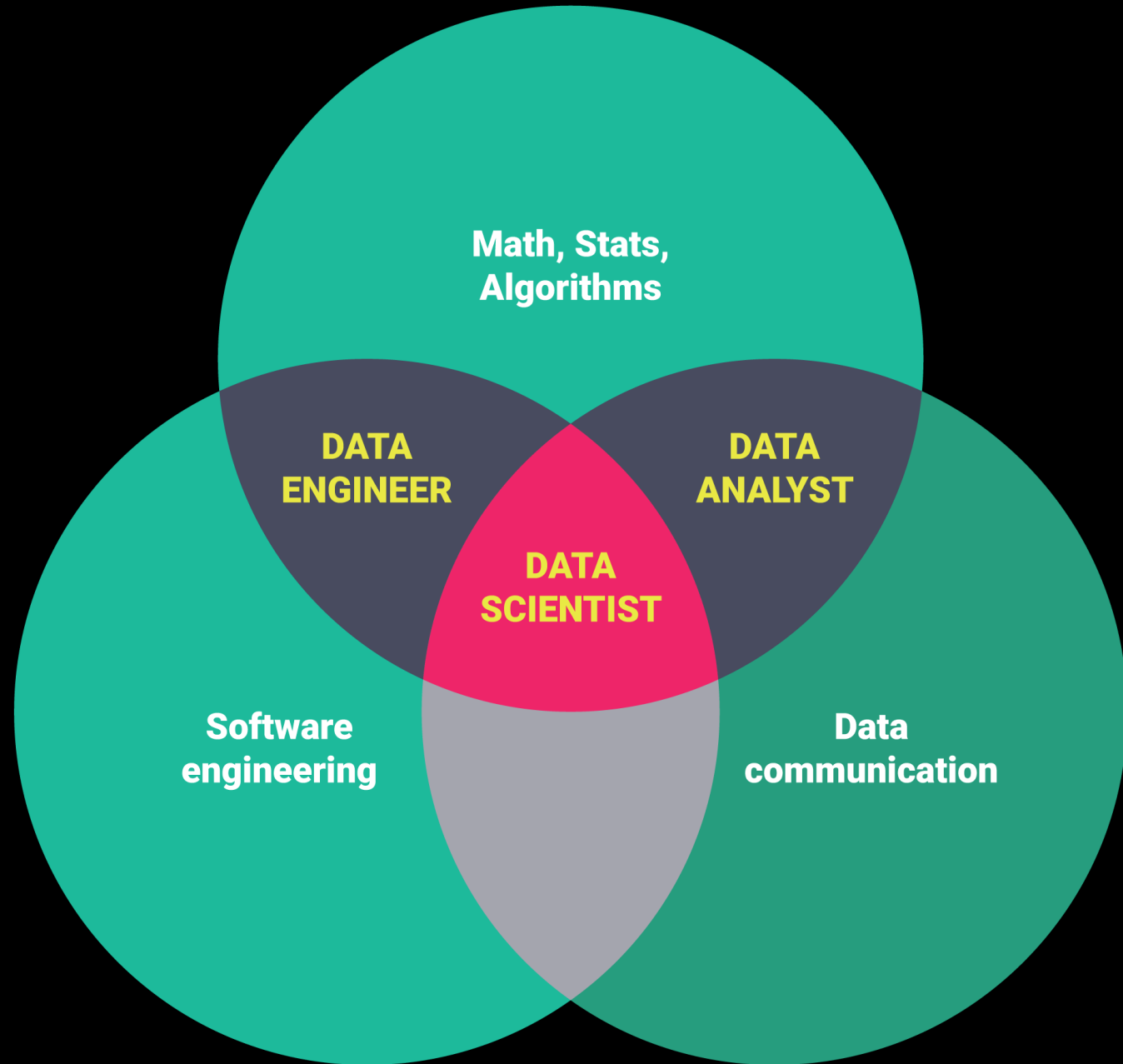


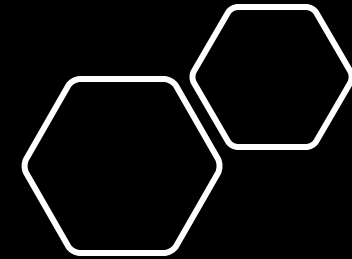
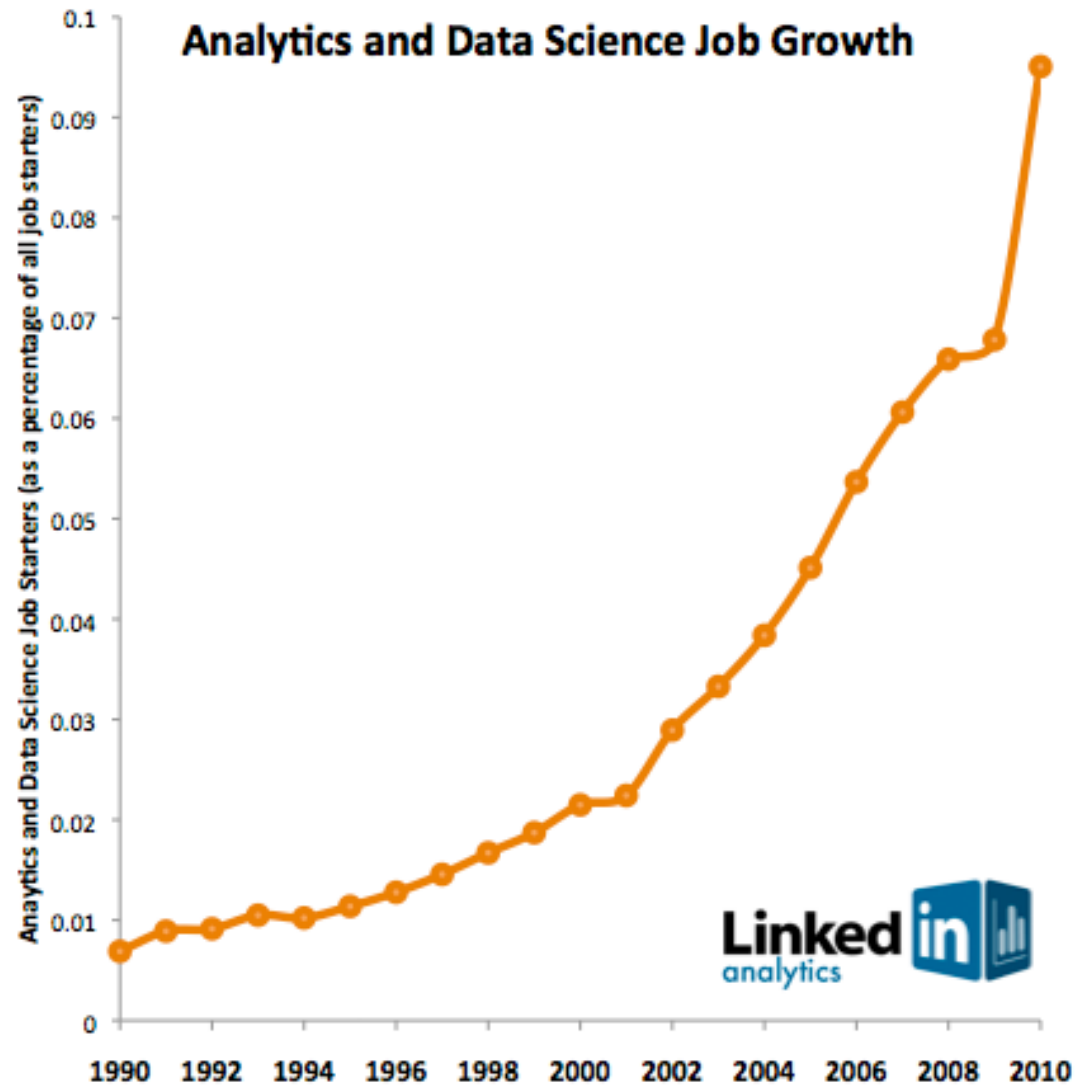
Experimentation and data analysis are key to the scientific process

Statistics are a tool to analyze data and quantitatively test hypothesis

Proper statistical inferences allows proper data interpretation

Sloppy statistical inference creates wrong interpretations





THE TYPICAL DATA SCIENTIST 2019

Predominantly Male
(69%)



8 years
in the workforce overall

Bilingual



Python/R
(73%)

2.3 years
as a Data Scientist



Master/PhD
(74%)





Introduction Bayesian statistics

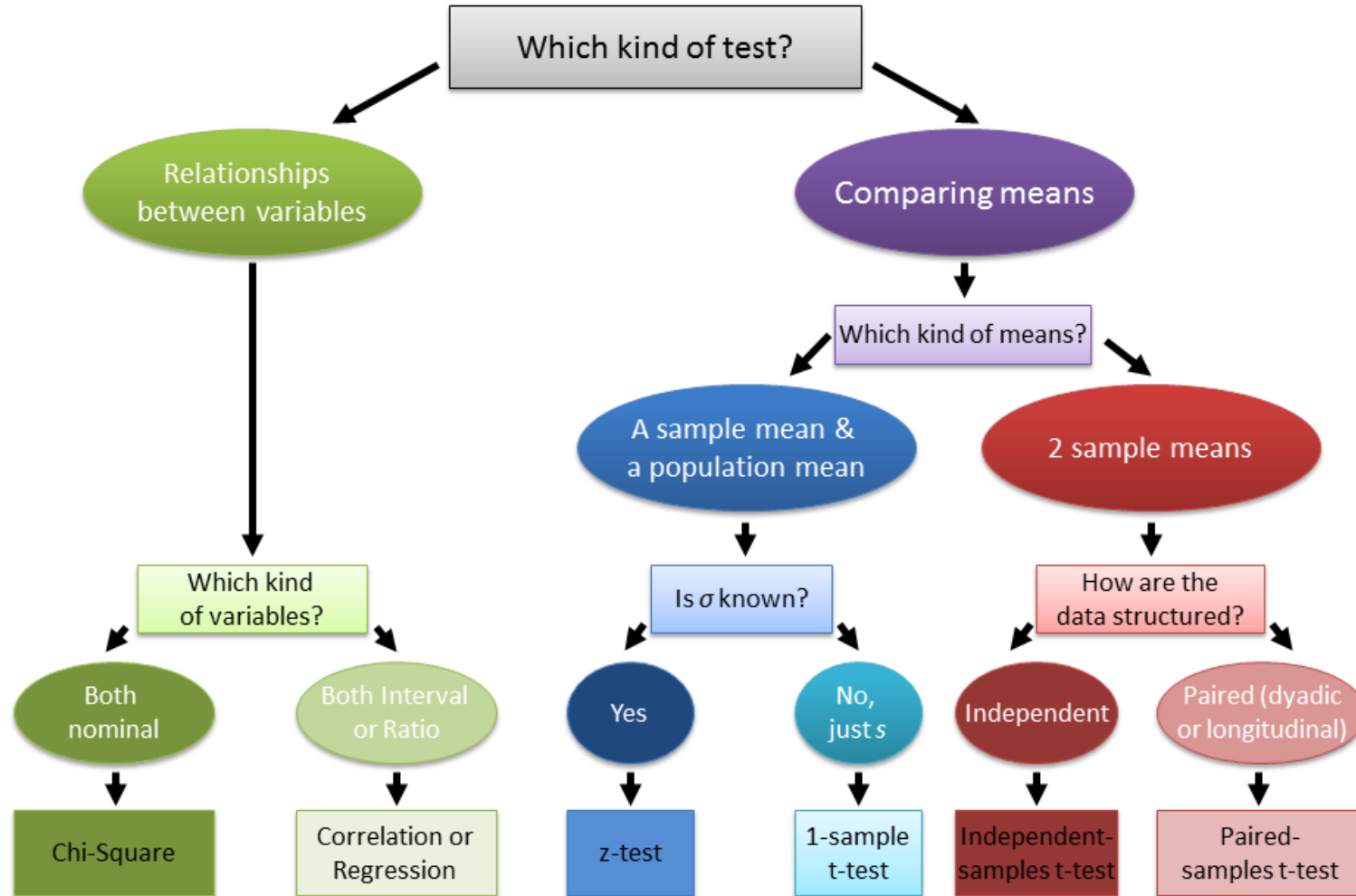
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Decision Tree



Classical statistical courses

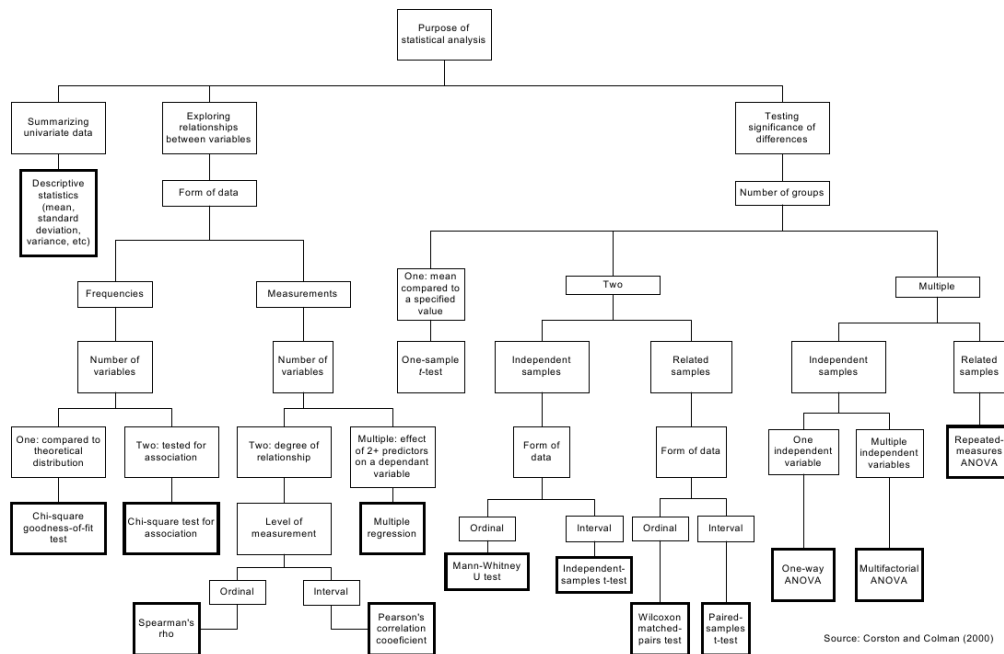
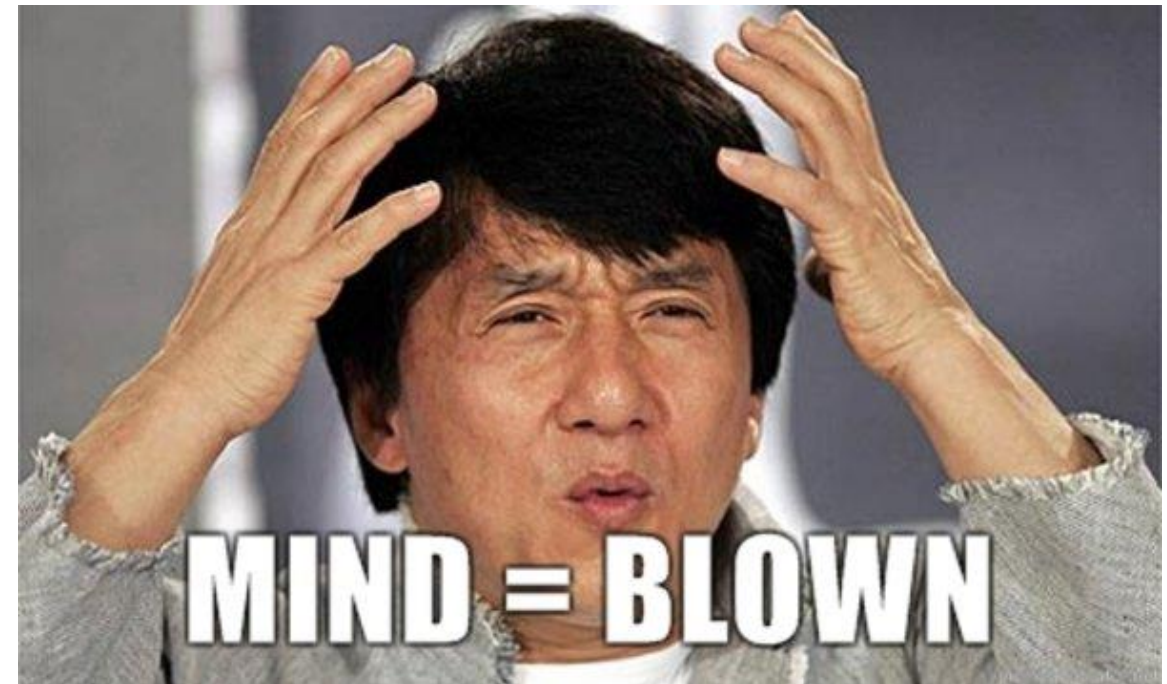


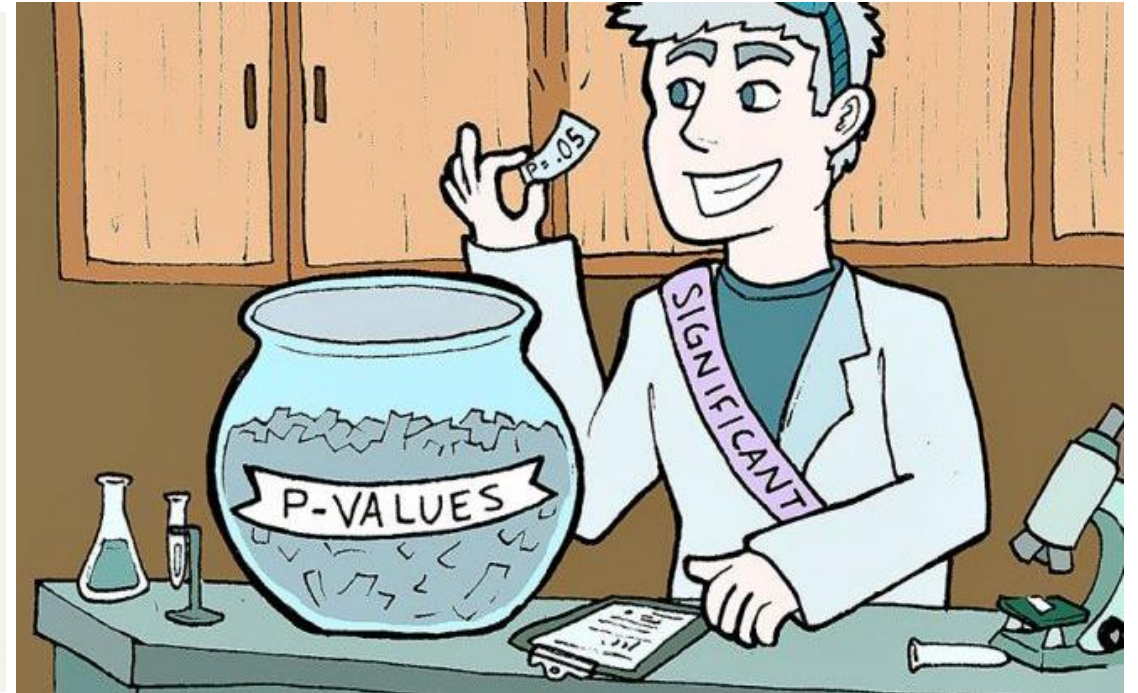
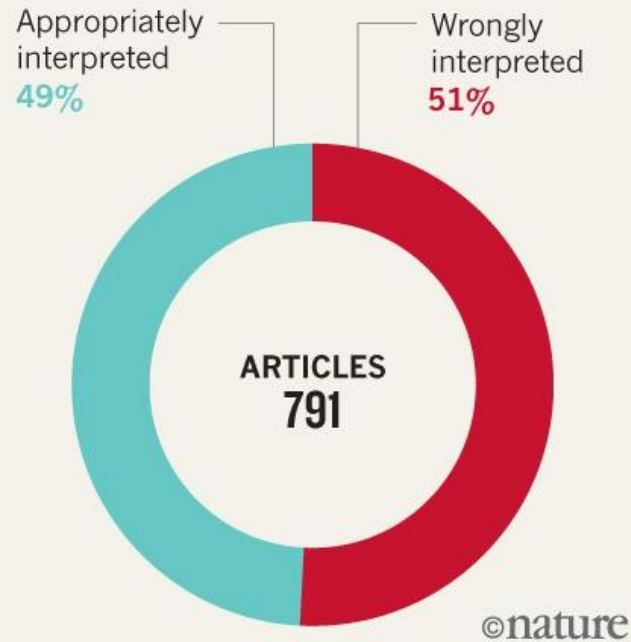
Figure 9. Choosing an appropriate statistical procedure



WRONG INTERPRETATIONS

An analysis of 791 articles across 5 journals* found that around half mistakenly assume non-significance means no effect.

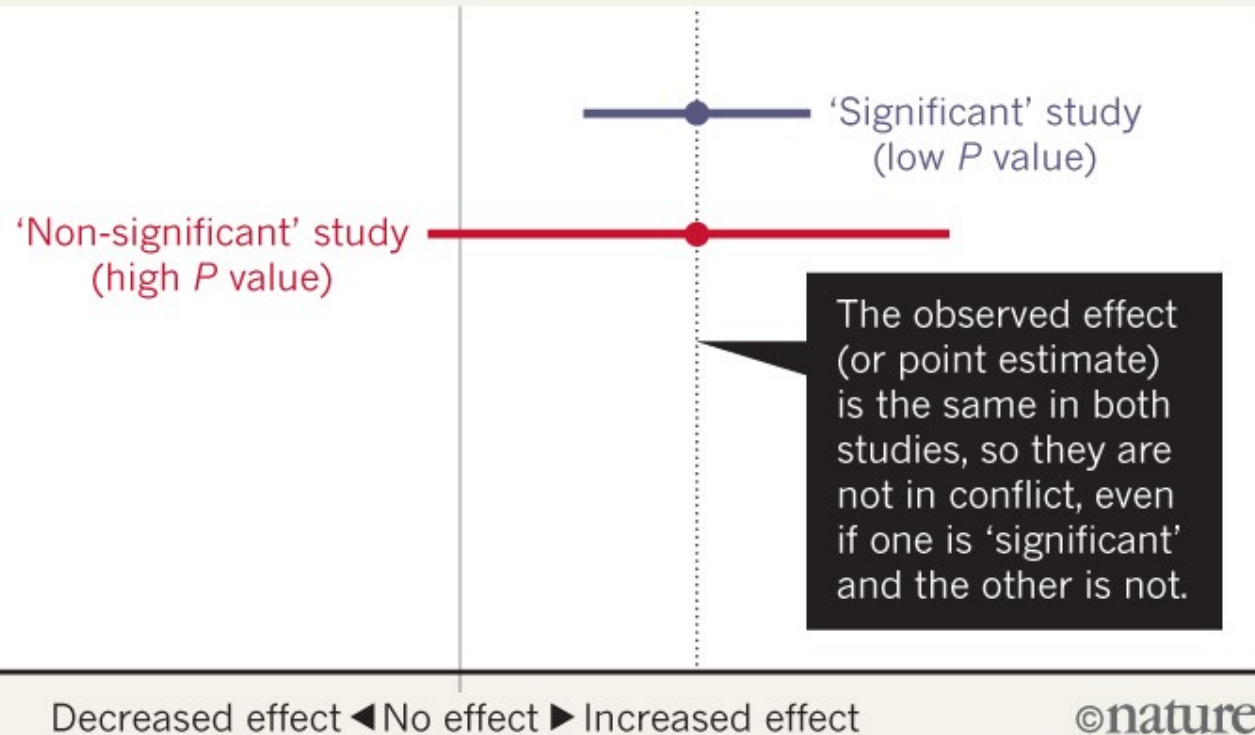
*Data taken from: P. Schatz et al. *Arch. Clin. Neuropsychol.* **20**, 1053–1059 (2005); F. Fidler et al. *Conserv. Biol.* **20**, 1539–1544 (2006); R. Hoekstra et al. *Psychon. Bull. Rev.* **13**, 1033–1037 (2006); F. Bernardi et al. *Eur. Sociol. Rev.* **33**, 1–15 (2017).

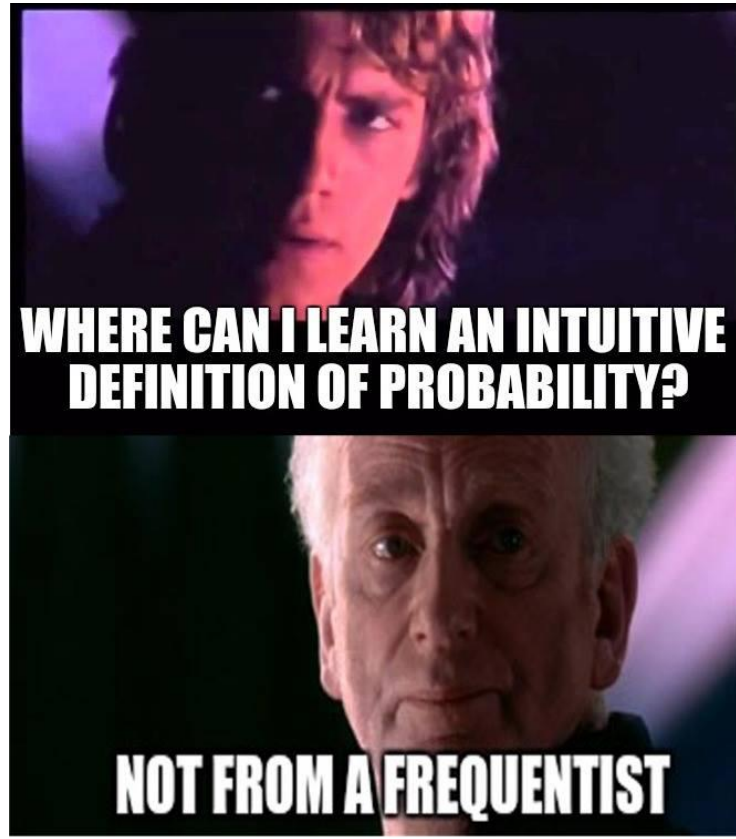


Significant or not significant? $\alpha < 0.05$

BEWARE FALSE CONCLUSIONS

Studies currently dubbed 'statistically significant' and 'statistically non-significant' need not be contradictory, and such designations might cause genuine effects to be dismissed.





No more p-values

What is Bayesian data analysis?

Use of probabilities to represent uncertainty in all parts of a statistical model



Information efficient but computational expensive



A method to figure out unknowns:

Data

A generative model

Priors

Understanding statistics

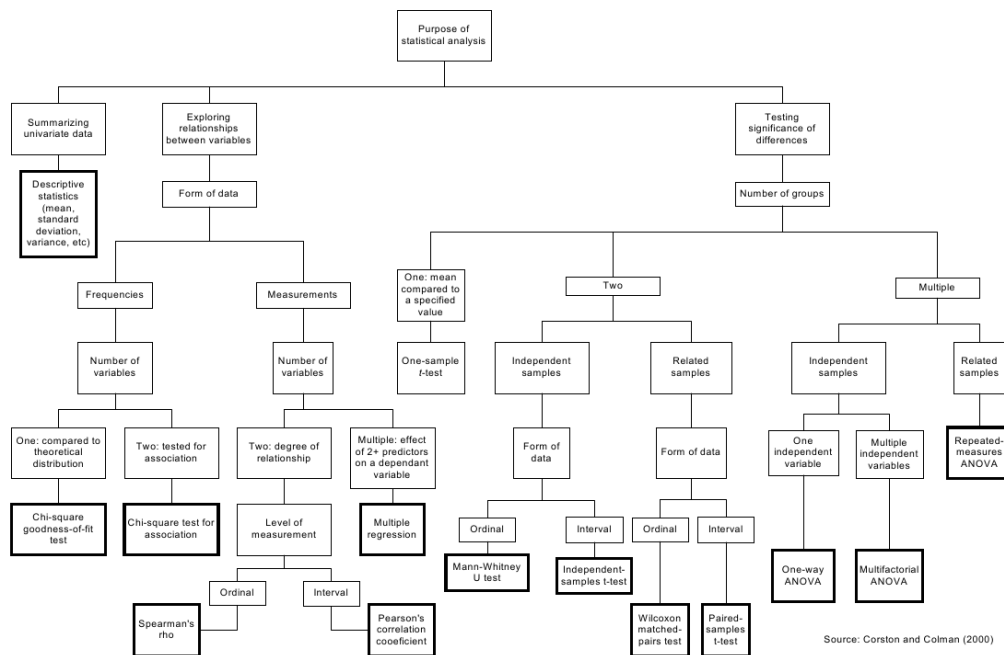


Figure 9. Choosing an appropriate statistical procedure

$$outcome \sim Normal(\mu_i, \sigma)$$

$$\mu_i = \beta x Predictor_i$$

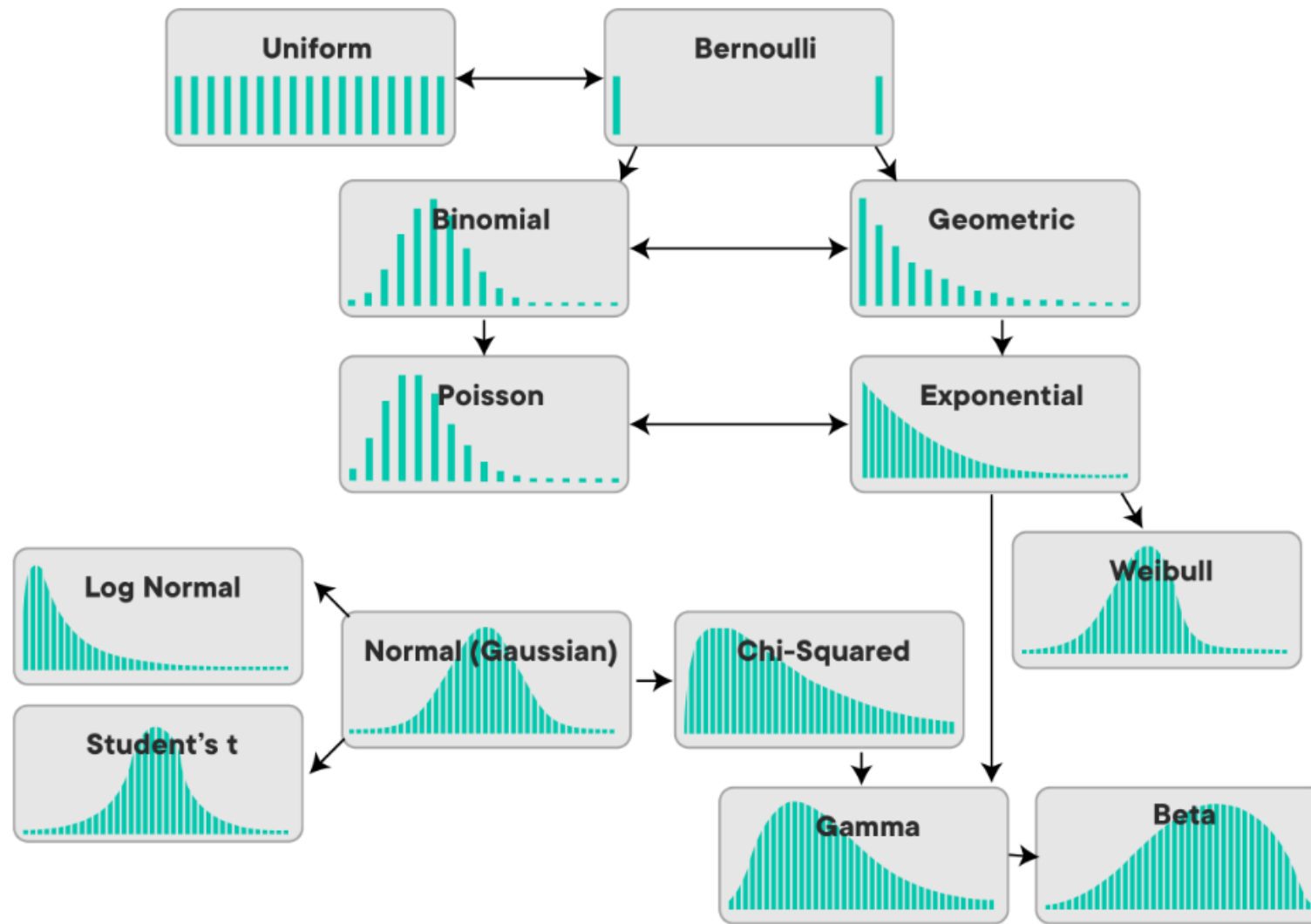
$$\beta \sim Normal(0, 10)$$

$$\sigma \sim HalfCauchy(0, 1)$$

A language for describing models:

1. ID the outcome variables
2. Define the likelihood distribution (e.g. Gaussian)
3. ID the predictors
4. Relate the predictors to the outcome
5. Choose your priors

outcome ~ *Normal*(μ_i, σ)
 $\mu_i = \beta x \text{Predictor}_i$
 β ~ *Normal*(0,10)
 σ ~ *HalfCauchy*(0,1)



Family
distributions

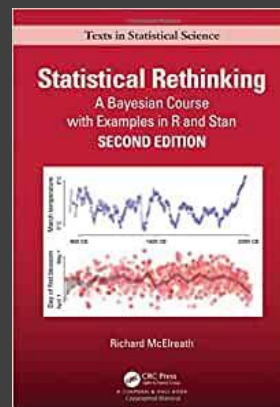
Running Bayesian statistics in R

1. Free, powerful, and efficient
2. You should know what you are doing
3. Keep your information for ever
4. Prefect for collaborations



Running Bayesian statistics in Stan

1. Free, powerful, and efficient
2. You should know what you are doing
3. Flexible



Partial census data for the Dobe area !Kung San. A foraging human population of the 20th century

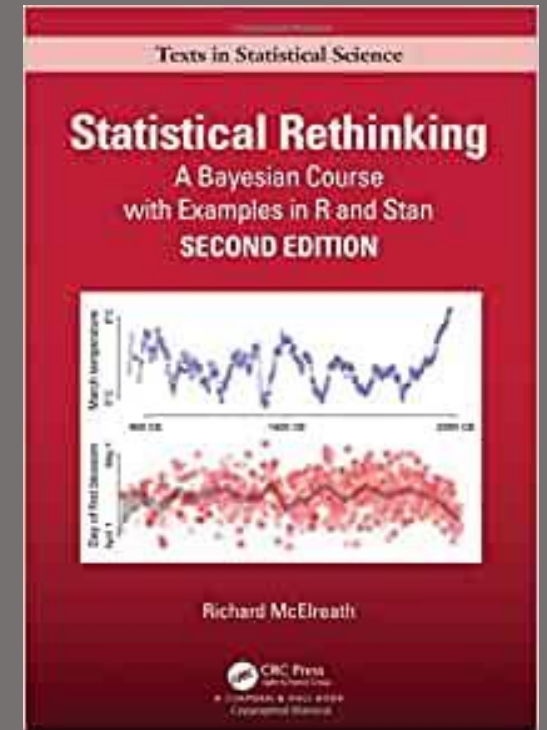
~/Dropbox/Muenster 2020-2026/R projects/Experimental |

> data

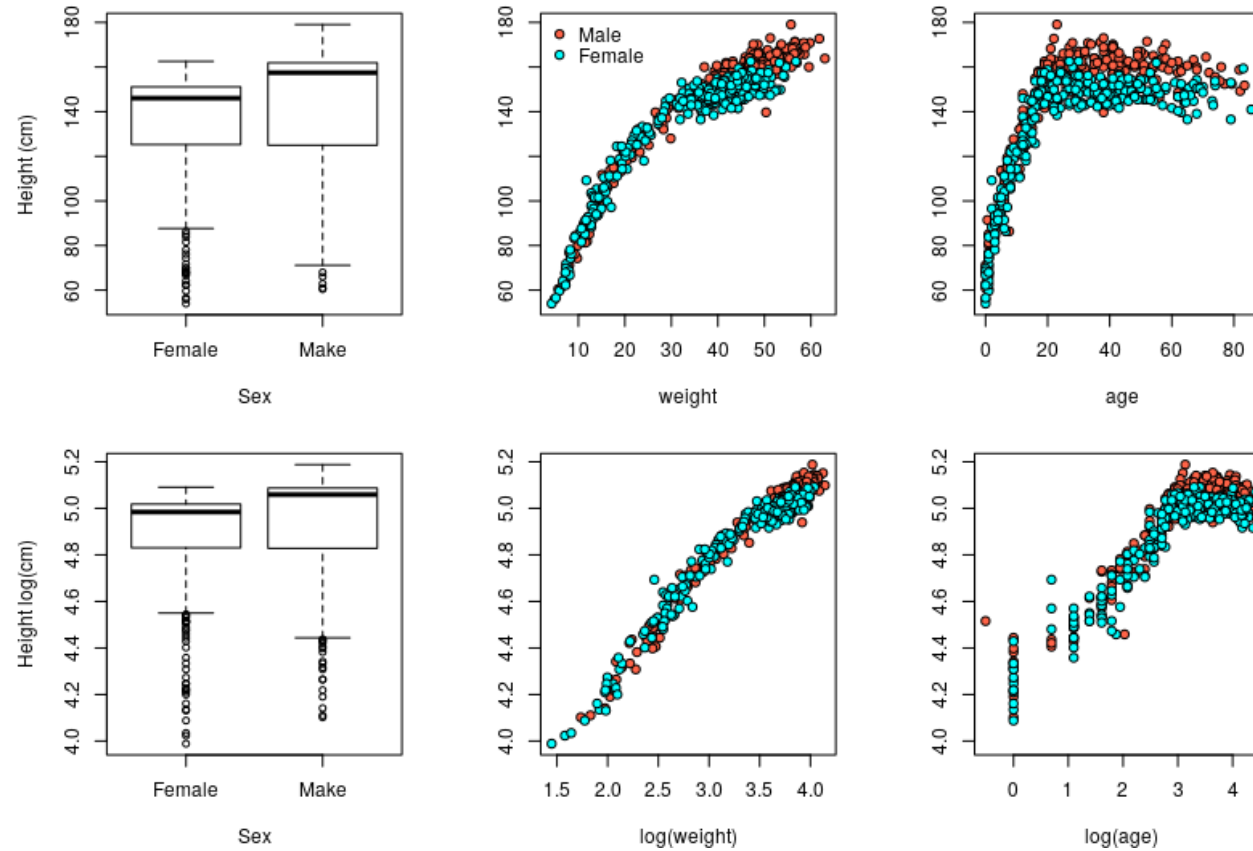
	height	weight	age	male
1	151.7650	47.825606	63.00	1
2	139.7000	36.485807	63.00	0
3	136.5250	31.864838	65.00	0
4	156.8450	53.041914	41.00	1
5	145.4150	41.276872	51.00	0
6	163.8300	62.992589	35.00	1
7	149.2250	38.243476	32.00	0
8	168.9100	55.479971	27.00	1
9	147.9550	34.869885	19.00	0
10	165.1000	54.487739	54.00	1
11	154.3050	49.895120	47.00	0
12	151.1300	41.220173	66.00	1
13	144.7800	36.032215	73.00	0
14	149.9000	47.700000	20.00	0
15	150.4950	33.849303	65.30	0
16	163.1950	48.562694	36.00	1
17	157.4800	42.325803	44.00	1
18	143.9418	38.356873	31.00	0
19	121.9200	19.617854	12.00	1
20	105.4100	13.947954	8.00	0



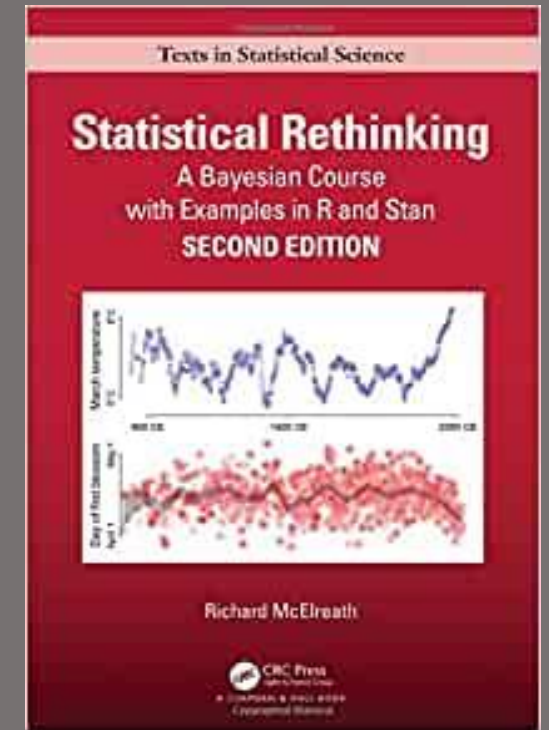
Howell data



Partial census data for the Dobe area !Kung San. A foraging human population of the 20th century



Howell data



Do men and women differ in body size?

Height \sim Normal(μ , σ) # likelihood

$\mu = \text{intercept} + \beta \times \text{male}$ # linear model

Intercept \sim Normal(0,10)

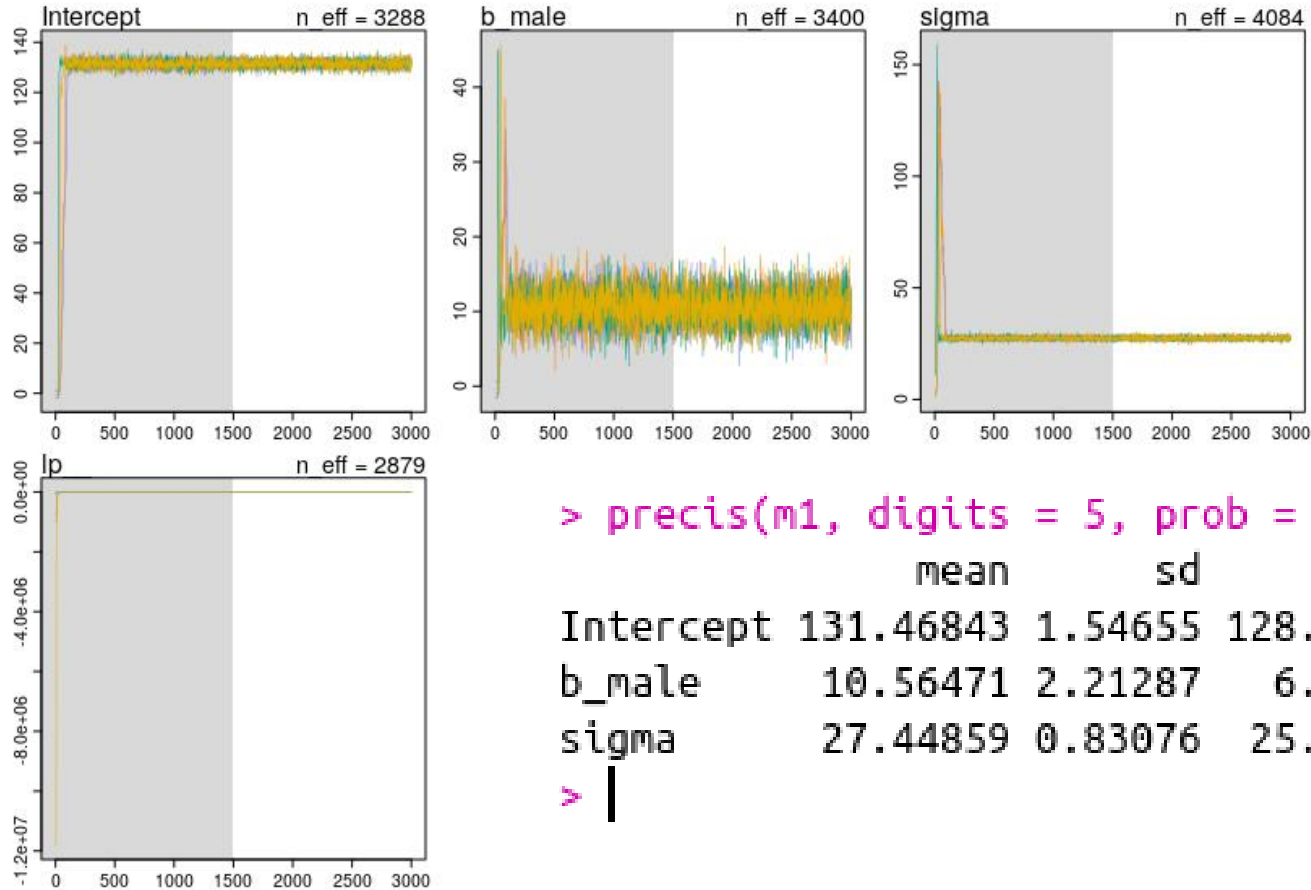
$\beta \sim$ Normal(0,10)

$\sigma \sim$ Normal(0,10)

```
# Run the model with the map2stan function from the rethinking package
m1 <- map2stan(
  alist(
    height ~ dnorm( mu , sigma ), # likelihood
    mu <- Intercept + b_male*male, # linear model
    Intercept ~ dnorm(0,10), # priors for intercept
    b_male ~ dnorm(0,10), # priors for the slope
    sigma ~ dcauchy(0,2) # priors for model error
  ), data = data, chains = 4, cores = 4, iter = 3000, warmup = 1500, WAIC = TRUE
)

tracerplot(m1)
precis(m1, digits = 5, prob = .95) # summary statistics with High Probability Densit
```


Check if the HMC chains converge



Rhat < 1.05

```
> precis(m1, digits = 5, prob = .95) # summary statistics with Hi
```

	mean	sd	2.5%	97.5%	n_eff	Rhat
Intercept	131.46843	1.54655	128.35394	134.42366	3288	1.00138
b_male	10.56471	2.21287	6.30106	14.90219	3400	1.00051
sigma	27.44859	0.83076	25.88773	29.13187	4084	1.00075

```
> |
```

Interprete your results and test the hypothesis

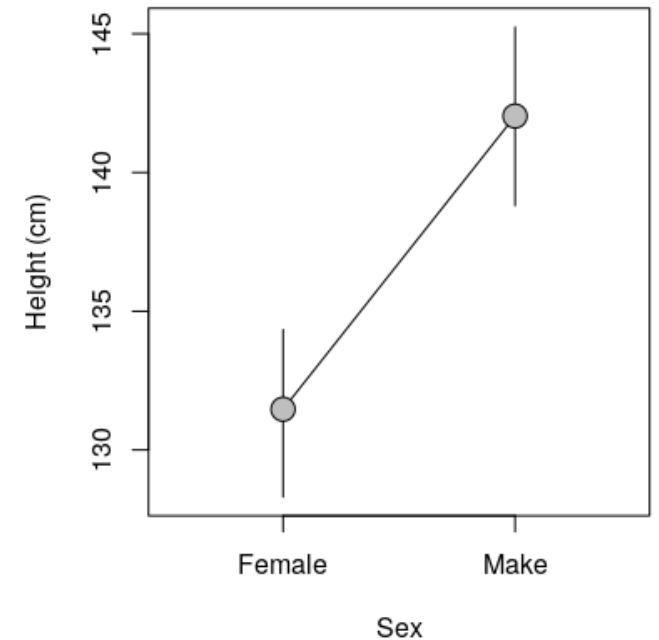
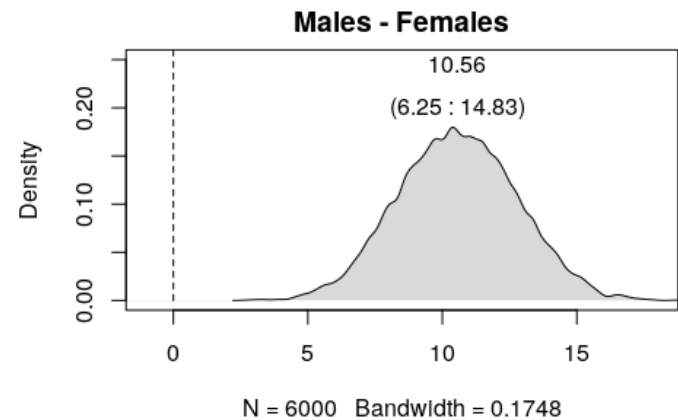
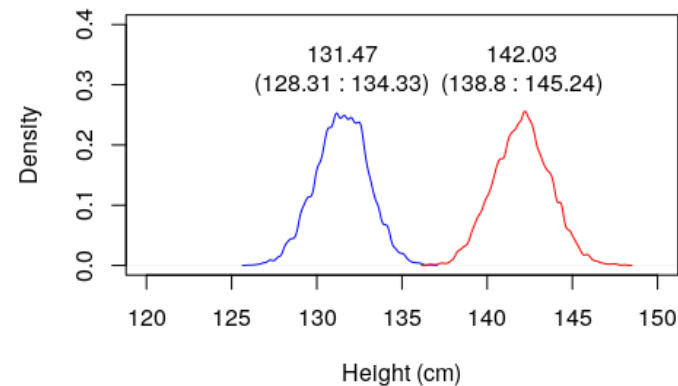
Males are taller than females with a ~100%

```
> precis(m1, digits = 5, prob = .95) # summary statistics with Hi
      mean      sd    2.5%   97.5% n_eff  Rhat
Intercept 131.46843 1.54655 128.35394 134.42366 3288 1.00138
b_male    10.56471 2.21287  6.30106 14.90219 3400 1.00051
sigma     27.44859 0.83076 25.88773 29.13187 4084 1.00075
> |
```

Intercept = predictions when all the response variables = 0.

```
~/Dropbox/Muenster 2020-2026/R projects/Experimental I
> data
  height  weight  age male
1  151.7650 47.825606 63.00  1
2  139.7000 36.485807 63.00  0
3  136.5250 31.864838 65.00  0
4  156.8450 53.041914 41.00  1
5  145.4150 41.276872 51.00  0
```

b_male = male effect = difference



How is it done in the frequentist way?

"Classical approach"

```
> summary(lm(height ~ male, data))
```

Call:
lm(formula = height ~ male, data = data)

Residuals:

Min	1Q	Median	3Q	Max
-81.87	-12.73	12.65	18.33	36.75

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	134.630	1.615	83.366	< 2e-16 ***
male	7.691	2.350	3.273	0.00113 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 27.36 on 542 degrees of freedom
Multiple R-squared: 0.01938, Adjusted R-squared: 0.01758
F-statistic: 10.71 on 1 and 542 DF, p-value: 0.001131

Bayesian approach

Bad priors

```
> precis(m1, digits = 5, prob = .95) # summary statistics with Hi
```

	mean	sd	2.5%	97.5%	n_eff	Rhat
Intercept	131.46843	1.54655	128.35394	134.42366	3288	1.00138
b_male	10.56471	2.21287	6.30106	14.90219	3400	1.00051
sigma	27.44859	0.83076	25.88773	29.13187	4084	1.00075

```
> |
```

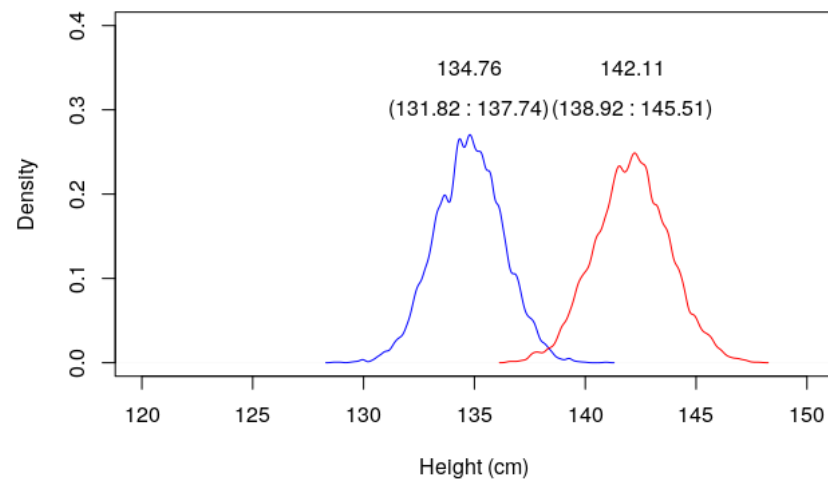
Good priors

```
> precis(m1, digits = 5, prob = .95) # summary statistics with H
```

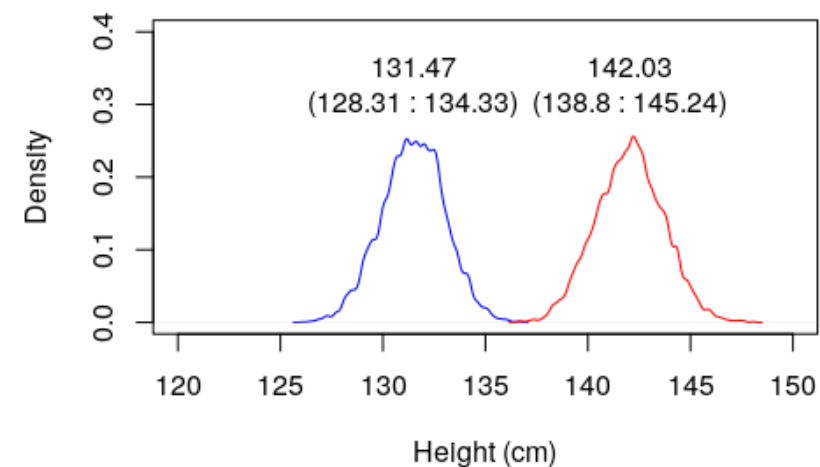
	mean	sd	2.5%	97.5%	n_eff	Rhat
Intercept	134.75950	1.52473	131.79127	137.72854	3668	1.00085
b_male	7.34556	2.26452	2.86005	11.71811	3614	1.00055
sigma	27.36680	0.82991	25.83096	29.04147	4335	1.00000

```
> |
```

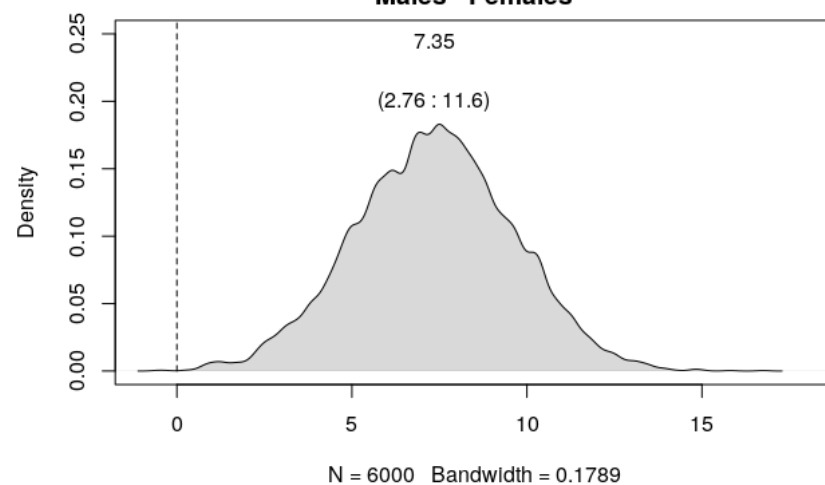
Good priors



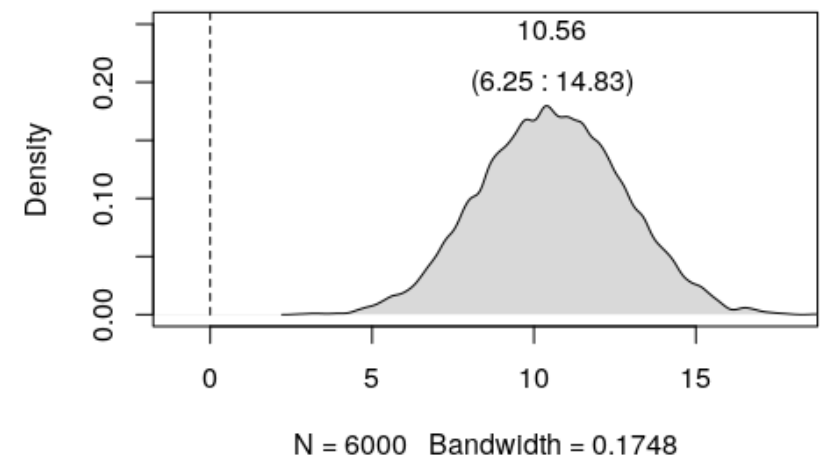
Bad priors



Males - Females



Males - Females



Height and weight relationship

```
data <- subset(data, age >= 18)
data$weight_c =(data$weight) - 45 # center at 30 kg

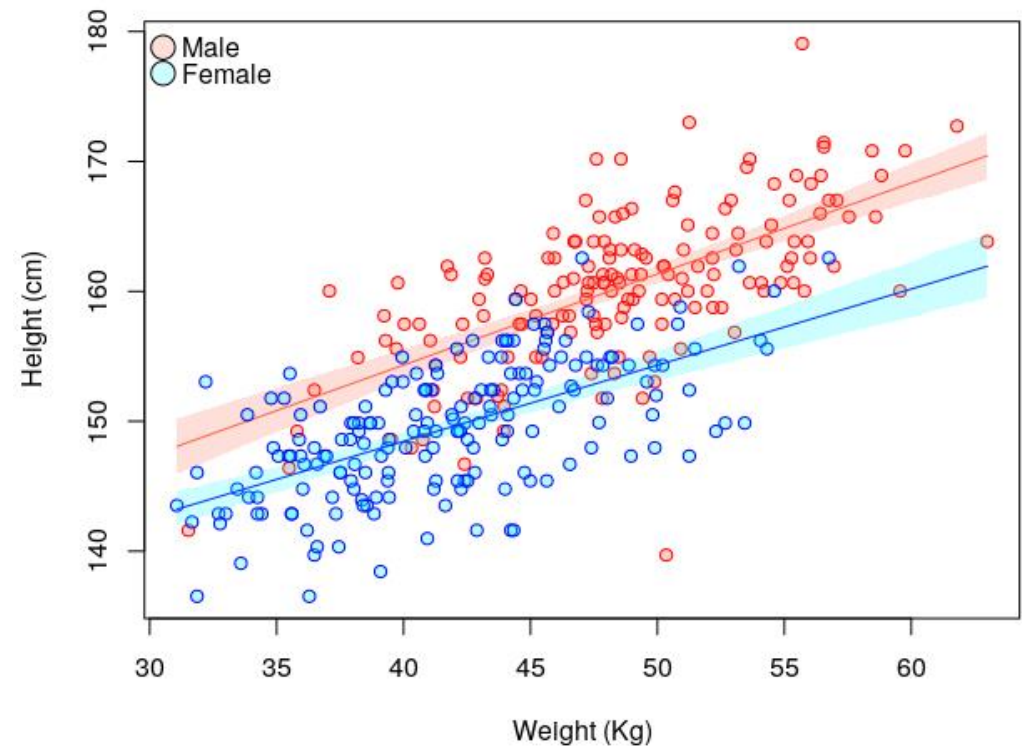
plot(data$height ~ data$weight)

m2 <- map2stan(
  alist(
    height ~ dnorm( mu , sigma ), # likelihood
    mu <- Intercept + b_weight*weight_c + b_male*male + b_WxM * (weight_c*male), # line
    Intercept ~ dnorm(134,100), # priors for intercept
    b_male ~ dnorm(0,10), # priors for the slope
    b_weight ~ dnorm(0,10), # priors for the slope
    b_WxM ~ dnorm(0,10), # priors for the slope
    sigma ~ dcauchy(0,10) # priors for model error
  ), data = data, chains = 4, cores = 4, iter = 3000, warmup = 1500, WAIC = TRUE
)
```

```
> precis(m2, digits = 5, prob = .95, depth = 2) # summary stats
```

	mean	sd	2.5%	97.5%	n_eff	Rhat
Intercept	151.38655	0.36098	150.67991	152.10977	3339	1.00036
b_male	6.45558	0.53269	5.40797	7.52473	3692	0.99983
b_weight	0.58522	0.05823	0.46971	0.69881	3251	1.00104
b_WxM	0.11454	0.08252	-0.04421	0.27869	3557	1.00129
sigma	4.27916	0.16323	3.97619	4.61445	4359	1.00087

```
> |
```



Evaluate model fit

