

Linear Regression

with Categories

Incorporating Categories

Categories

- Goal: Model causes that are not continuous

Categories

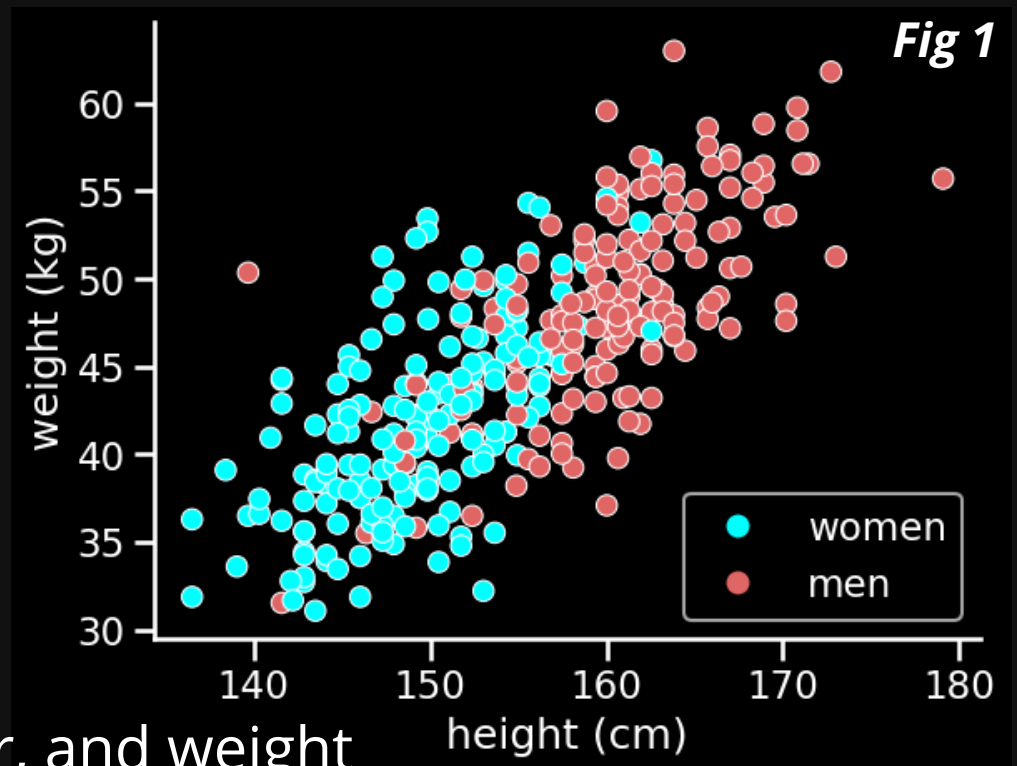
- Goal: Model causes that are not continuous
- Categories: discrete, unordered types

Categories

- Goal: Model causes that are not continuous
- Categories: discrete, unordered types
- Approach: **stratify** by categories

Categories

- Goal: Model causes that are not continuous
- Categories: discrete, unordered types
- Approach: **stratify** by categories
 - fit separate line for each category



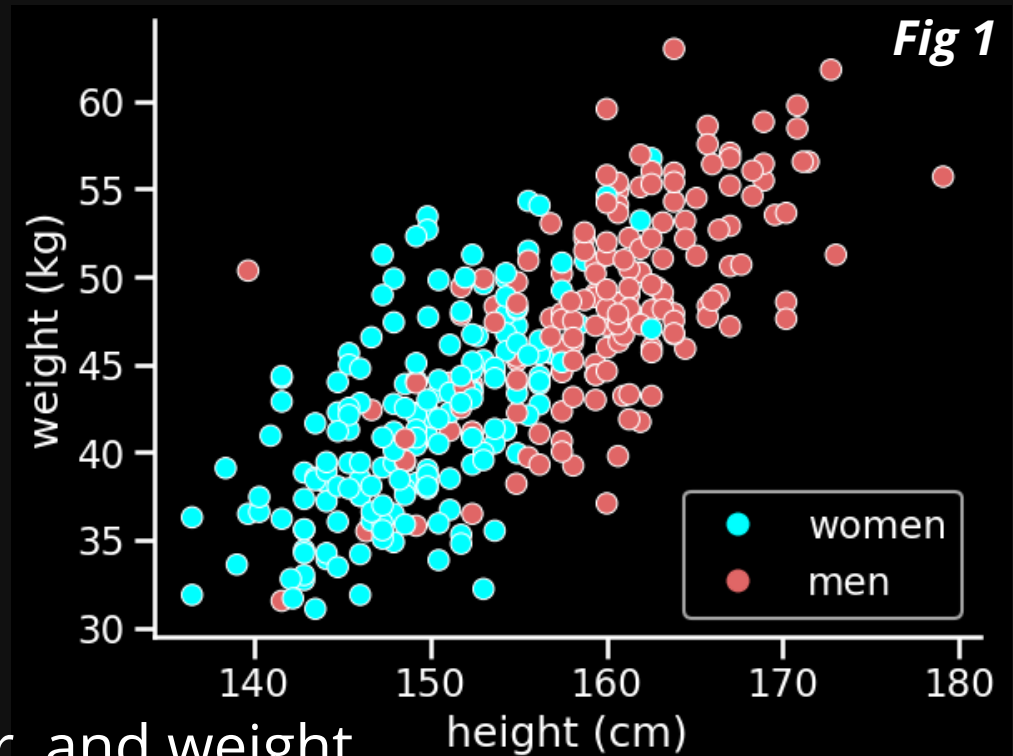
Adult height, gender, and weight

```
import pandas as pd
```

Code 1

```
df = pd.read_csv(  
    "Data/Howell1.csv",  
    sep=';',  
    header=0  
)  
df2 = df[df.age >= 18]  
df2.head()
```

	height	weight	age	male
0	151.765	47.825606	63.0	1
1	139.700	36.485807	63.0	0
2	136.525	31.864838	65.0	0
3	156.845	53.041914	41.0	1
4	145.415	41.276872	51.0	0



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Code 1

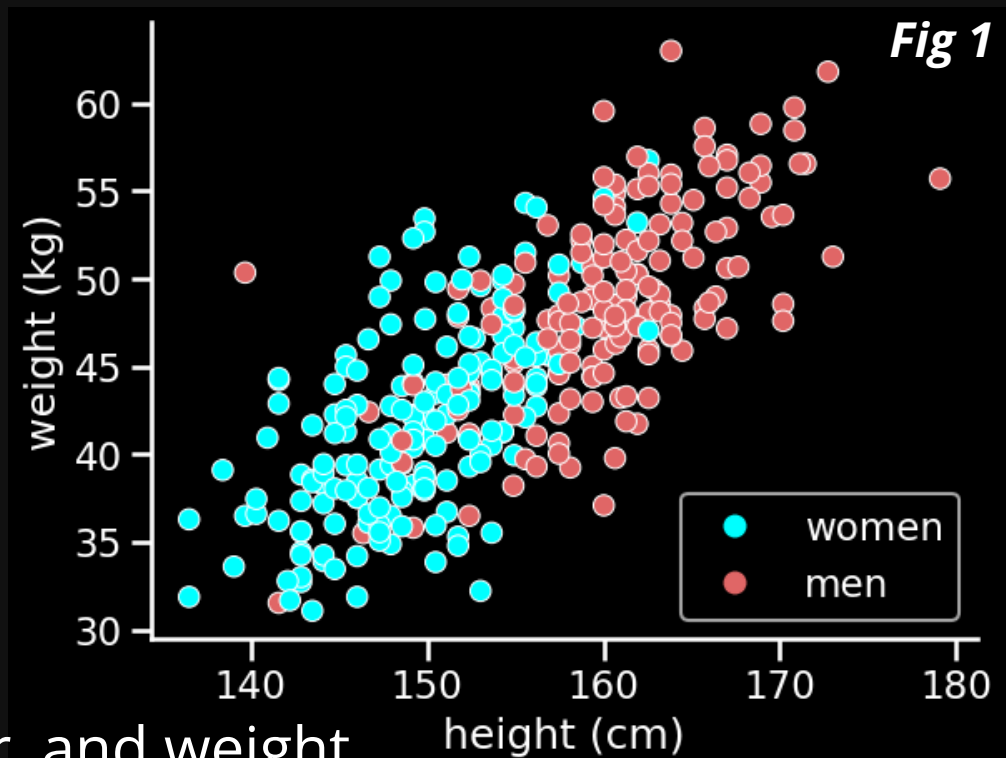
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```
import seaborn as sns  
from matplotlib.lines import Line2D
```

Code 2

```
ax = sns.scatterplot(data=df2, x="height", y="weight", hue="male",  
    palette=["cyan", "#e06666"]  
)  
  
custom = [Line2D([], [], marker='o', color="cyan", linestyle='None'),  
    Line2D([], [], marker='o', color="#e06666", linestyle='None')]  
  
_ = plt.legend(custom, ['women', 'men'], loc='lower right')  
  
_ = ax.set_xlabel("height (cm)")  
_ = ax.set_ylabel("weight (kg)")
```



Adult height, gender, and weight

generates points

- uses **height** column for x values
- uses **weight** column for y values
- uses **male** column to color ("hue") points

```
import pandas as pd
```

Code 1

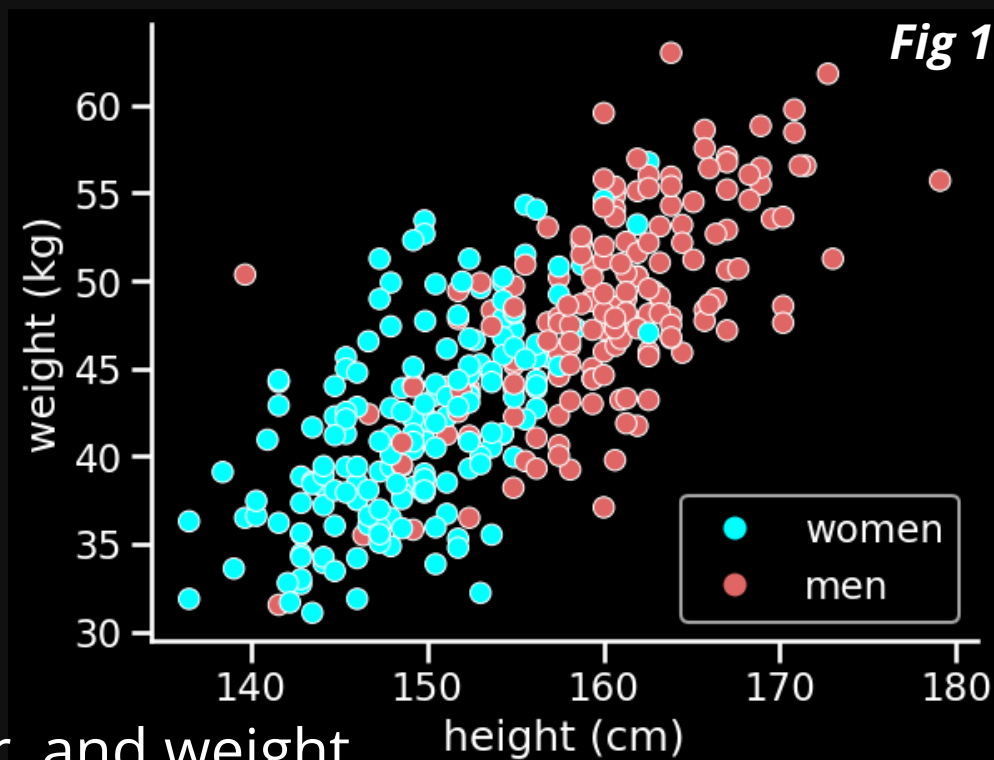
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Adult height, gender, and weight

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)
df2 = df[df.age >= 18]
df2.head()
```

Code 1

custom provides specifications for legend

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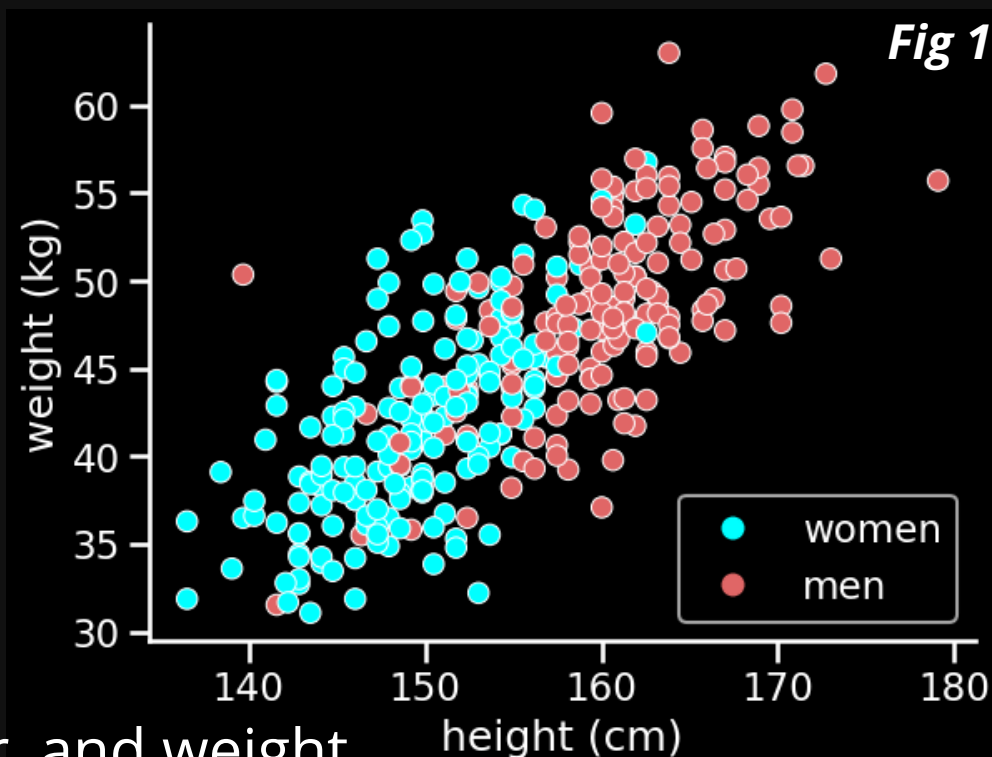
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Adult height, gender, and weight

Think scientifically first

How are height, gender, and weight ***causally*** related?

Think scientifically first

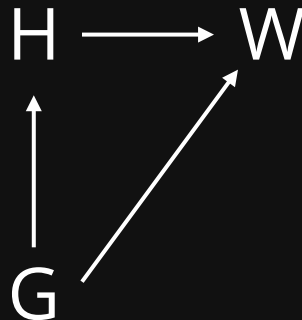
How are height, gender, and weight ***causally*** related?

How are height, gender, and weight ***statistically*** related?

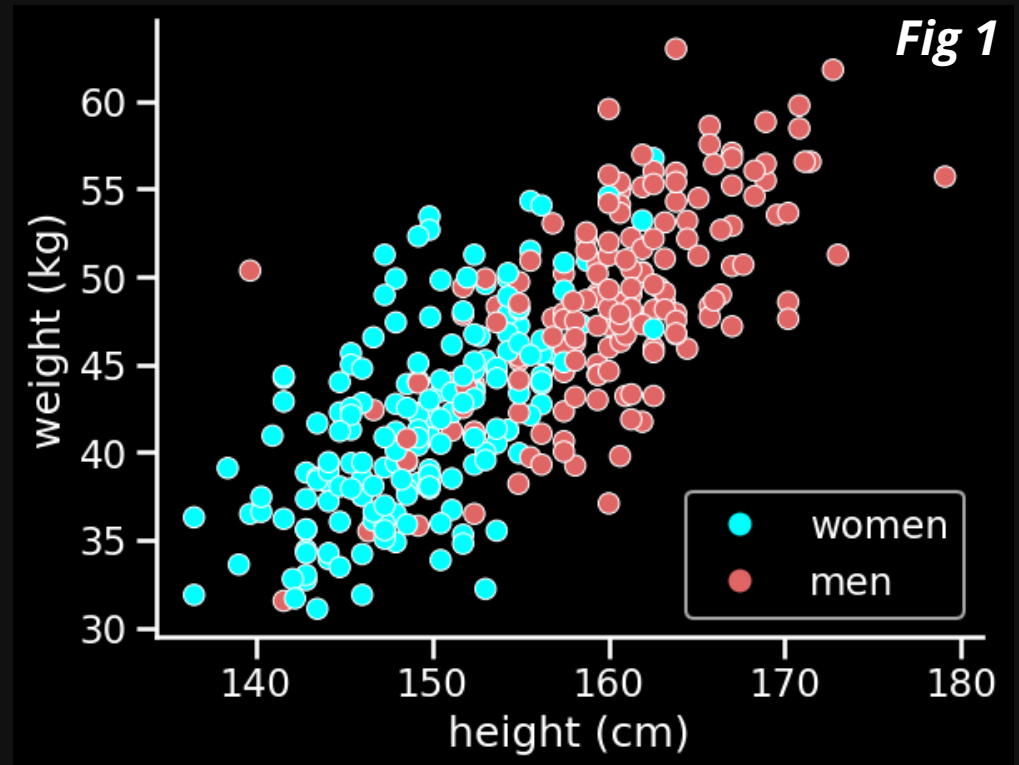
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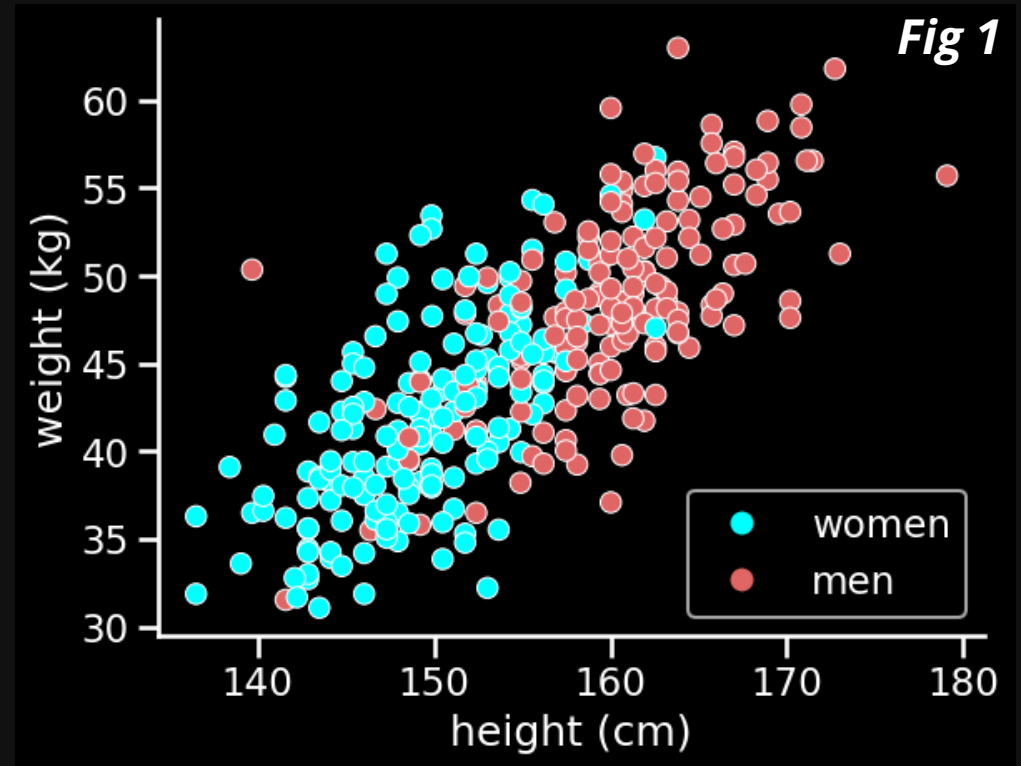


Causes are not included in data



Causes are not included in data

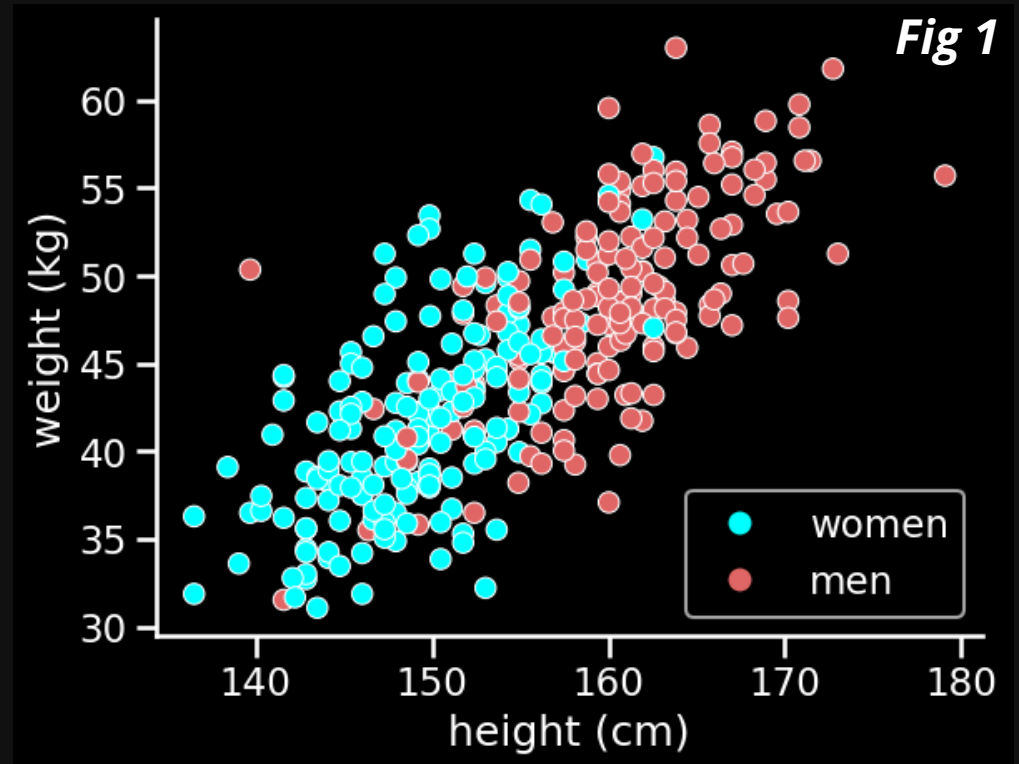
H \longrightarrow W



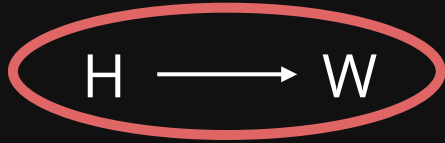
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H → W

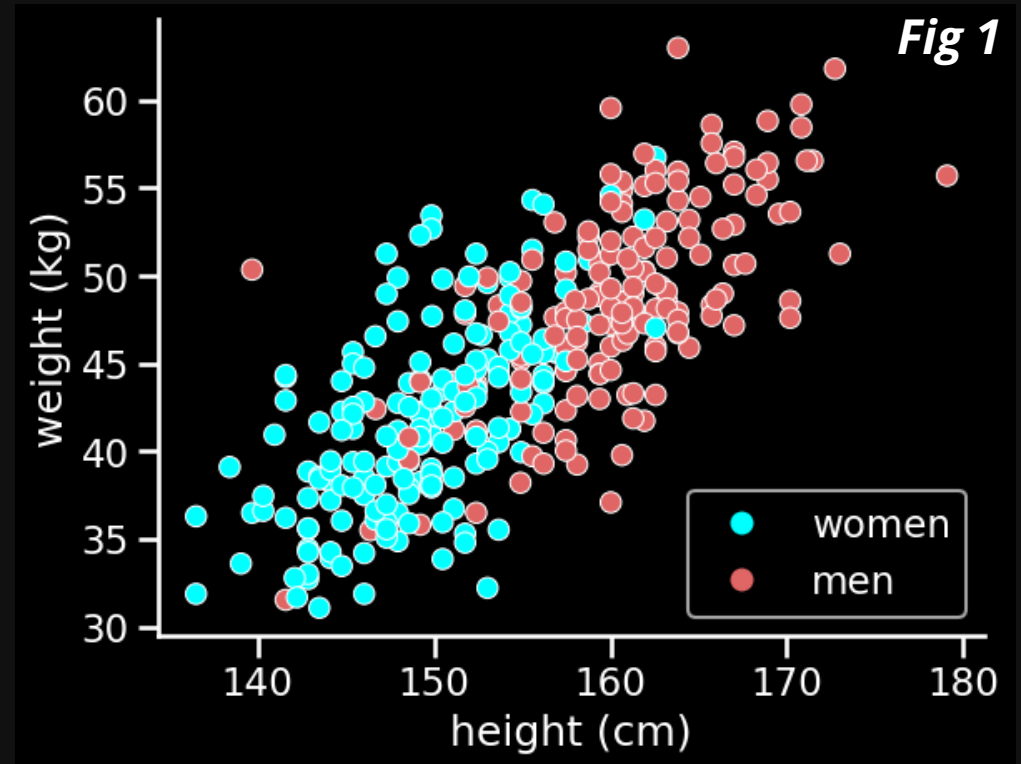
H ← W



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H ← W



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_ = ax.set_xlabel("height (cm)")  
_ = ax.set_ylabel("density")  
_ = sns.despine()
```

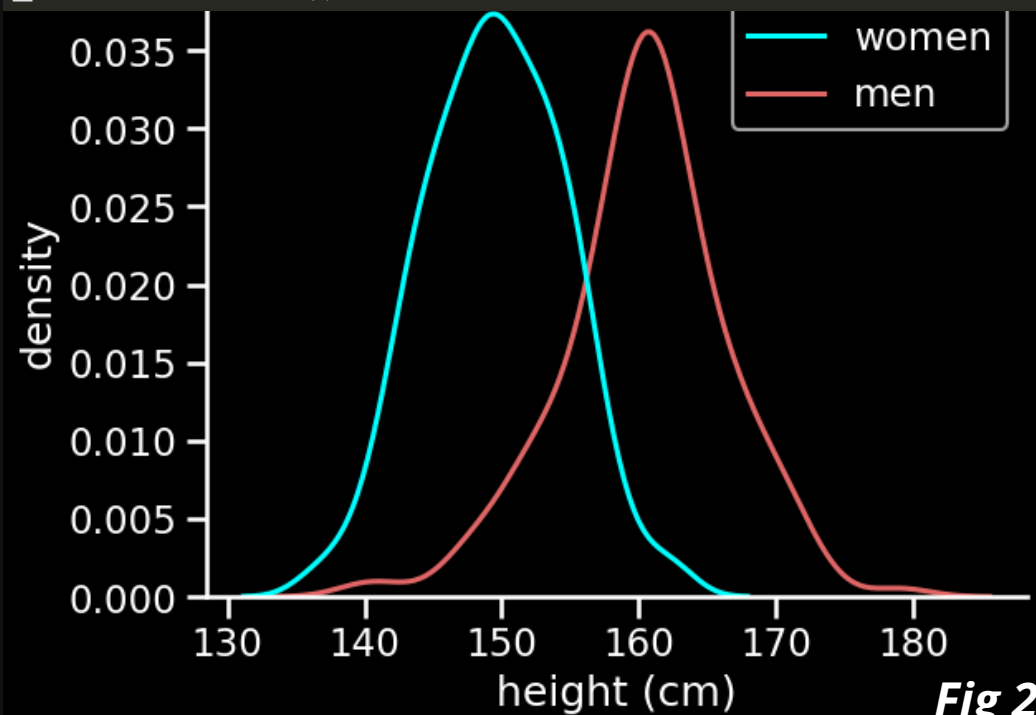


Fig 2

Causes are not included in data

H \longrightarrow G

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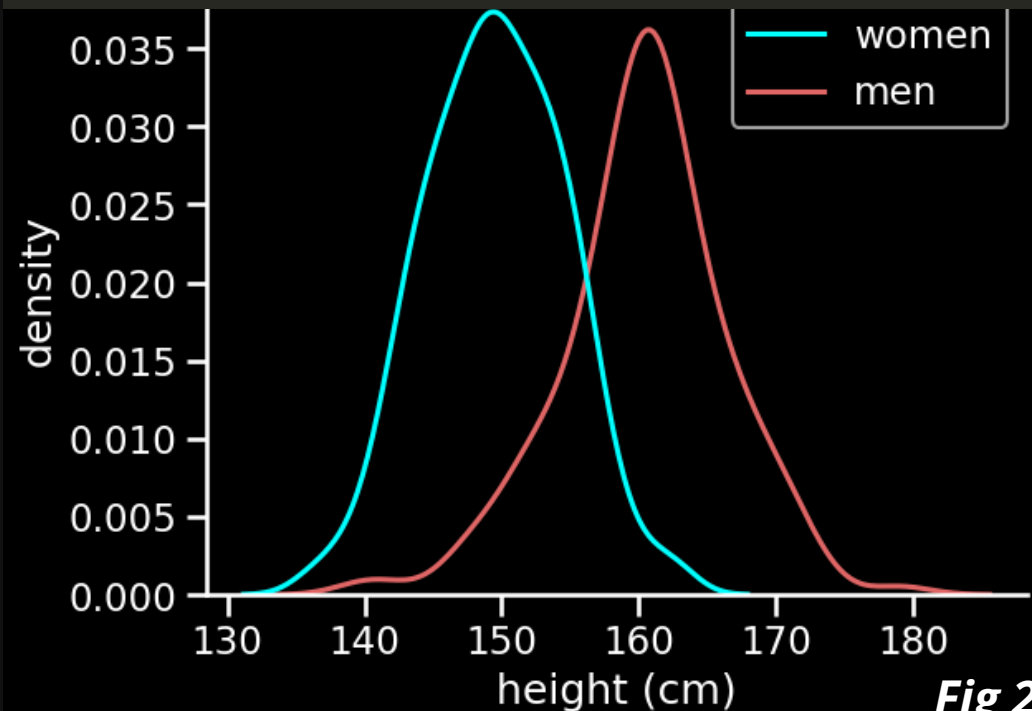


Fig 2

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H \longrightarrow G

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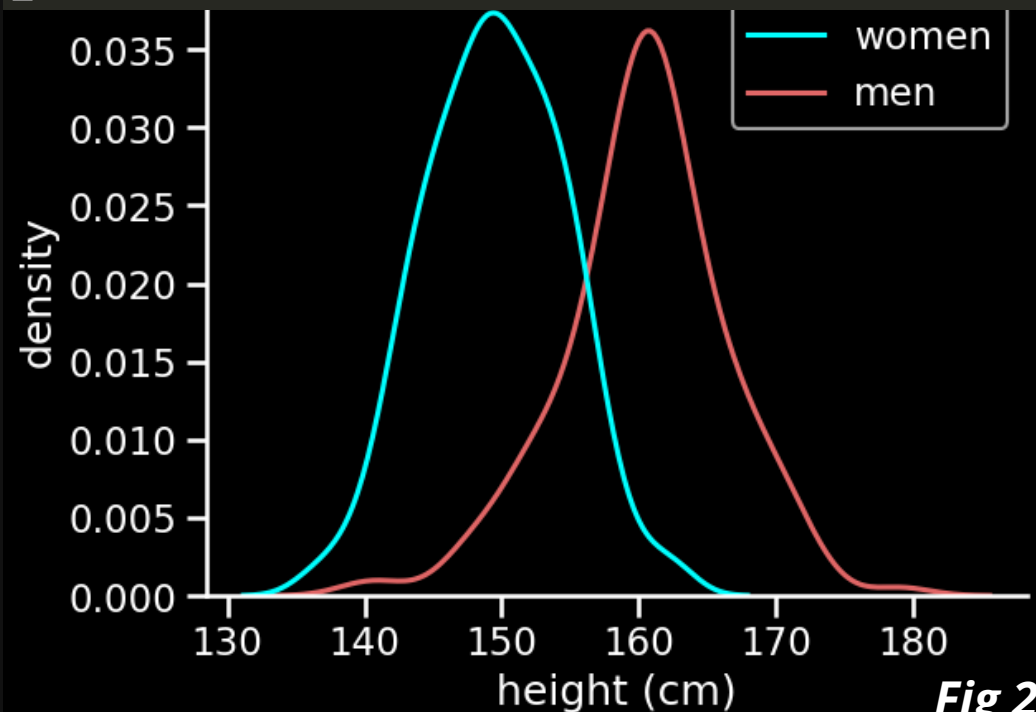
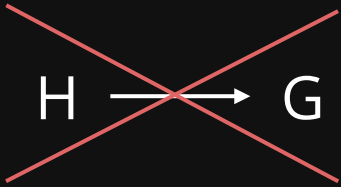


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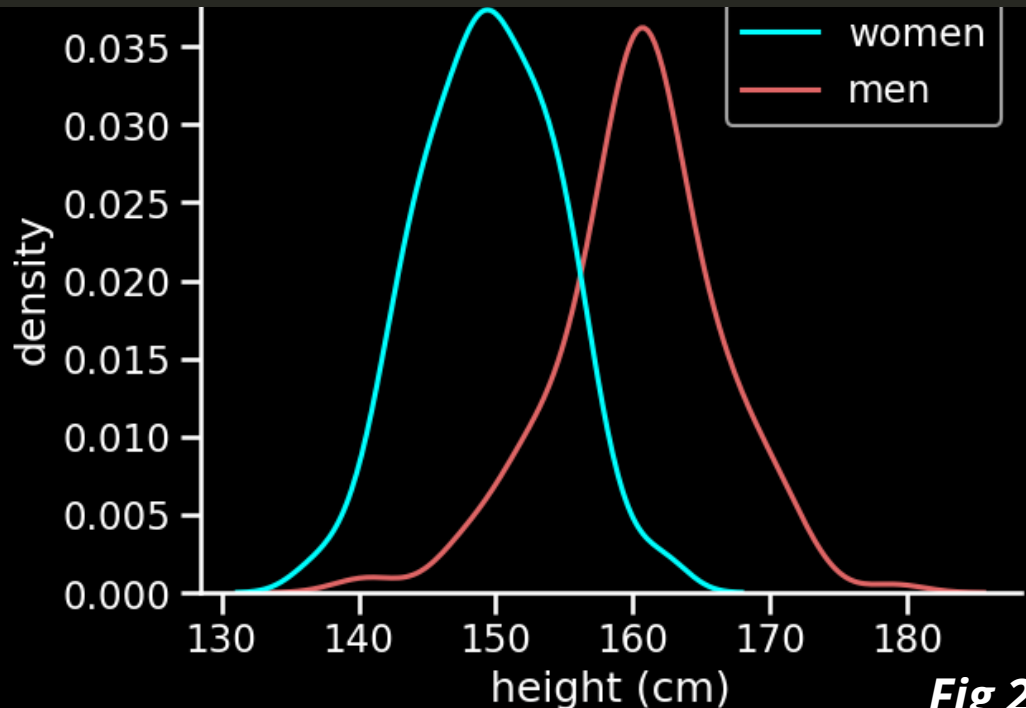
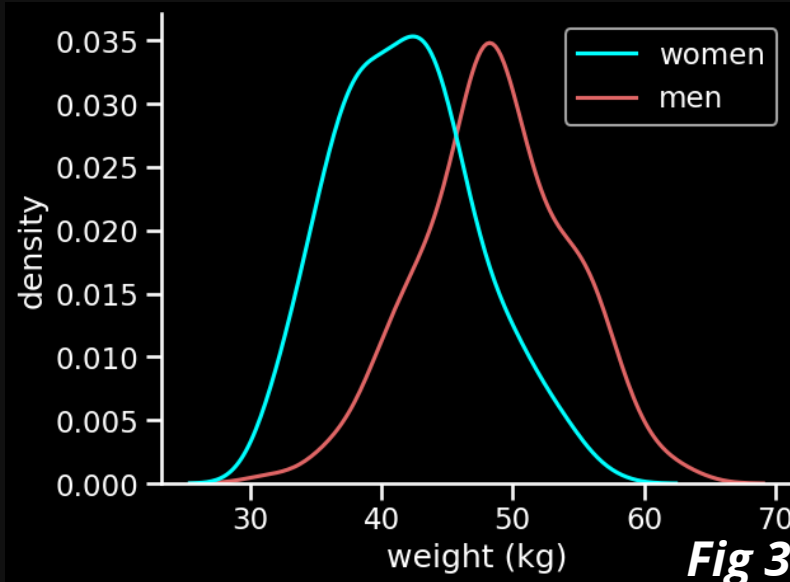
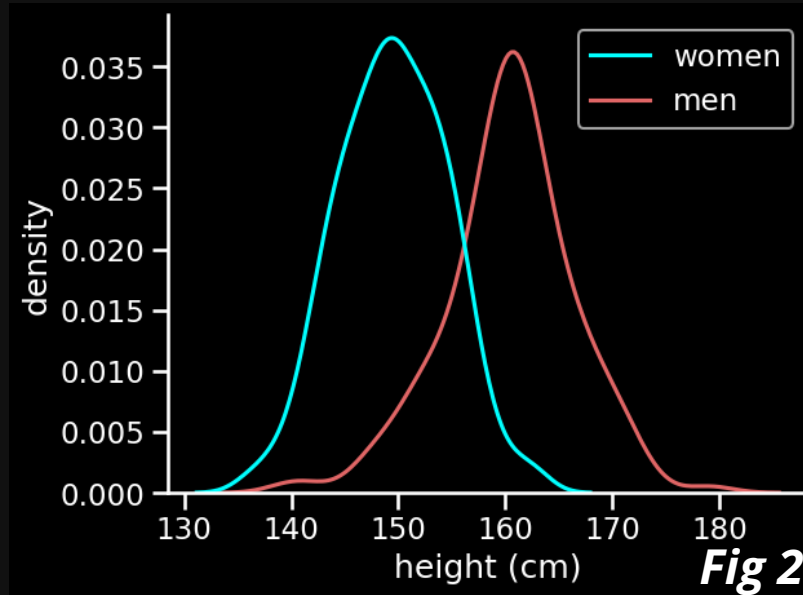
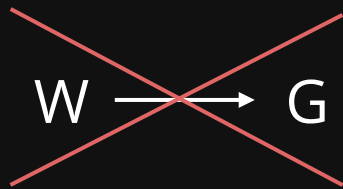
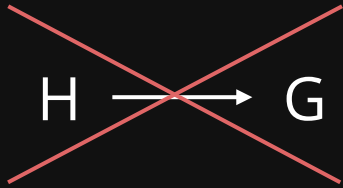


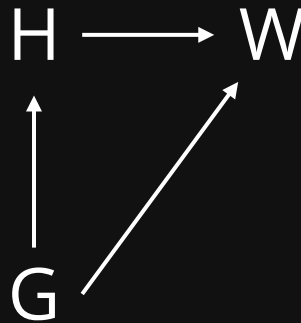
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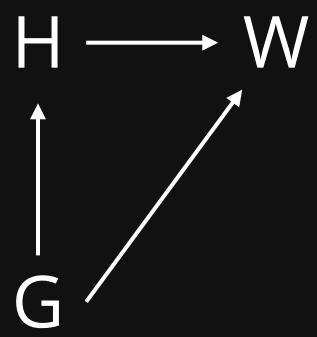


height influences
weight

weight influenced by
gender & height

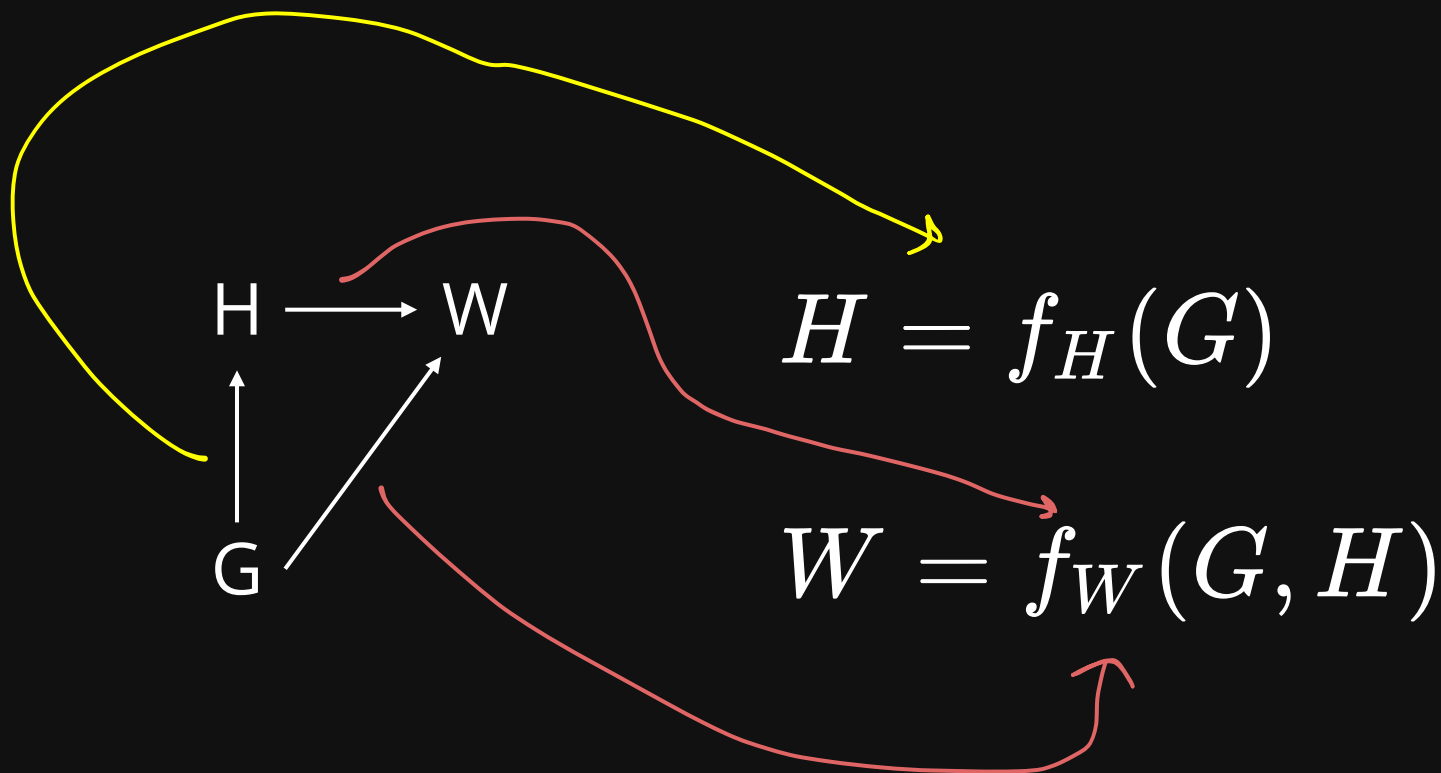


gender influences
height & weight





$$H = f_H(G)$$



height

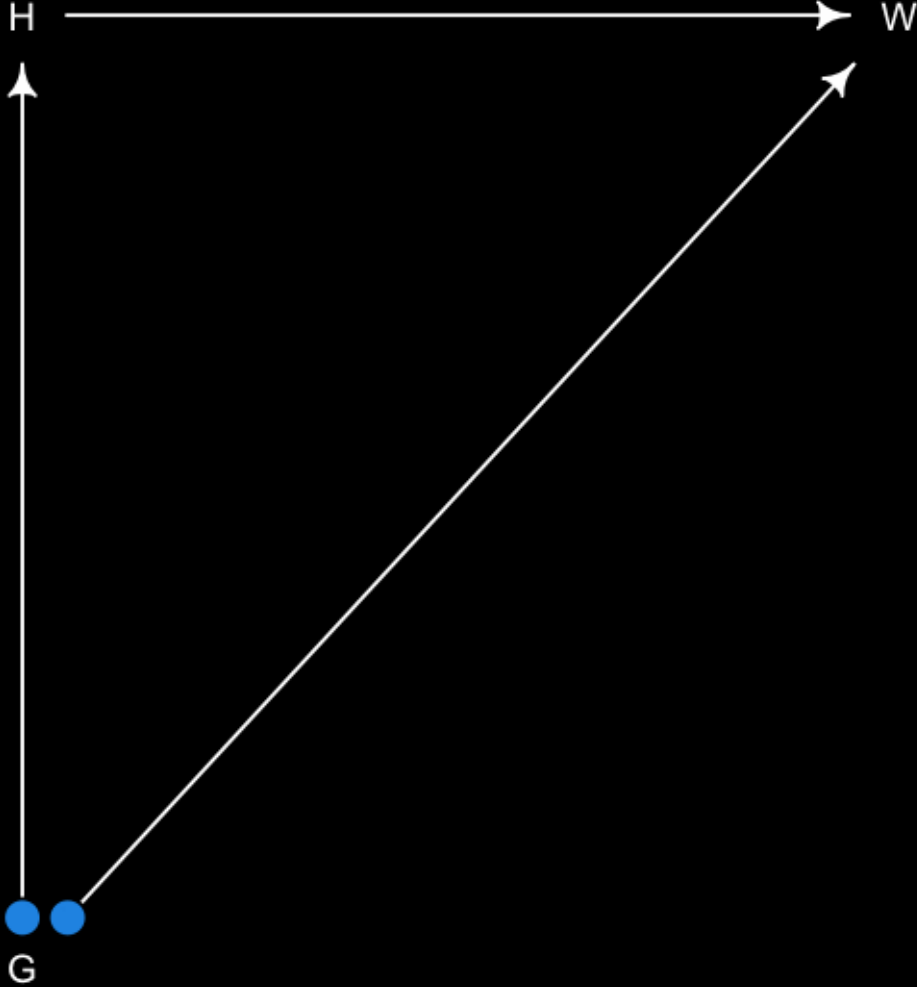
weight

H

W

G

gender at birth



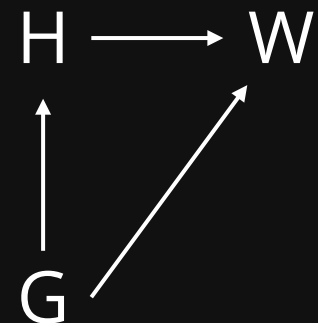
Think scientifically first

Different causal questions need different statistical models

Q: Causal effect of H on W?

Q: Total causal effect of G on W?

Q: Direct causal effect of G on W?



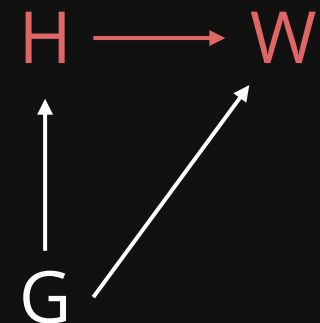
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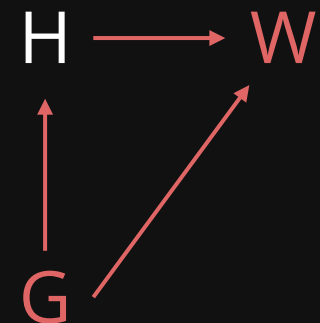
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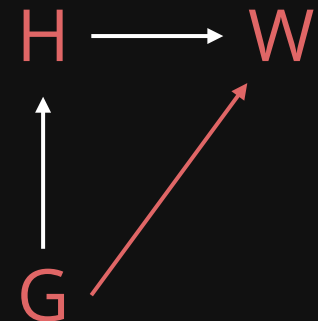
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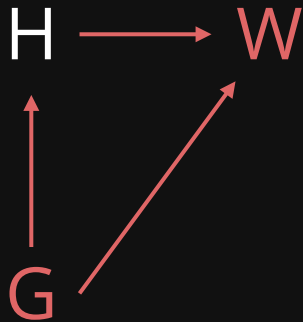
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From estimand to estimate

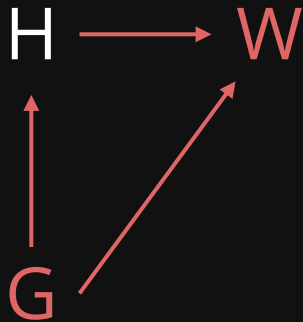
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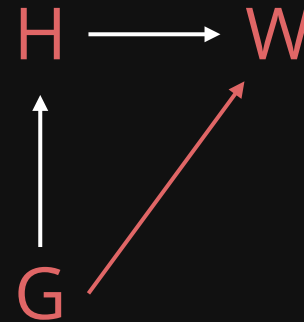


From estimand to estimate

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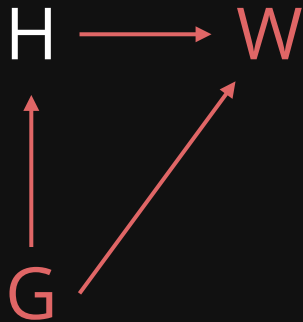


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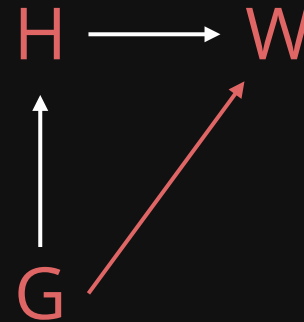


From estimand to estimate

Q: Total causal effect of G on W?



Q: Direct causal effect of G on W?



Need to model G as ***categorical*** variable

Working with categories

Several ways to code categorical variables

Working with categories

Several ways to code categorical variables

1. "dummy" (indicator) variables (0/1)

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1. "dummy" (indicator) variables (0/1)

2. index variables: 0,1,2,3,...

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extend to many categories without change in code

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better for specifying priors

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extend to many categories without change in code

better for specifying priors

straight forward extension to multi-level models





Working with categories

Working with categories

Example: How does color influence t-shirt sales?





Working with categories

Example: How does color influence t-shirt sales?

				
Category	Cyan	Magenta	Yellow	Black
Index Value	0	1	2	3

Working with categories

Example: How does color influence t-shirt sales?

				
Category	Cyan	Magenta	Yellow	Black
Index Value	0	1	2	3

Influence of color coded by

$$\alpha = [\alpha_0, \alpha_1, \alpha_2, \alpha_3]$$




Working with categories

$$\alpha = [\alpha_0, \alpha_1, \alpha_2, \alpha_3]$$




Working with categories

$$\alpha = [\alpha_0, \alpha_1, \alpha_2, \alpha_3]$$
Four colored circles are arranged horizontally below the vector notation. From left to right, they are cyan, magenta, yellow, and black. Each circle is a solid color with a thin white outline.

$$y_i \sim \text{Normal}(\mu_i, \sigma)$$

$$\mu_i = \alpha_{\text{COLOR}[i]}$$

Working with categories


$$\alpha = [\alpha_0, \alpha_1, \alpha_2, \alpha_3]$$
Four colored circles are arranged horizontally below the vector α . From left to right, they are cyan, magenta, yellow, and black. Each circle is a solid color with a thin black outline.

profits from sales of t-shirt i


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Working with categories

$$\alpha = [\alpha_0, \alpha_1, \alpha_2, \alpha_3]$$



profits from sales of t-shirt i

↪ $y_i \sim \text{Normal}(\mu_i, \sigma)$

↪ $\mu_i = \alpha_{\text{COLOR}[i]}$

expected profits from
sales of t-shirt i

Working with categories

$$\alpha = [\alpha_0, \alpha_1, \alpha_2, \alpha_3]$$


profits from sales of t-shirt i

↪ $y_i \sim \text{Normal}(\mu_i, \sigma)$

↪ $\mu_i = \alpha_{\text{COLOR}[i]}$

↪ expected profits from
sales of t-shirt i

↪ color of t-shirt i

Using index variables

$$W_i \sim \text{Normal}(\mu_i, \sigma)$$

$$\mu_i = \alpha$$



intercept

Using index variables

	H	W	G
0	152	48	1
1	140	36	0
2	137	32	0
3	157	53	1
4	141	45	0
5	164	63	1
6	149	38	0
7	169	55	1
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9	165	54	1
10	154	50	0
11	151	41	1

$$W_i \sim \text{Normal}(\mu_i, \sigma)$$

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Using index variables

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gender of
i-th person

Using index variables

	H	W	G
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$$W_i \sim \text{Normal}(\mu_i, \sigma)$$

$$\mu_i = \alpha_{G[i]}$$

gender of
 i -th person

$G[i] = 0$ (female)

$G[i] = 1$ (male)

Using index variables

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gender of
 i -th person

$G[i] = 0$ (female)

$G[i] = 1$ (male)

$$\alpha = [\alpha_0, \alpha_1]$$

two intercepts, one
for each value of G

Using index variables

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6	149	38	0
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8	148	35	0
9	165	54	1
10	154	50	0
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$i = 0$

$$W_i \sim \text{Normal}(\mu_i, \sigma)$$

$$\mu_i = \alpha G[i]$$

$$G[0] = 1$$

$$\alpha = [\alpha_0, \alpha_1]$$

Using index variables

	H	W	G
0	152	48	1
1	140	36	0
2	137	32	0
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10	154	50	0
11	151	41	1

$i = 1$

$$W_i \sim \text{Normal}(\mu_i, \sigma)$$

$$\mu_i = \alpha G[i]$$

$$G[1] = 0$$

$$\alpha = [\alpha_0, \alpha_1]$$

Using index variables

$$W_i \sim \text{Normal}(\mu_i, \sigma)$$

$$\mu_i = \alpha_{G[i]}$$

Using index variables

$$W_i \sim \text{Normal}(u_i, \sigma)$$

$$\mu_i = \alpha_{G[i]}$$

Priors

$$\alpha = [\alpha_0, \alpha_1] \quad \alpha_j \sim \text{Normal}(60, 10)$$
$$j \in [0, 1]$$

Using index variables

```
import pandas as pd
import pymc as pm
from quap import quap

df = pd.read_csv("Data/Howell1.csv", sep=';', header=0)
df2 = df[df.age >= 18]
gen = df2.male #gender for each individual

with pm.Model() as m_GW:
    a = pm.Normal('a', 60, 10, shape=2)
    mu = pm.Deterministic("mu", a[gen])
    sigma = pm.Uniform("sigma", 0, 10)

    weight = pm.Normal("weight", mu, sigma, observed=df2.weight)

    m_GW_idata, _ = quap([a, sigma])
```

Code 4

$$W_i \sim \text{Normal}(u_i, \sigma)$$

$$\mu_i = \alpha_{G[i]}$$

$$\alpha_j \sim \text{Normal}(60, 10)$$

$$\sigma \sim \text{Uniform}(0, 10)$$

Using index variables

Code 4

```
import pandas as pd
import pymc as pm
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    mu = pm.Deterministic("mu", a[gen])
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    weight = pm.Normal("weight", mu, sigma, observed=df2.weight)

    m_GW_idata, _ = quap([a, sigma])
```

$$W_i \sim \text{Normal}(u_i, \sigma)$$

$$\mu_i = \alpha_{G[i]}$$

$$\alpha_j \sim \text{Normal}(60, 10)$$

$$\sigma \sim \text{Uniform}(0, 10)$$

Using index variables

```
import pandas as pd
import pymc as pm
from quap import quap

df = pd.read_csv("Data/Howell1.csv", sep=';', header=0)
df2 = df[df.age >= 18]
gen = df2.male #gender for each individual

with pm.Model() as m_GW:
    a = pm.Normal('a', 60, 10, shape=2) need 2 alphas in model
    mu = pm.Deterministic("mu", a[gen])
    sigma = pm.Uniform("sigma", 0, 10)

    weight = pm.Normal("weight", mu, sigma, observed=df2.weight)

    m_GW_idata, _ = quap([a, sigma])
```

Code 4

$$W_i \sim \text{Normal}(u_i, \sigma)$$

$$\mu_i = \alpha_{G[i]}$$

$$\underline{\alpha_j} \sim \text{Normal}(60, 10) \quad j \in [0, 1]$$

$$\sigma \sim \text{Uniform}(0, 10)$$

Using index variables

```
import pandas as pd
import pymc as pm
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df = pd.read_csv("Data/Howell1.csv", sep=';', header=0)
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Code 4

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```

pandas Series of 0/1 values

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```

pandas Series of 0/1 values

```
with pm.Model() as m_GW:
```

```
    a = pm.Normal('a', 60, 10, shape=2)
```

```
    mu = pm.Deterministic("mu", a[gen])
```

```
    sigma = pm.Uniform("sigma", 0, 10)
```

select the alpha value from
vector based on value of
gen for *i*th individual

```
    weight = pm.Normal("weight", mu, sigma, observed=df2.weight)
```

```
    m_GW_idata, _ = quap([a, sigma])
```

$$W_i \sim \text{Normal}(u_i, \sigma)$$

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    a = pm.Normal('a', 60, 10, shape=2)
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```
m_GW_idata, _ = quap([a, sigma])
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$$\alpha_j \sim \text{Normal}(60, 10)$$

$$\sigma \sim \text{Uniform}(0, 10)$$

Posterior means & predictions

posterior mean weight (by gender)

```
1 import arviz as az
2 import seaborn as sns
3
4 post = az.extract(m_GW_idata, num_samples=1000)
5
6 # posterior mean weight
7 sns.kdeplot(post.a.values[1], color = "#e06666")
8 ax = sns.kdeplot(post.a.values[0], color = "cyan")
9 ax.set_xlabel("posterior mean weight (kg)")
10 sns.despine();
```

Code 5

Posterior means & predictions

posterior mean weight (by gender)

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1 import arviz as az
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Code 5

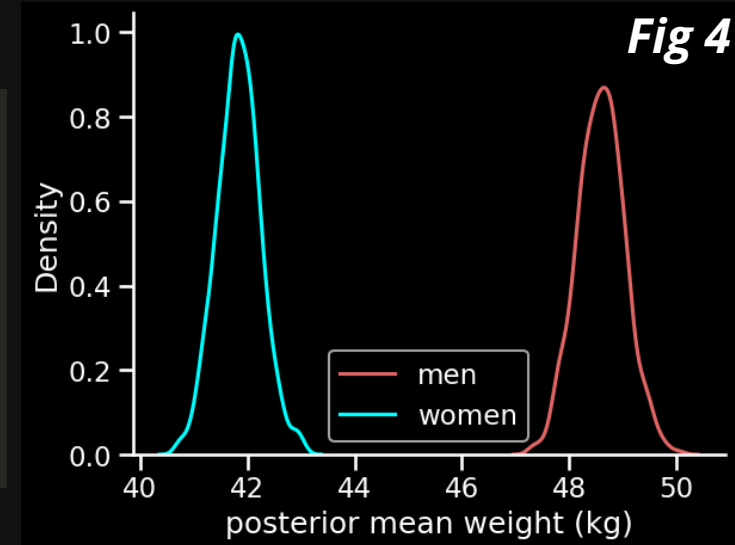


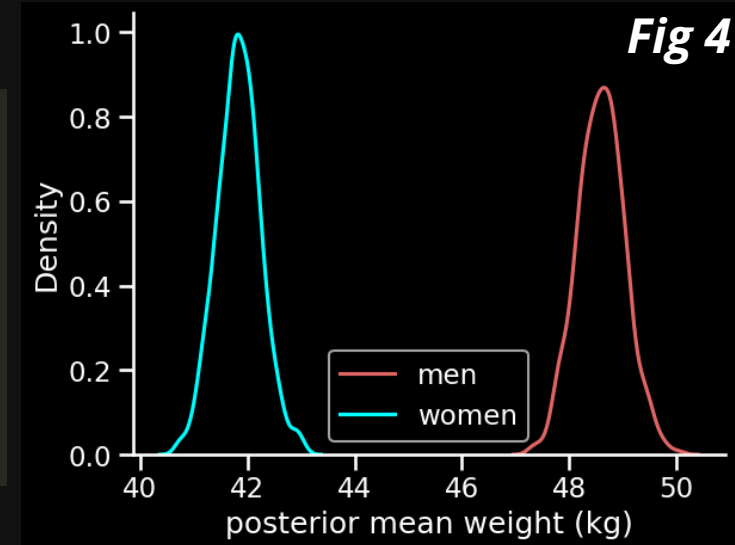
Fig 4

Posterior means & predictions

posterior mean weight (by gender)

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9 ax.set_xlabel("posterior mean weight (kg)")
10 sns.despine();
```

Code 5



posterior predicted weight (by gender)

```
1 w_W = stats.norm.rvs(post.a.values[0], post.sigma.values)
2 w_M = stats.norm.rvs(post.a.values[1], post.sigma.values)
3
4 _ = sns.kdeplot(w_W, color = "r")
5 ax = sns.kdeplot(w_M, color = "g")
6 _ = ax.set_xlabel("posterior predicted weight (kg)")
```

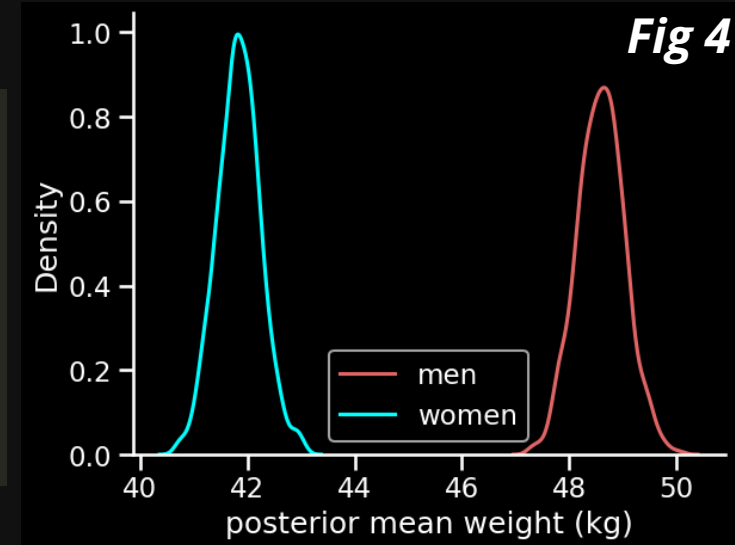
Code 6

Posterior means & predictions

posterior mean weight (by gender)

```
1 import arviz as az
2 import seaborn as sns
3
4 post = az.extract(m_GW_idata, num_samples=1000)
5
6 # posterior mean weight
7 sns.kdeplot(post.a.values[1], color = "#e06666")
8 ax = sns.kdeplot(post.a.values[0], color = "cyan")
9 ax.set_xlabel("posterior mean weight (kg)")
10 sns.despine();
```

Code 5



posterior predicted weight (by gender)

μ σ **Code 6**

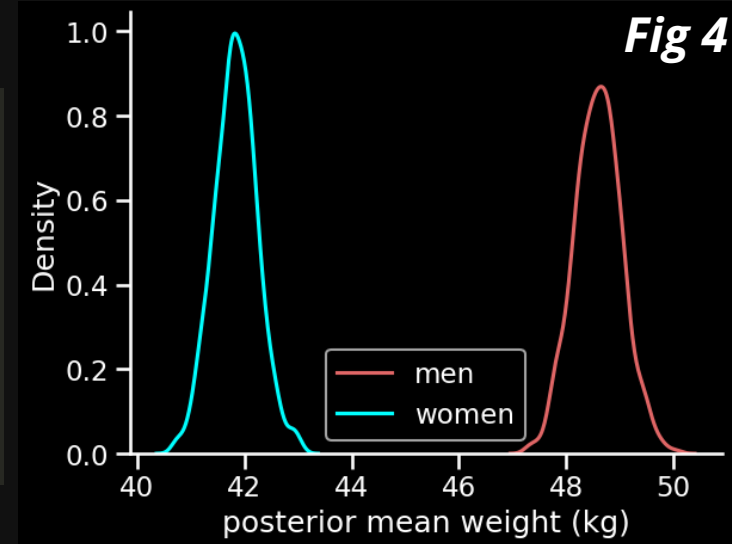
```
1 w_W = stats.norm.rvs(post.a.values[0], post.sigma.values)
2 w_M = stats.norm.rvs(post.a.values[1], post.sigma.values)
3
4 _ = sns.kdeplot(w_W, color = "r")
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```

Posterior means & predictions

posterior mean weight (by gender)

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```

Code 5



posterior predicted weight (by gender)

μ σ **Code 6**

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5 ax = sns.kdeplot(w_M, color = "g")
6 _ = ax.set_xlabel("posterior predicted weight (kg)")
```

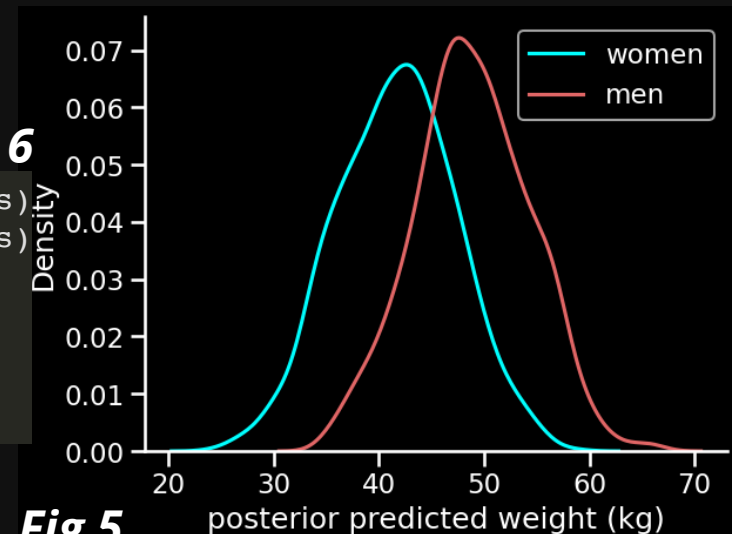
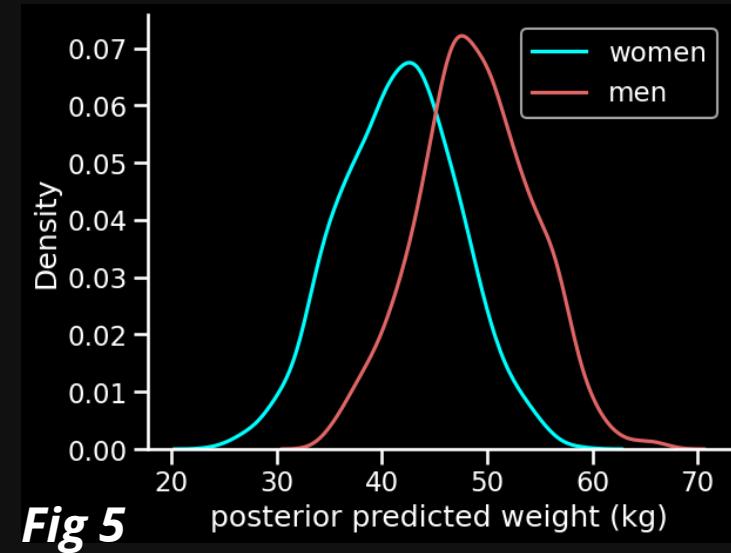


Fig 5

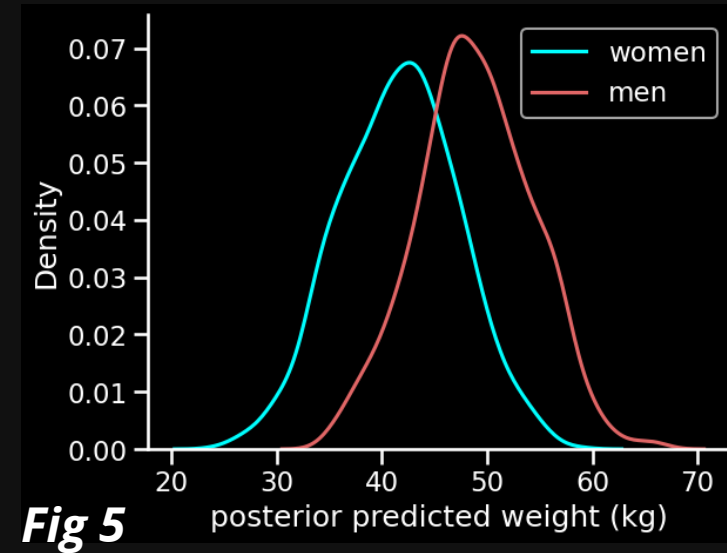
Always compute contrasts

Need to compute **contrast**



Always compute contrasts

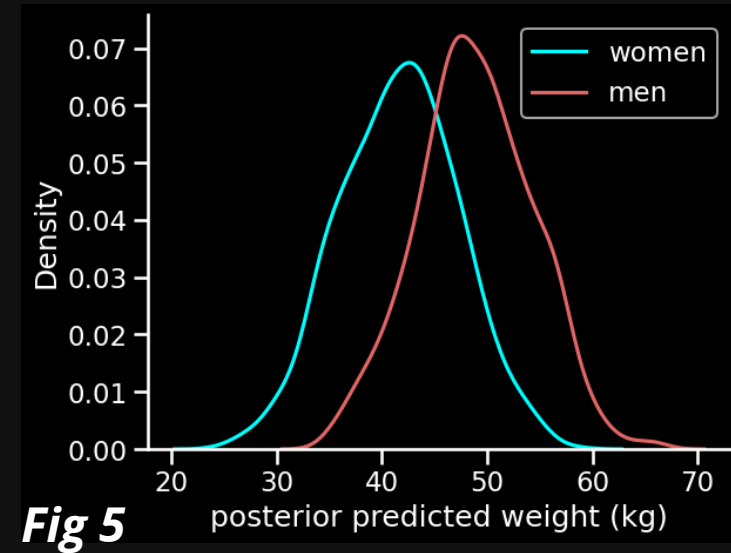
Need to compute **contrast**
- difference between the categories



Always compute contrasts

Need to compute **contrast**
- difference between the categories

Don't want to simply compare
overlap in parameters

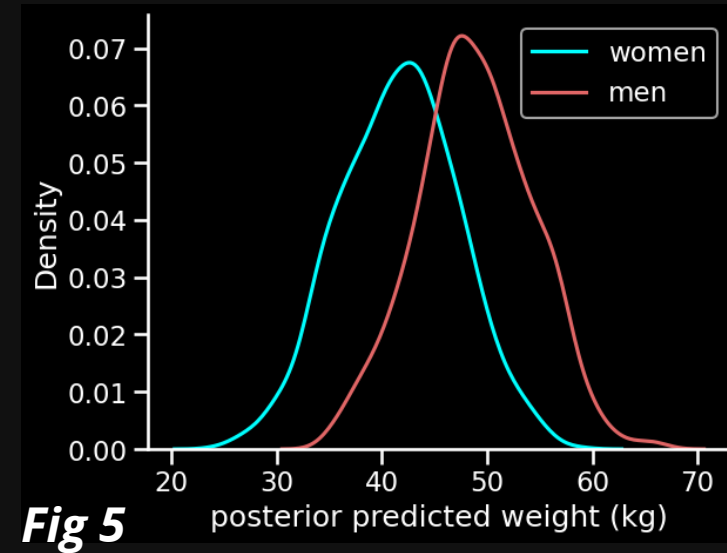


Always compute contrasts

Need to compute **contrast**
- difference between the categories

Don't want to simply compare
overlap in parameters

Samples are not independent!



Always compute contrasts

Need to compute **contrast**
- difference between the categories

Don't want to simply compare
overlap in parameters

Samples are not independent!

Compute **contrast distribution**

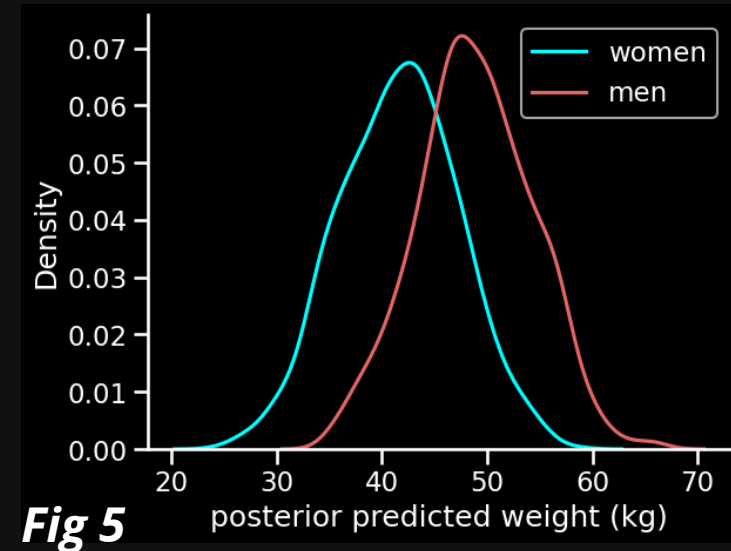
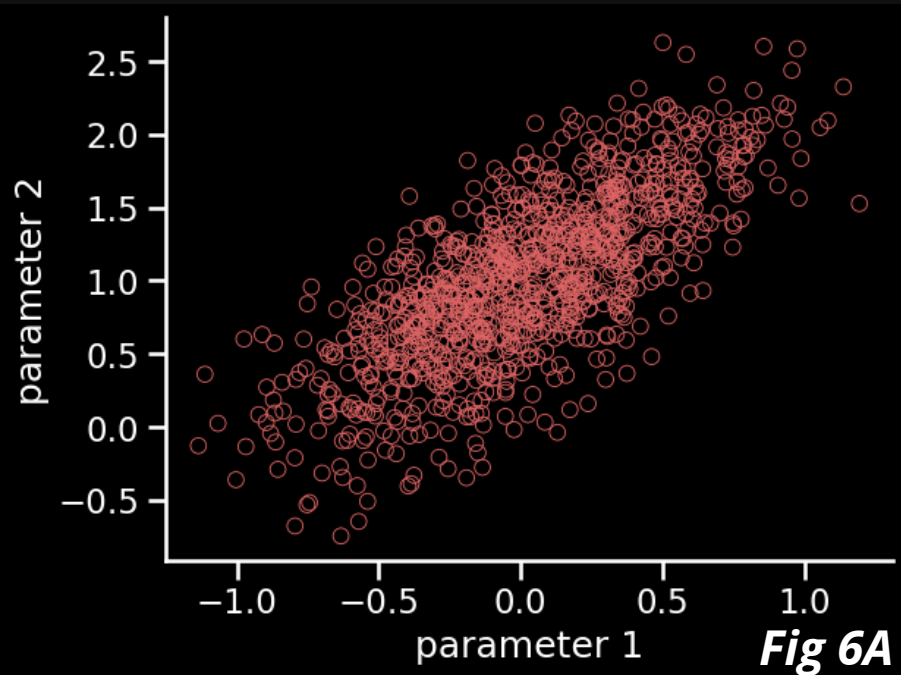


Fig 5

A motivation for computing contrasts

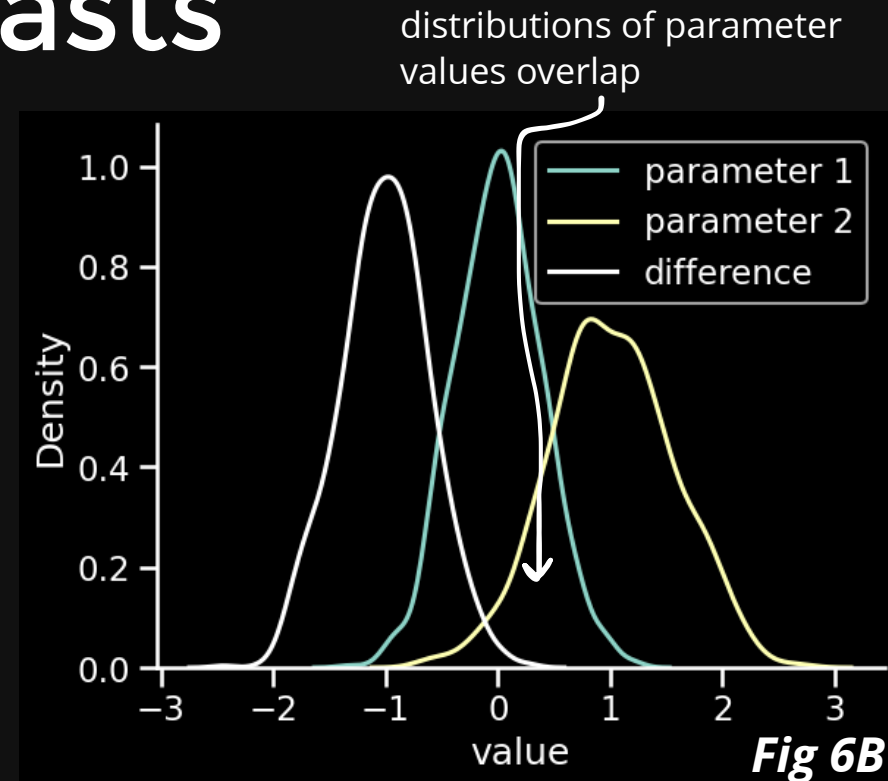
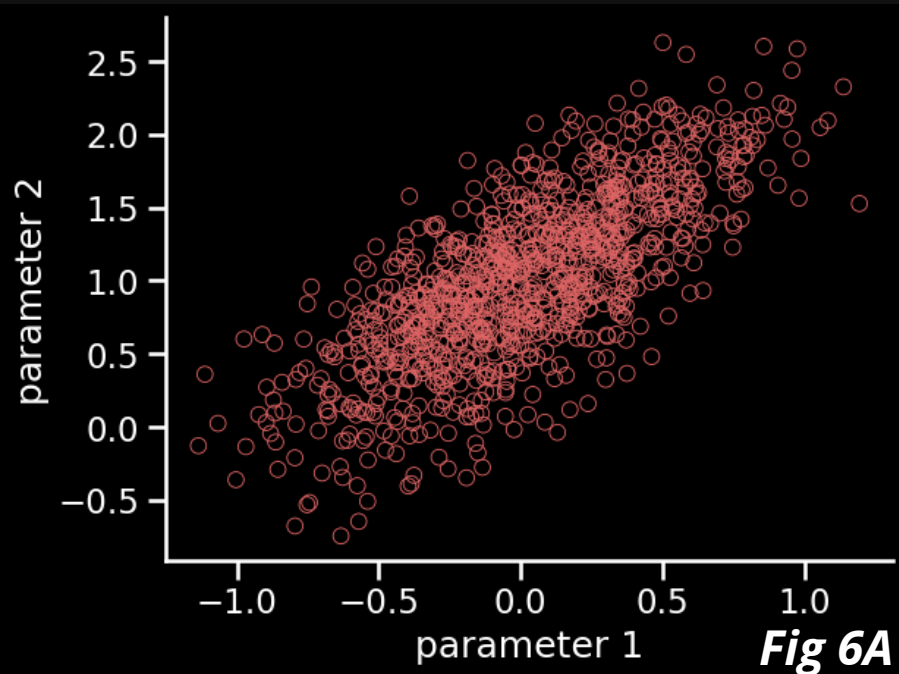


$$p_{1,i} \sim \text{Normal}(0, 0.4)$$

$$p_{2,i} \sim \text{Normal}(p_{1,i} + 1, 0.4)$$

$$i \in [1, 1000]$$

A motivation for computing contrasts

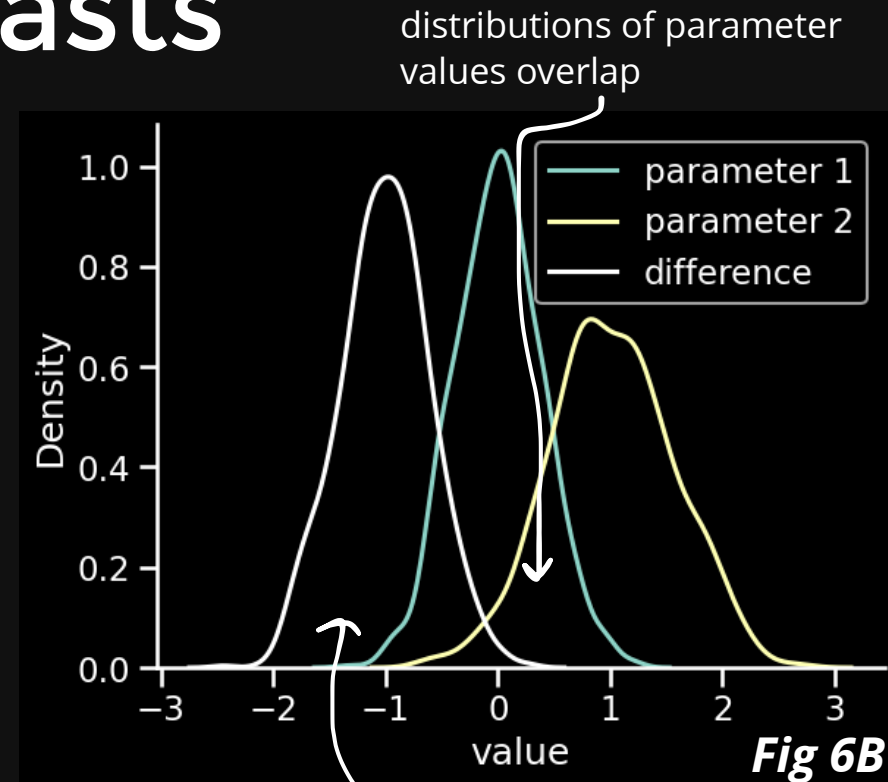
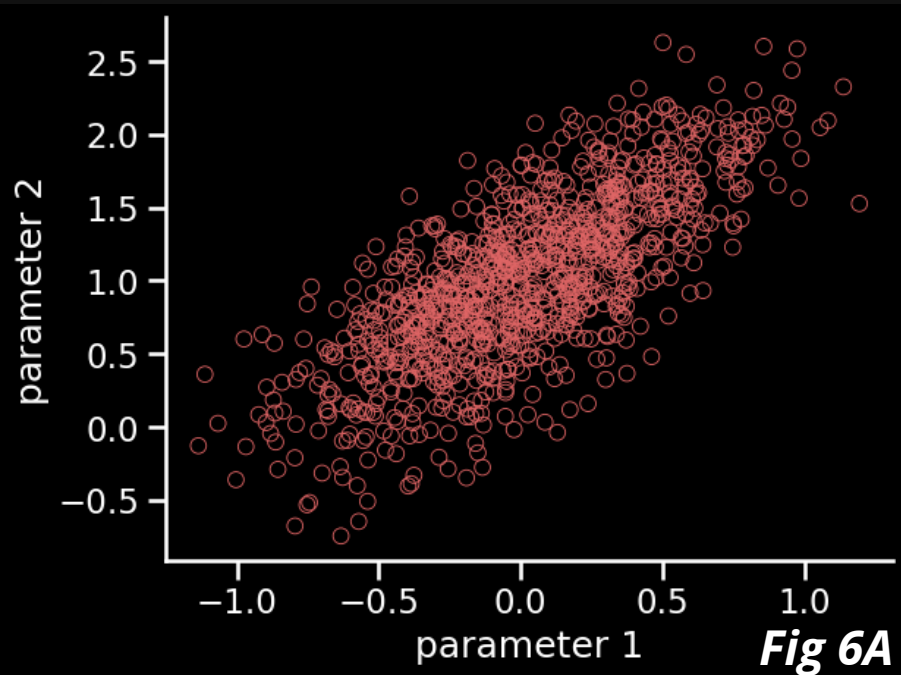


$$p_{1,i} \sim \text{Normal}(0, 0.4)$$

$$p_{2,i} \sim \text{Normal}(p_{1,i} + 1, 0.4)$$

$$i \in [1, 1000]$$

A motivation for computing contrasts



contrast distribution shows non-zero difference between paired parameters





Causal Contrast

post





xarray.Dataset

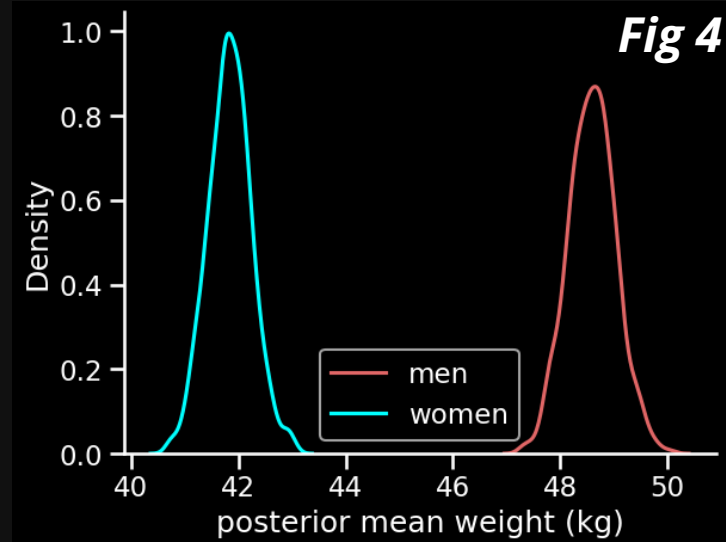
► Dimensions: (a_dim_0: 2, sample: 1000)

▼ Coordinates:

a_dim_0	(a_dim_0)	int64	0 1	 
sample	(sample)	MultiIndex	(chain, draw)	 
chain	(sample)	int64	0 0 0 0 0 0 0 0 ... 0 0 0 0 0 0 0 0	 
draw	(sample)	int64	2597 3123 2861 ... 1921 4875 1934	 

▼ Data variables:

a	(a_dim_0, sample)	float64	41.79 42.22 41.84 ... 48.81 49.16	 
sigma	(sample)	float64	5.541 5.359 5.627 ... 5.483 5.095	 







Causal Contrast

post





xarray.Dataset

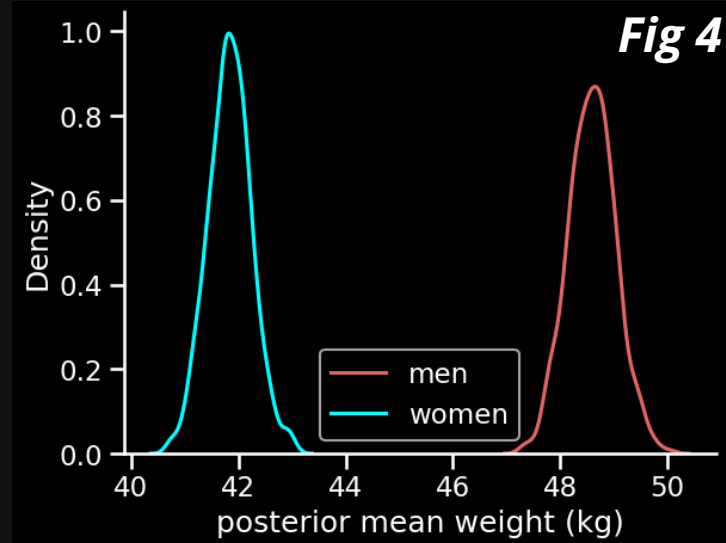
► Dimensions: (a_dim_0: 2, sample: 1000)

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a_dim_0	(a_dim_0)	int64	0 1	 
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sigma	(sample)	float64	5.541 5.359 5.627 ... 5.483 5.095	 



```
import seaborn as sns
```

Code 7

```
# causal contrast in means (male=1, female=0)
mu_contrast = post.a.values[1] - post.a.values[0]

ax = sns.kdeplot(mu_contrast, color = "w")
_ = ax.set_xlabel("posterior mean weight contrast (kg)")
```


Causal Contrast

post





xarray.Dataset

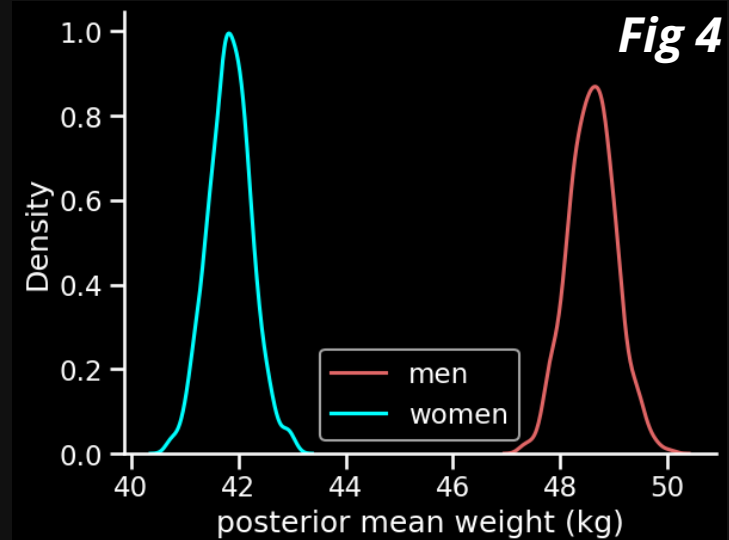
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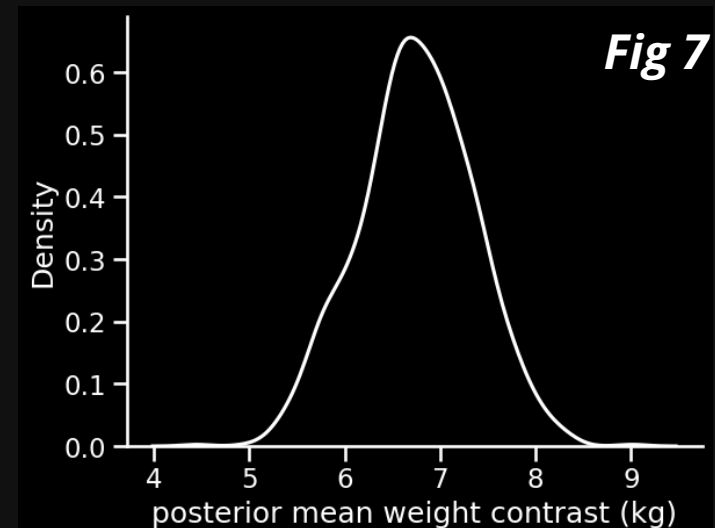


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Causal Contrast

post

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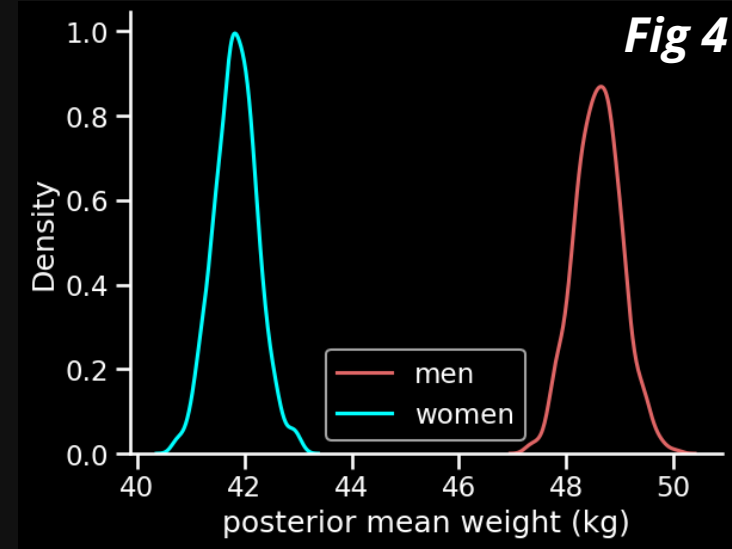
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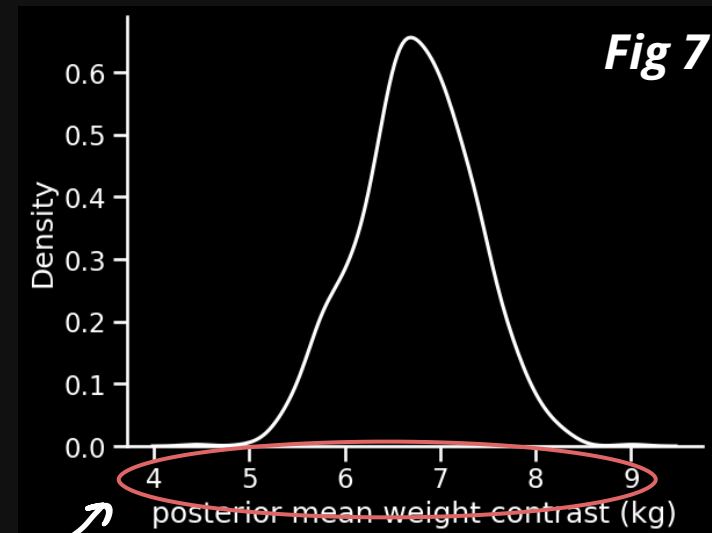
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```

Code 7

reliably positive difference for
men vs. women (on average)



Simulated Weight Contrast

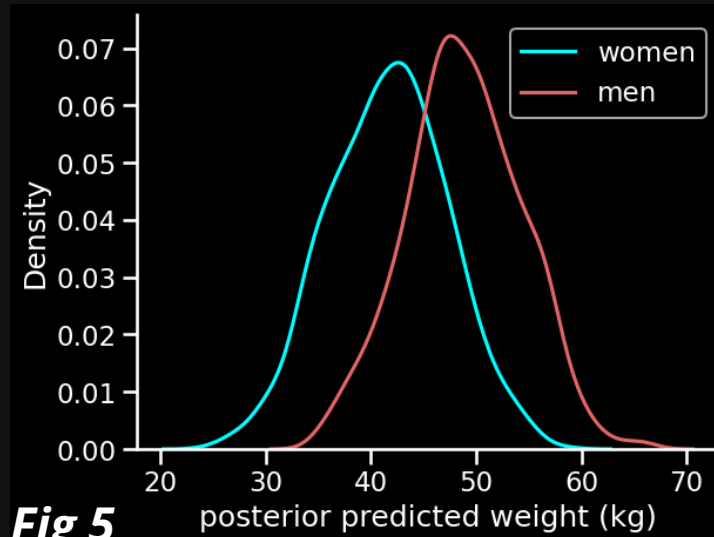
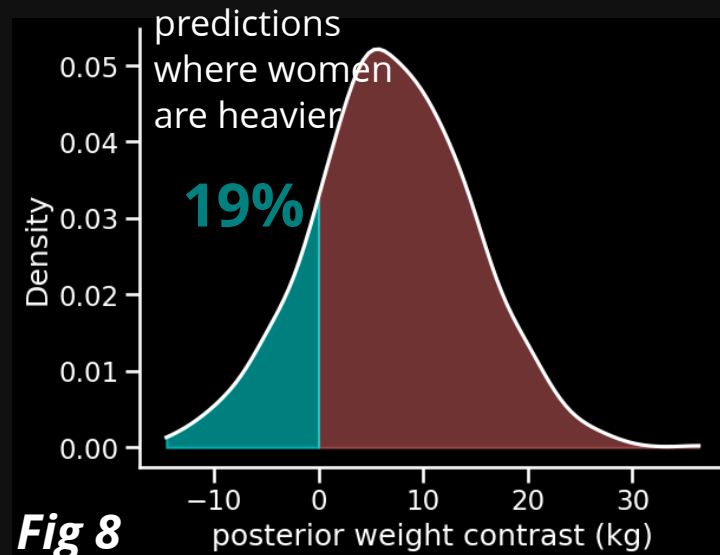
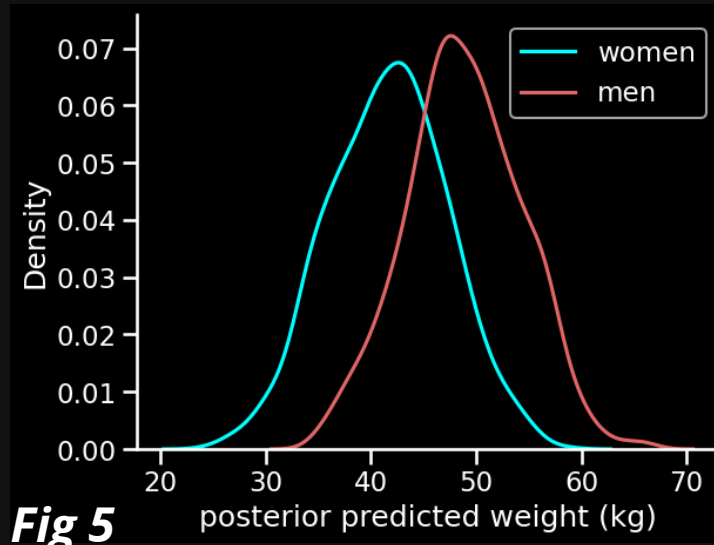
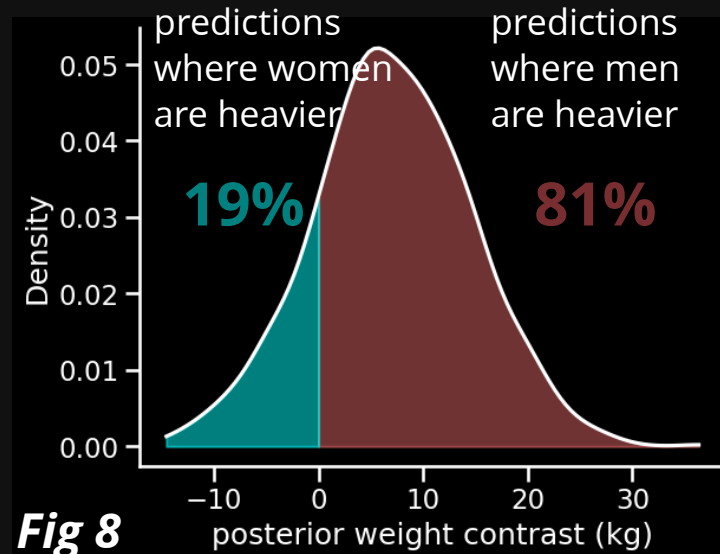
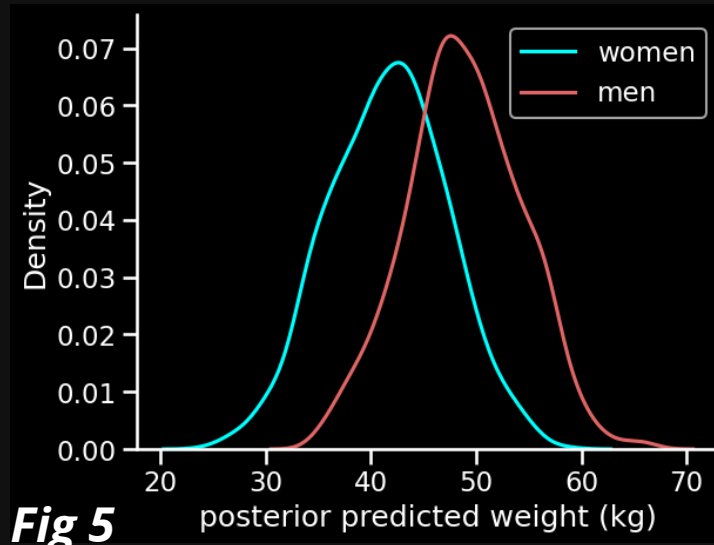


Fig 5

Simulated Weight Contrast

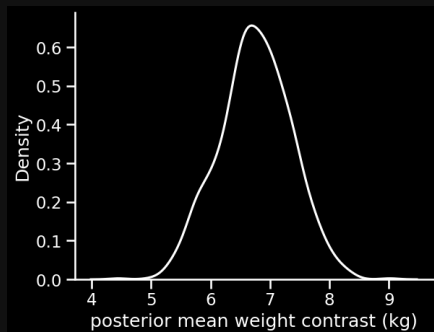
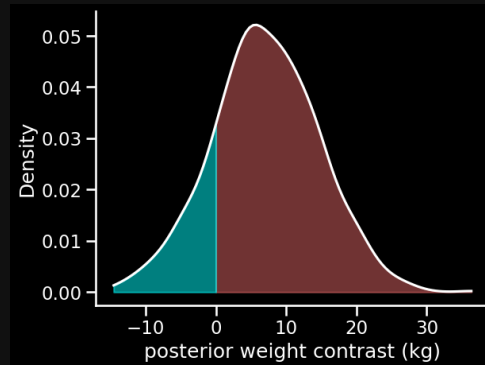


Simulated Weight Contrast



From estimand to estimate

Q: Total causal effect of G on W?

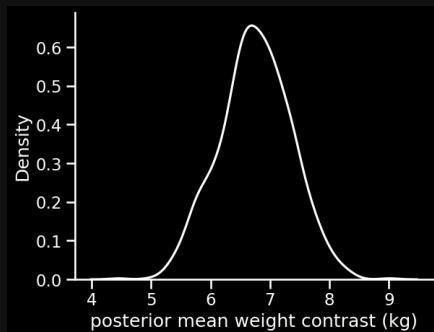
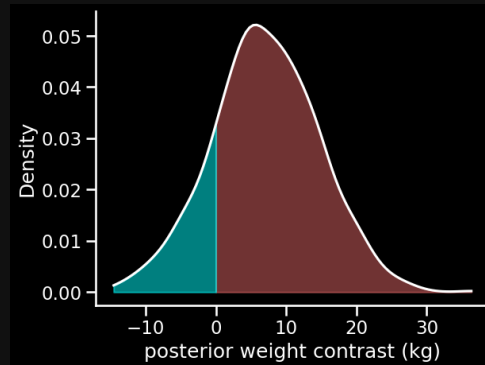


From estimand to estimate

influence of G on W

- direct influence
- AND influence through H

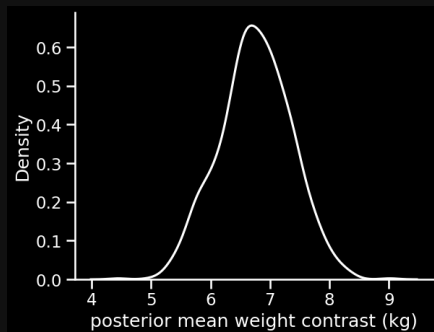
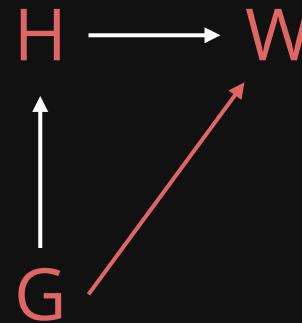
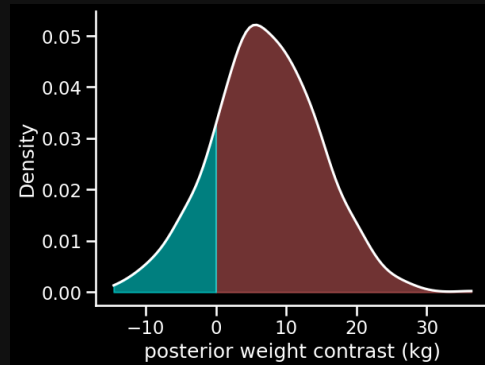
Q: Total causal effect of G on W?



From estimand to estimate

Q: Total causal effect of G on W?

Q: Direct causal effect of G on W?

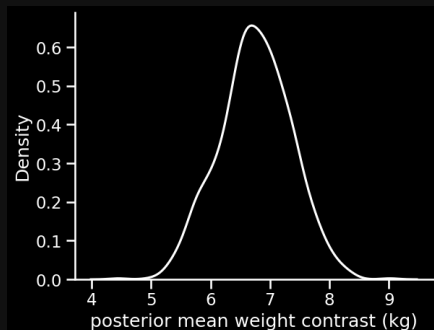
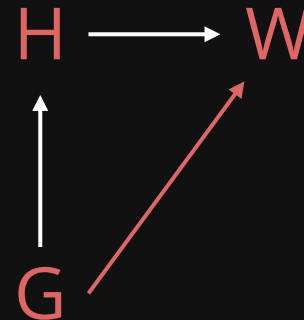
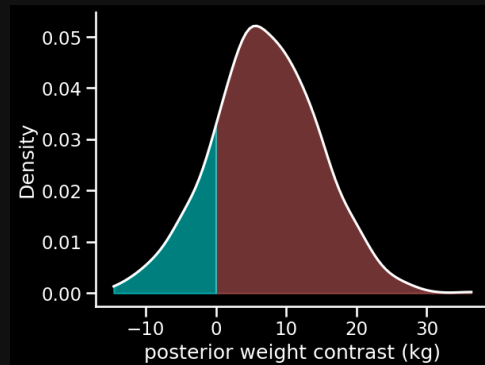
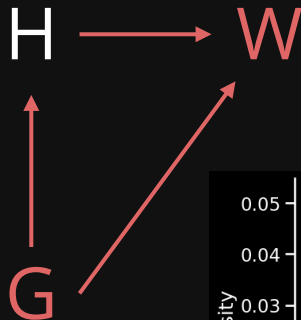


From estimand to estimate

direct influence of G on W (ONLY)

Q: Total causal effect of G on W?

Q: Direct causal effect of G on W?

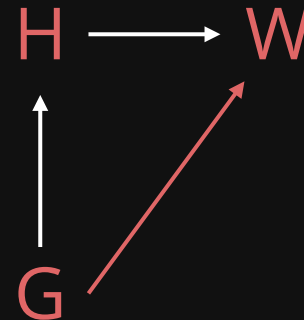
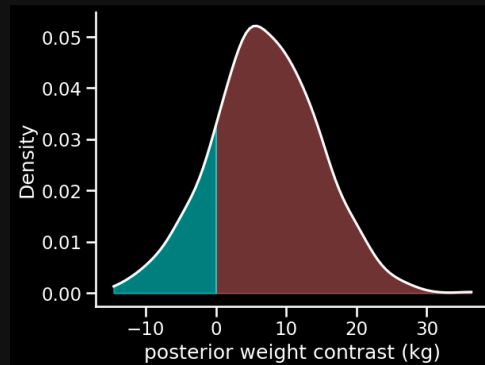


From estimand to estimate

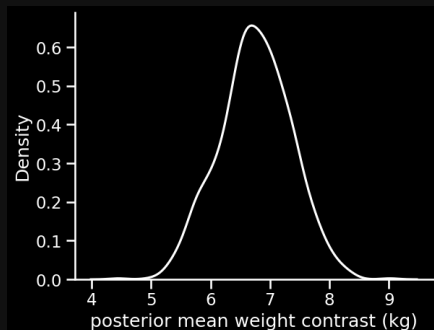
direct influence of G on W (ONLY)

Q: Total causal effect of G on W?

Q: Direct causal effect of G on W?



need a different statistical model for estimate...



Index variables and lines

model without stratification by gender

$$W_i \sim \text{Normal}(u_i, \sigma)$$

$$\mu_i = \alpha + \beta(H_i - \bar{H})$$

Index variables and lines

model without stratification by gender

$$W_i \sim \text{Normal}(u_i, \sigma)$$

$$\mu_i = \alpha + \beta(H_i - \bar{H})$$

intercept

slope

Index variables and lines

model with stratification by gender

$$W_i \sim \text{Normal}(u_i, \sigma)$$

$$\mu_i = \alpha_{G[i]} + \beta_{G[i]}(H_i - \bar{H})$$

Index variables and lines

	H	W	G
0	152	48	1
1	140	36	0
2	137	32	0
3	157	53	1
4	141	45	0
5	164	63	1
6	149	38	0
7	169	55	1
8	148	35	0
9	165	54	1
10	154	50	0
11	151	41	1

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$$W_i \sim \text{Normal}(u_i, \sigma)$$

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model with stratification by gender

$$W_i \sim \text{Normal}(u_i, \sigma)$$

$$\mu_i = \alpha_{G[i]} + \beta_{G[i]}(H_i - \bar{H})$$

gender of
i-th person

Index variables and lines

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$$W_i \sim \text{Normal}(u_i, \sigma)$$

$$\mu_i = \alpha_{G[i]} + \beta_{G[i]}(H_i - \bar{H})$$

gender of
i-th person

$G[i] = 0$ (female)
 $G[i] = 1$ (male)

Index variables and lines

	H	W	G
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1	140	36	0
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gender of
i-th person

$G[i] = 0$ (female)

$G[i] = 1$ (male)

$$\alpha = [\alpha_0, \alpha_1]$$

Index variables and lines

	H	W	G
0	152	48	1
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2	137	32	0
3	157	53	1
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0	152	48	1
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9	165	54	1
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model with stratification by gender

$$W_i \sim \text{Normal}(u_i, \sigma)$$

$$\mu_i = \alpha_{G[i]} + \beta_{G[i]}(H_i - \bar{H})$$

gender of
i-th person

$G[i] = 0$ (female)
 $G[i] = 1$ (male)

$$\alpha = [\alpha_0, \alpha_1] \quad \beta = [\beta_0, \beta_1]$$

Two intercepts and two slopes
- one for each value in G

Index variables and lines

	H	W	G
0	152	48	1
1	140	36	0
2	137	32	0
3	157	53	1
4	141	45	0
5	164	63	1
6	149	38	0
7	169	55	1
8	148	35	0
9	165	54	1
10	154	50	0
11	151	41	1

$i = 0$

$$W_i \sim \text{Normal}(u_i, \sigma)$$

$$\mu_i = \alpha_{G[i]} + \beta_{G[i]}(H_i - \bar{H})$$

$$G[0] = 1$$

$$\alpha = [\alpha_0, \alpha_1] \quad \beta = [\beta_0, \beta_1]$$

Index variables and lines

	H	W	G
0	152	48	1
1	140	36	0
2	137	32	0
3	157	53	1
4	141	45	0
5	164	63	1
6	149	38	0
7	169	55	1
8	148	35	0
9	165	54	1
10	154	50	0
11	151	41	1

$i = 1$

$$W_i \sim \text{Normal}(u_i, \sigma)$$

$$\mu_i = \alpha_{G[i]} + \beta_{G[i]}(H_i - \bar{H})$$

$$G[1] = 0$$

$$\alpha = [\alpha_0, \alpha_1] \quad \beta = [\beta_0, \beta_1]$$

Using index variables

Code 8

```
import pandas as pd
import pymc as pm
from quap import quap

df = pd.read_csv("Data/Howell1.csv", sep=';', header=0)
df2 = df[df.age >= 18]
gen = df2.male

with pm.Model() as m_GHW:
    a = pm.Normal('a', 60, 10, shape=2)
    b = pm.Lognormal('b', 0, 2, shape=2)
    mu = pm.Deterministic("mu", a[gen] + b[gen] * (df2.height - df2.height.mean()))
    sigma = pm.Uniform("sigma", 0, 10)

    weight = pm.Normal("weight", mu, sigma, observed=df2.weight)

m_GHW_idata, _ = quap([a, b, sigma])
```

$$W_i \sim \text{Normal}(u_i, \sigma)$$

$$\mu_i = \alpha_{G[i]} + \beta_{G[i]}(H_i - \bar{H})$$

$$\alpha_j \sim \text{Normal}(60, 10)$$

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    sigma = pm.Uniform("sigma", 0, 10)

    weight = pm.Normal("weight", mu, sigma, observed=df2.weight)

m_GHW_idata, _ = quap([a, b, sigma])
```

$$W_i \sim \text{Normal}(u_i, \sigma)$$

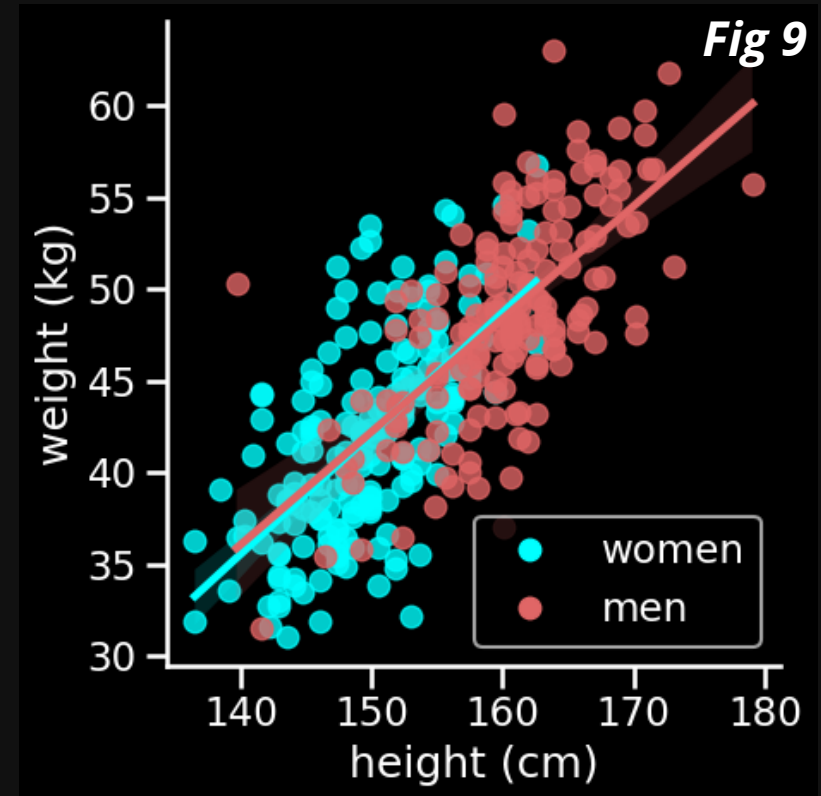
$$\mu_i = \alpha_{G[i]} + \beta_{G[i]}(H_i - \bar{H})$$

$$\alpha_j \sim \text{Normal}(60, 10)$$

$$\beta_j \sim \text{LogNormal}(0, 2)$$

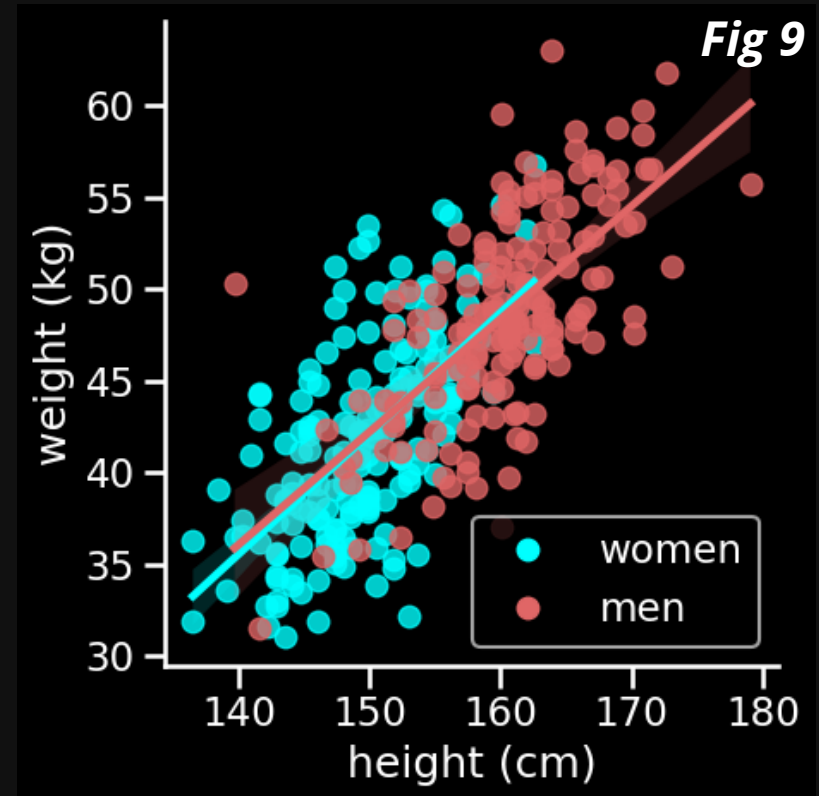
$$\sigma \sim \text{Uniform}(0, 10)$$

Contrasts at each height



Contrasts at each height

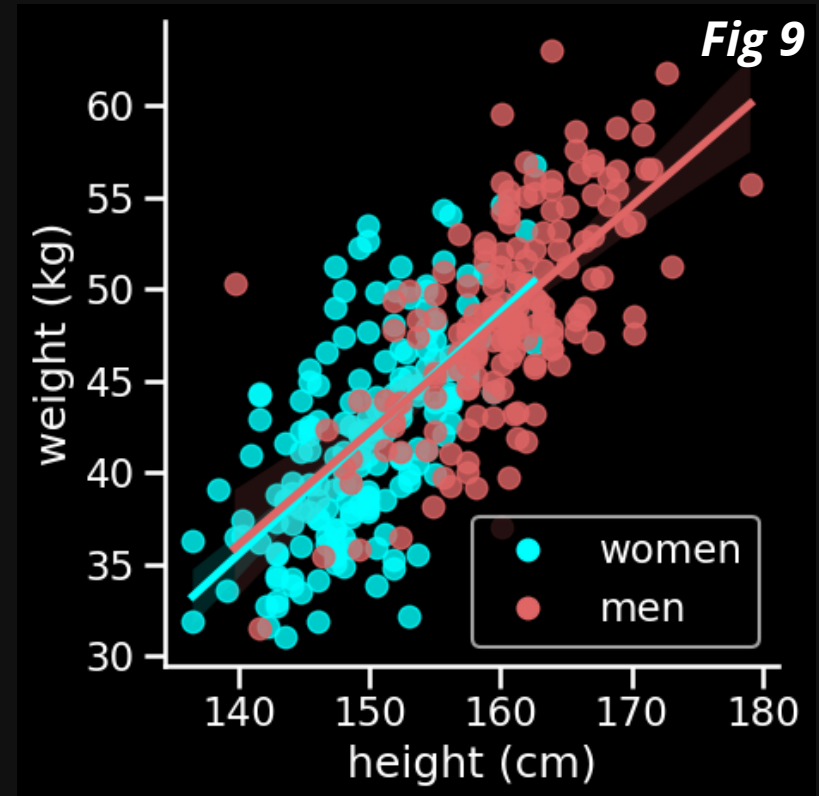
Don't rely on a plot such as this one for determining differences in influence of gender on weight



Contrasts at each height

(1) Compute posterior mean weight for women

Don't rely on a plot such as this one for determining differences in influence of gender on weight

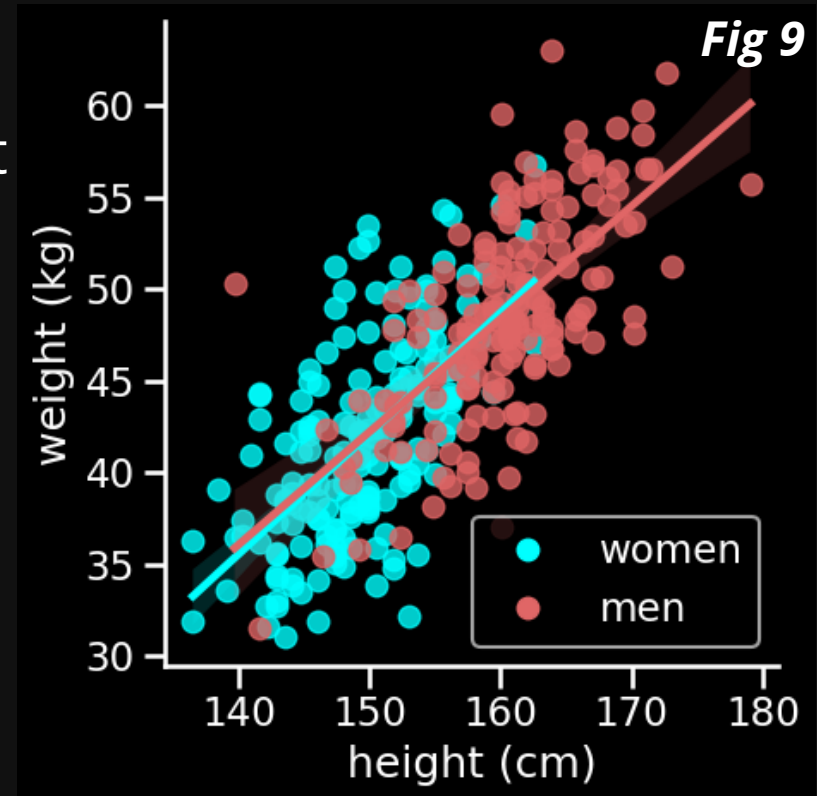


Contrasts at each height

(1) Compute posterior mean weight for women

(2) Compute posterior mean weight for men

Don't rely on a plot such as this one for determining differences in influence of gender on weight



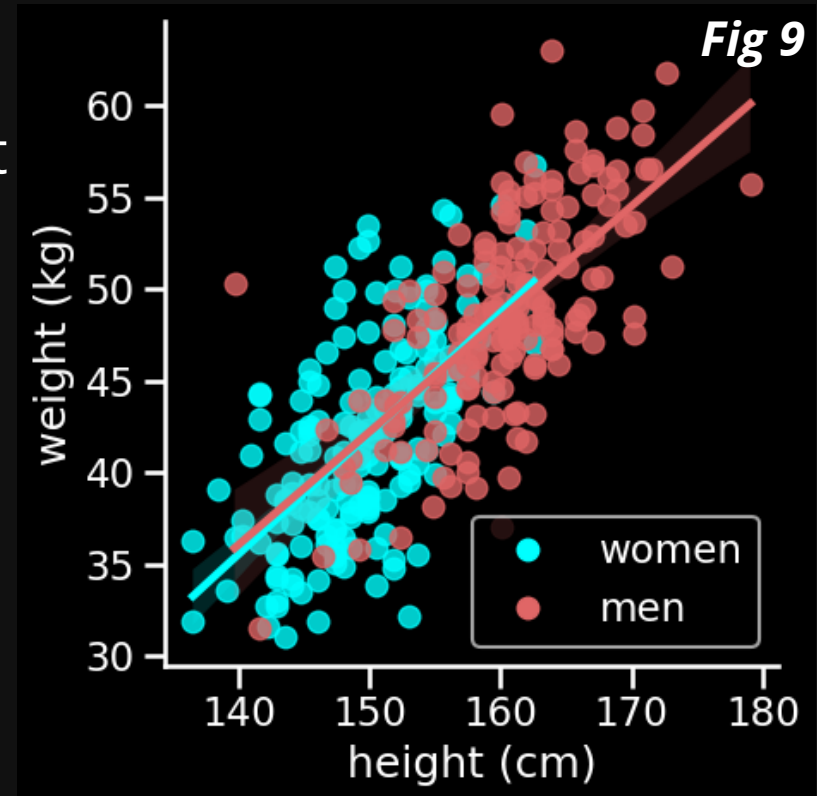
Contrasts at each height

(1) Compute posterior mean weight for women

(2) Compute posterior mean weight for men

(3) Subtract (2) from (1)

Don't rely on a plot such as this one for determining differences in influence of gender on weight



Contrasts at each height

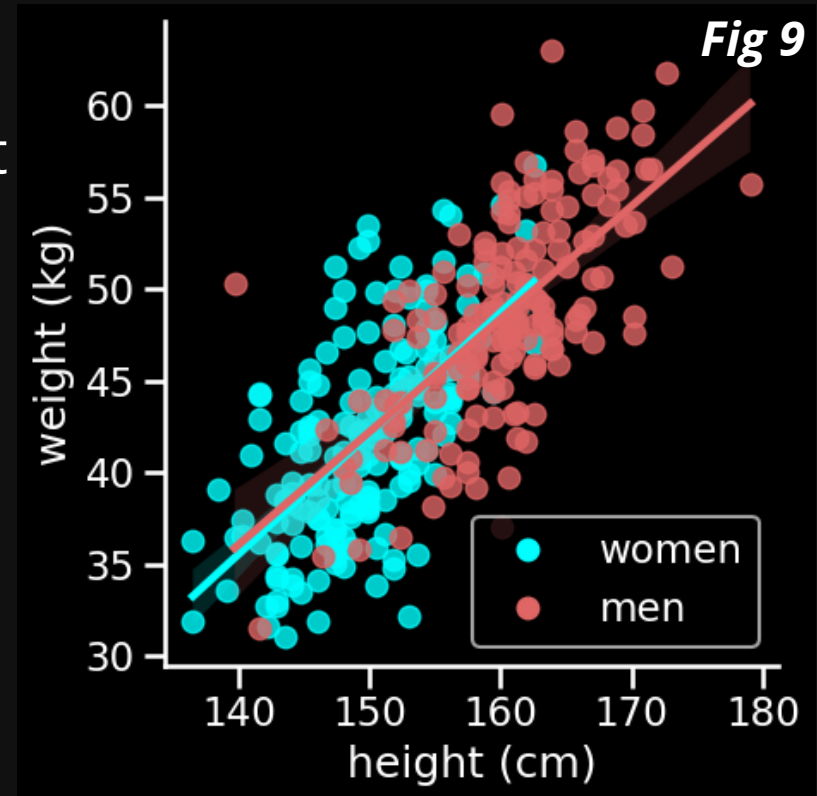
(1) Compute posterior mean weight for women

(2) Compute posterior mean weight for men

(3) Subtract (2) from (1)

(4) Plot contrast distribution at each height

Don't rely on a plot such as this one for determining differences in influence of gender on weight



Contrasts at each height

Code 9

```
import arviz as az

height_seq = np.linspace(130, 180, 30)

data_thin = az.extract(m_GHW_idata, num_samples = 1000)
mu_pred_W = np.empty((len(height_seq), data_thin.sizes["sample"]))
mu_pred_M = np.empty((len(height_seq), data_thin.sizes["sample"]))

for i, ht in enumerate(height_seq):
    mu_pred_W[i] = data_thin.a.values[0] + data_thin.b.values[0] * (ht - df2.height.mean())
    mu_pred_M[i] = data_thin.a.values[1] + data_thin.b.values[1] * (ht - df2.height.mean())

mu_pred_contrast = mu_pred_W - mu_pred_M

for p in [0.5, 0.6, 0.7, 0.8, 0.9, 0.99]:
    _ = az.plot_hdi(height_seq, mu_pred_contrast.T, hdi_prob=p)

_ = plt.plot(height_seq, [0] * len(height_seq), "_", color='k')
_ = plt.xlabel("height (cm)")
_ = plt.ylabel("weight contrast (F - M)")
_ = sns.despine()
```


Contrasts at each height

Code 9

```
import arviz as az

height_seq = np.linspace(130, 180, 30)  # grid of heights to use
                                       # for predictions

data_thin = az.extract(m_GHW_idata, num_samples = 1000)
mu_pred_W = np.empty((len(height_seq), data_thin.sizes["sample"]))
mu_pred_M = np.empty((len(height_seq), data_thin.sizes["sample"]))

for i, ht in enumerate(height_seq):
    mu_pred_W[i] = data_thin.a.values[0] + data_thin.b.values[0] * (ht - df2.height.mean())
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mu_pred_W = np.empty((len(height_seq), data_thin.sizes["sample"]))
mu_pred_M = np.empty((len(height_seq), data_thin.sizes["sample"]))

for i, ht in enumerate(height_seq):
    mu_pred_W[i] = data_thin.a.values[0] + data_thin.b.values[0] * (ht - df2.height.mean())
    mu_pred_M[i] = data_thin.a.values[1] + data_thin.b.values[1] * (ht - df2.height.mean())

mu_pred_contrast = mu_pred_W - mu_pred_M

for p in [0.5, 0.6, 0.7, 0.8, 0.9, 0.99]:
    _ = az.plot_hdi(height_seq, mu_pred_contrast.T, hdi_prob=p)

_ = plt.plot(height_seq, [0] * len(height_seq), "_", color='k')
_ = plt.xlabel("height (cm)")
_ = plt.ylabel("weight contrast (F - M)")
_ = sns.despine()
```

extract 1000 samples
from posterior

Contrasts at each height

Code 9

```
import arviz as az

height_seq = np.linspace(130, 180, 30)

data_thin = az.extract(m_GHW_idata, num_samples = 1000)
mu_pred_W = np.empty((len(height_seq), data_thin.sizes["sample"]))
mu_pred_M = np.empty((len(height_seq), data_thin.sizes["sample"]))

for i, ht in enumerate(height_seq):
    mu_pred_W[i] = data_thin.a.values[0] + data_thin.b.values[0] * (ht - df2.height.mean())
    mu_pred_M[i] = data_thin.a.values[1] + data_thin.b.values[1] * (ht - df2.height.mean())

mu_pred_contrast = mu_pred_W - mu_pred_M

for p in [0.5, 0.6, 0.7, 0.8, 0.9, 0.99]:
    _ = az.plot_hdi(height_seq, mu_pred_contrast.T, hdi_prob=p)

_ = plt.plot(height_seq, [0] * len(height_seq), "_", color='k')
_ = plt.xlabel("height (cm)")
_ = plt.ylabel("weight contrast (F - M)")
_ = sns.despine()
```

storage for posterior mean weights by gender

Contrasts at each height

Code 9

```
import arviz as az
```

```
height_seq = np.linspace(130, 180, 30)
```

```
data_thin = az.extract(m_GHW_idata, num_samples = 1000)
```

```
mu_pred_W = np.empty((len(height_seq), data_thin.sizes["sample"]))
```

```
mu_pred_M = np.empty((len(height_seq), data_thin.sizes["sample"]))
```

```
for i, ht in enumerate(height_seq):
```

```
    mu_pred_W[i] = data_thin.a.values[0] + data_thin.b.values[0] * (ht - df2.height.mean())
```

```
    mu_pred_M[i] = data_thin.a.values[1] + data_thin.b.values[1] * (ht - df2.height.mean())
```

```
mu_pred_contrast = mu_pred_W - mu_pred_M
```

```
for p in [0.5, 0.6, 0.7, 0.8, 0.9, 0.99]:
```

```
    _ = az.plot_hdi(height_seq, mu_pred_contrast.T, hdi_prob=p)
```

```
_ = plt.plot(height_seq, [0] * len(height_seq), "_", color='k')
```

```
_ = plt.xlabel("height (cm)")
```

```
_ = plt.ylabel("weight contrast (F - M)")
```

```
_ = sns.despine()
```



calculate 1000 expected weights for each height from posterior samples (by gender)

Contrasts at each height

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```
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data_thin = az.extract(m_GHW_idata, num_samples = 1000)
mu_pred_W = np.empty((len(height_seq), data_thin.sizes["sample"]))
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for i, ht in enumerate(height_seq):
    mu_pred_W[i] = data_thin.a.values[0] + data_thin.b.values[0] * (ht - df2.height.mean())
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```

compute contrast distribution
for expected weights

Contrasts at each height

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    mu_pred_W[i] = data_thin.a.values[0] + data_thin.b.values[0] * (ht - df2.height.mean())
    mu_pred_M[i] = data_thin.a.values[1] + data_thin.b.values[1] * (ht - df2.height.mean())

mu_pred_contrast = mu_pred_W - mu_pred_M

for p in [0.5, 0.6, 0.7, 0.8, 0.9, 0.99]: vary high density interval size
    _ = az.plot_hdi(height_seq, mu_pred_contrast.T, hdi_prob=p)

_ = plt.plot(height_seq, [0] * len(height_seq), "_", color='k')
_ = plt.xlabel("height (cm)")
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```

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mu_pred_M = np.empty((len(height_seq), data_thin.sizes["sample"]))

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    _ = az.plot_hdi(height_seq, mu_pred_contrast.T, hdi_prob=p)

_ = plt.plot(height_seq, [0] * len(height_seq), "_", color='k')
_ = plt.xlabel("height (cm)")
_ = plt.ylabel("weight contrast (F - M)")
```

plot high density interval for
contrast distribution

Contrasts at each height

Code 9

```
import arviz as az

height_seq = np.linspace(130, 180, 30)

data_thin = az.extract(m_GHW_idata, num_samples = 1000)
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_ = plt.plot(height_seq, [0] * len(height_seq), "_", color='k')
_ = plt.xlabel("height (cm)")
_ = plt.ylabel("weight contrast (F - M)")
```

plot line representing NO
difference in expected weights

Contrasts at each height

Code 9

```
import arviz as az

height_seq = np.linspace(130, 180, 30)

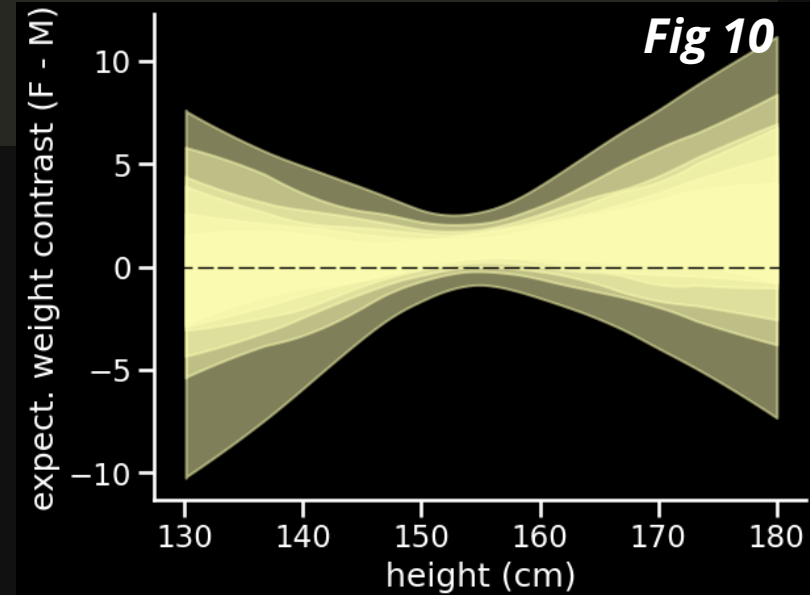
data_thin = az.extract(m_GHW_idata, num_samples = 1000)
mu_pred_W = np.empty((len(height_seq), data_thin.sizes["sample"]))
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Contrasts at each height

Code 9

```
import arviz as az

height_seq = np.linspace(130, 180, 30)

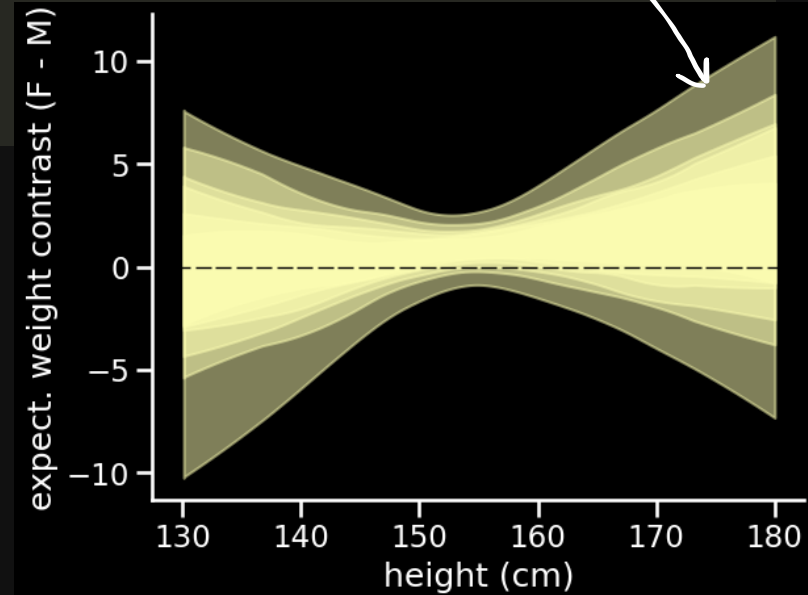
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Contrasts at each height

Code 9

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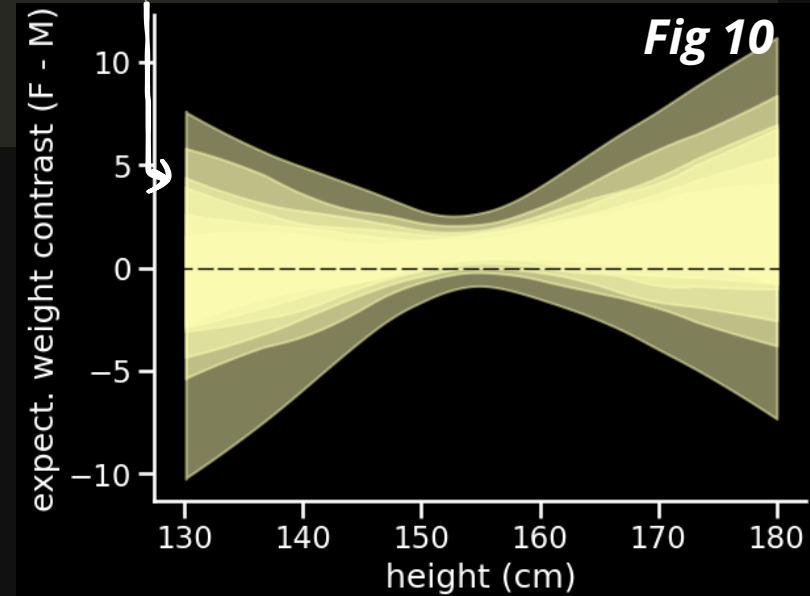
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Contrasts at each height

Code 9

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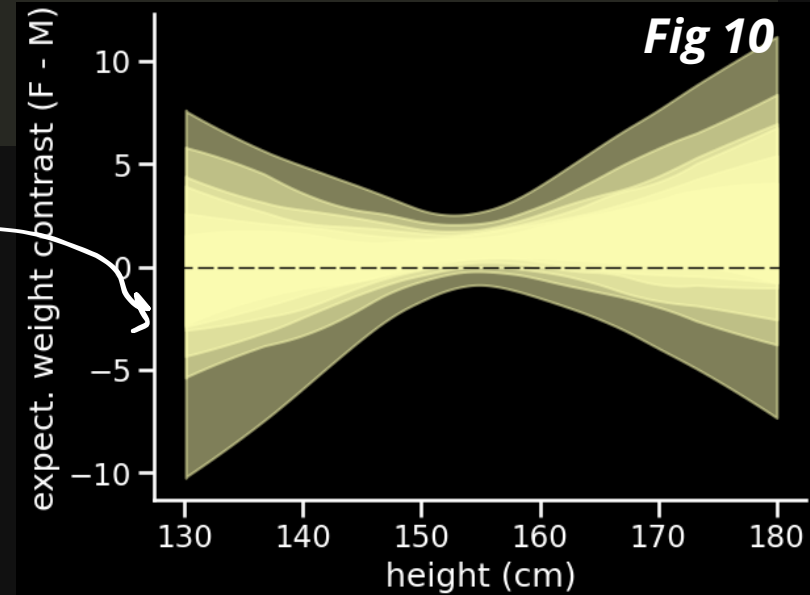
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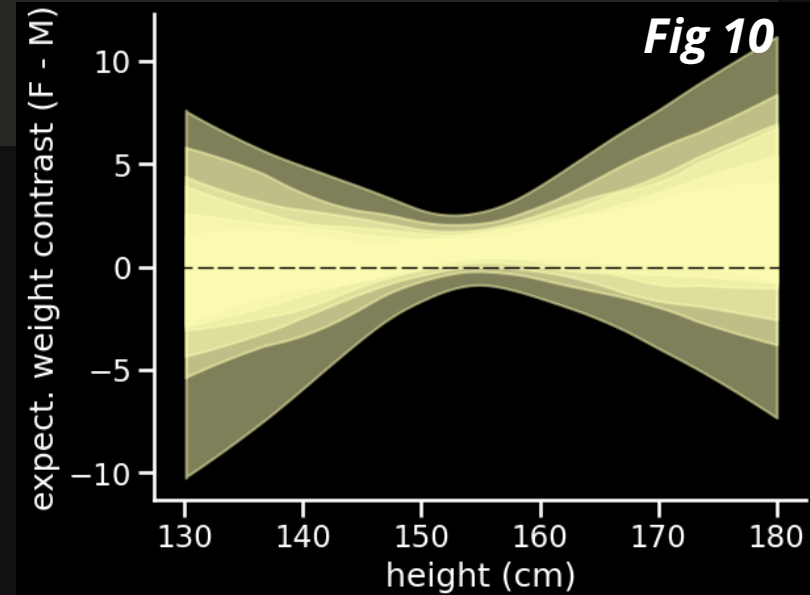
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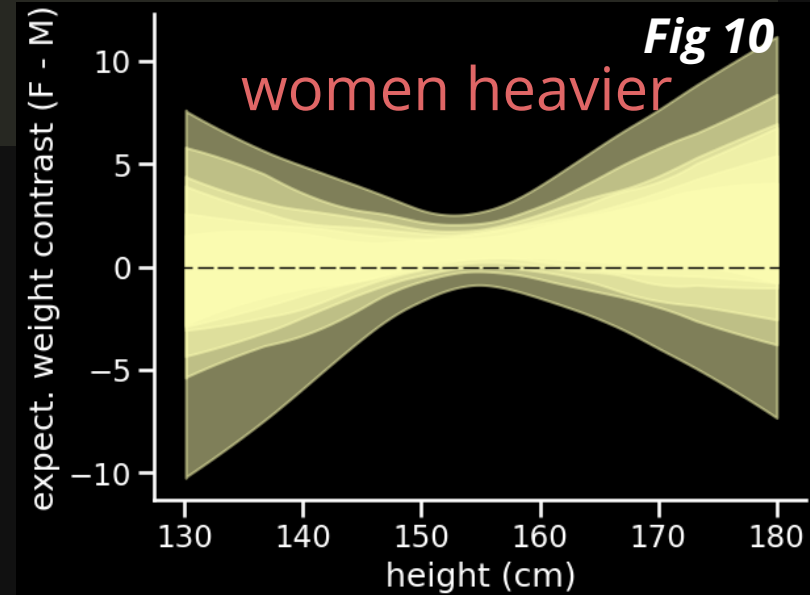
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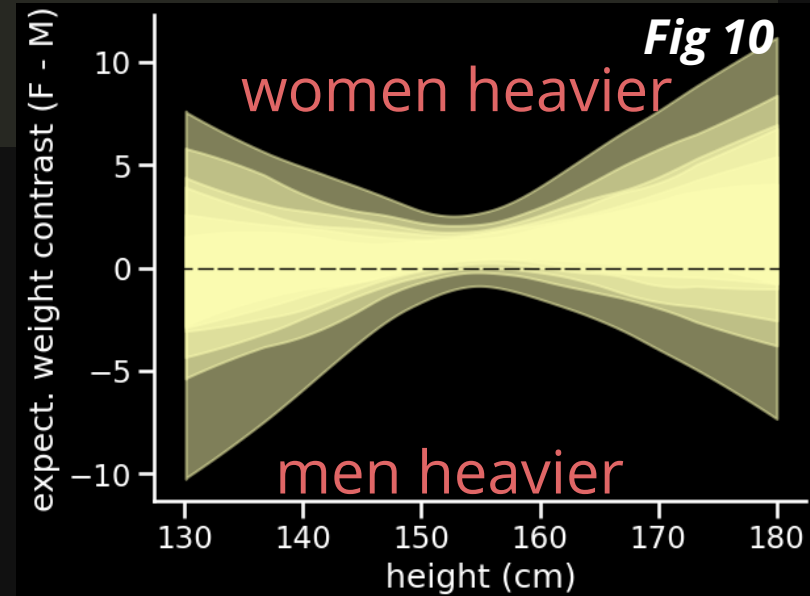
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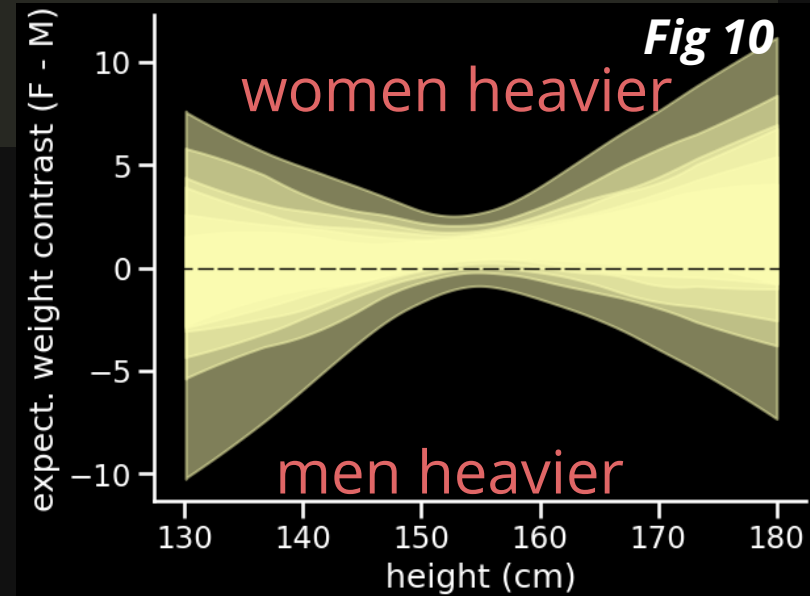
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contrast distribution *relatively*
symmetric around value for no
difference (0)



Contrasts at each height

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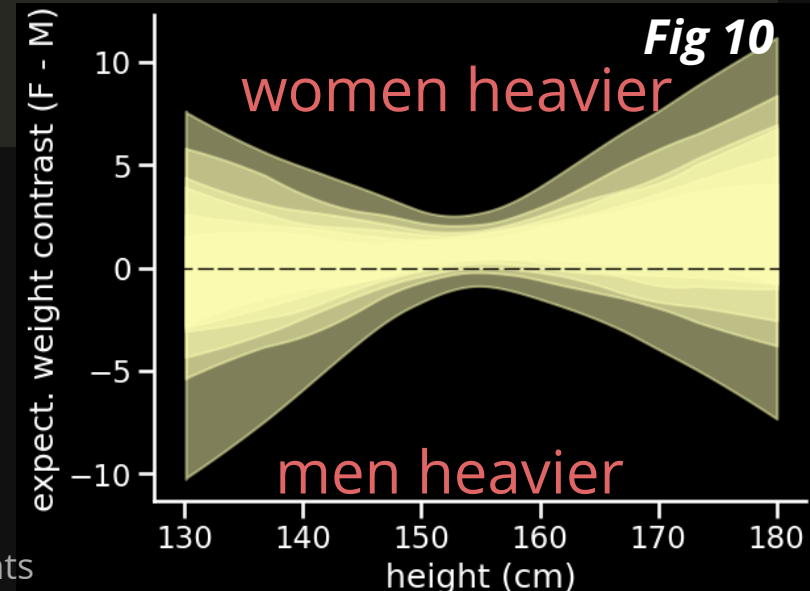
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```

contrast distribution *relatively*
symmetric around value for no
difference (0)

less symmetry at extreme heights



Contrasts at each height

Code 9

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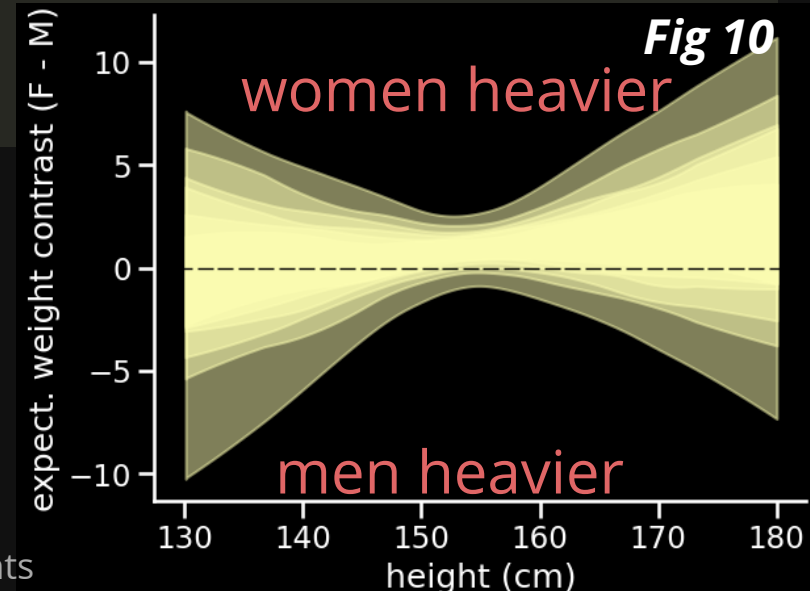
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```

contrast distribution *relatively*
symmetric around value for no
difference (0)

Nearly all of the causal
effect of G acts through H

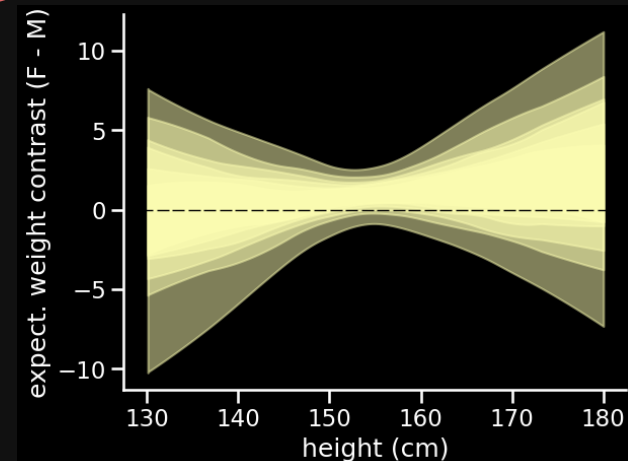
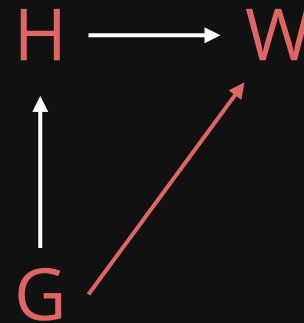
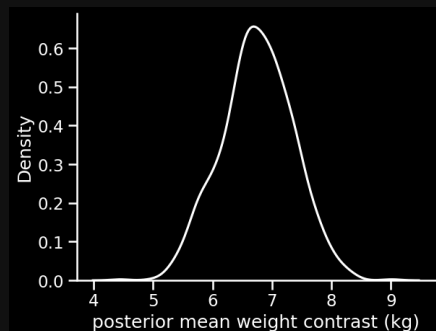
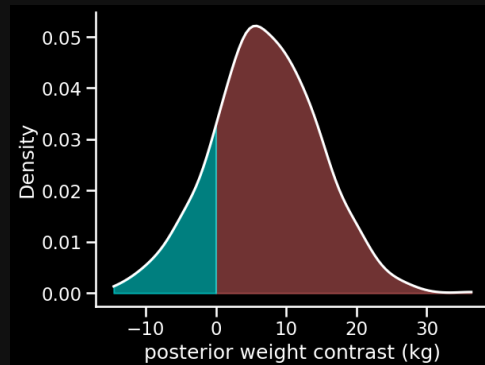
less symmetry at extreme heights



From estimand to estimate

Q: Total causal effect of G on W?

Q: Direct causal effect of G on W?



Summary

Linear regression

(1) Question/goal/estimand

(2) Scientific model

(3) Statistical model

(4) Validate model

(5) Analyze data

Inference with linear models

1. State each estimand

Inference with linear models

With more than two variables, scientific (causal) model and statistical model not always same

1. State each estimand
2. Design **unique statistical model** for each

**ONE STAT MODEL
FOR EACH ESTIMAND**

Inference with linear models

With more than two variables, scientific (causal) model and statistical model not always same

1. State each estimand
2. Design **unique statistical model** for each
3. **Compute** each estimand

**ONE STAT MODEL
FOR EACH ESTIMAND**

Inference with linear models

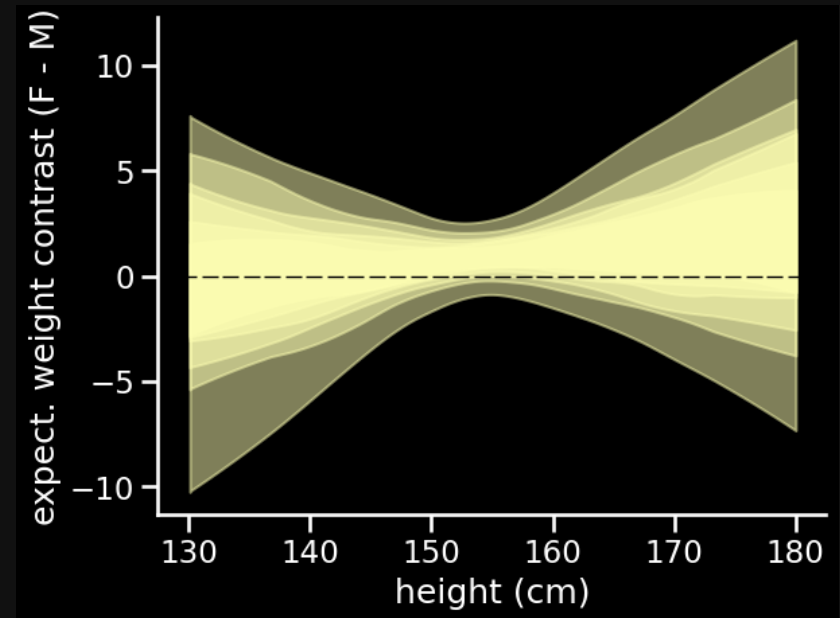
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Categorical variables

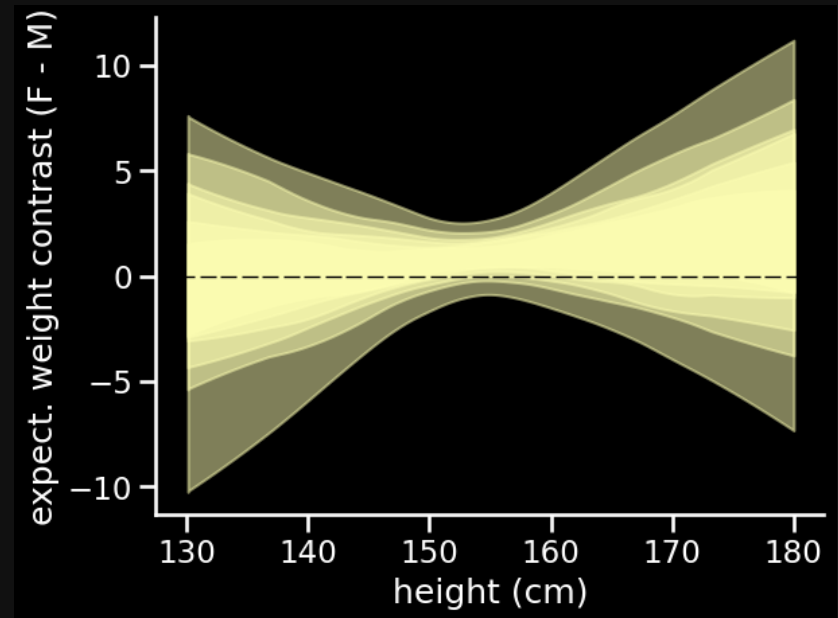
Easy to use with index coding



Categorical variables

Easy to use with index coding

Must later use samples to compute relevant contrasts

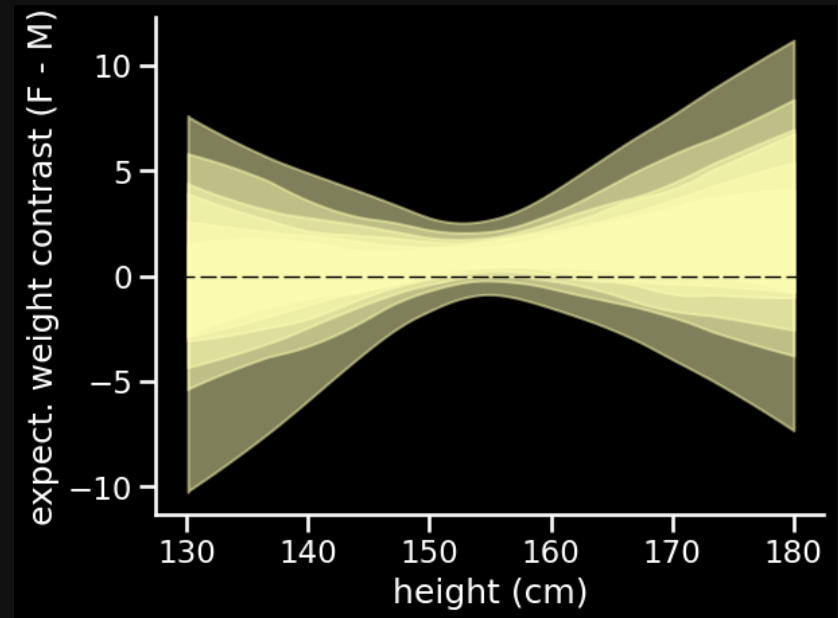


Categorical variables

Easy to use with index coding

Must later use samples to compute relevant contrasts

Always summarize (mean, interval) as last step



Categorical variables

Easy to use with index coding

Must later use samples to compute relevant contrasts

Always summarize (mean, interval) as last step

Want **mean difference** and not **difference of means**

