

# HST.508 HW2

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## 1 Problem 1

### 1.1 Problem 1 a

```
from utils import plot
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt

def probability_of_fixation(N,S,p):
    return (1-np.exp(-2*N*S*p))/(1-np.exp(-2*N*S))
N = 300
ps = [0.001,0.01,0.1]

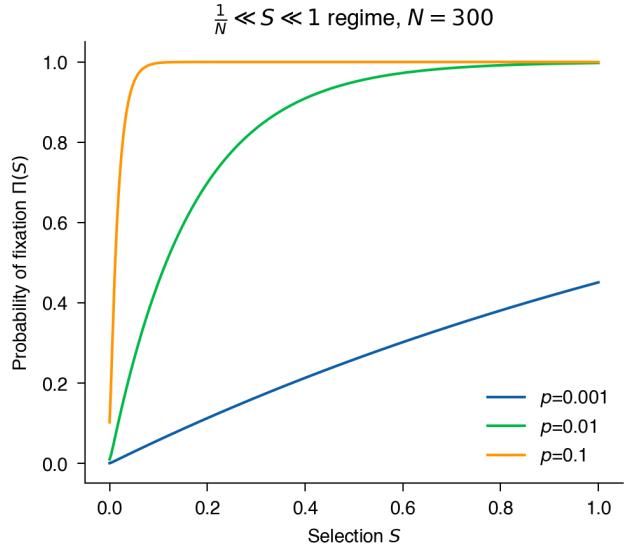
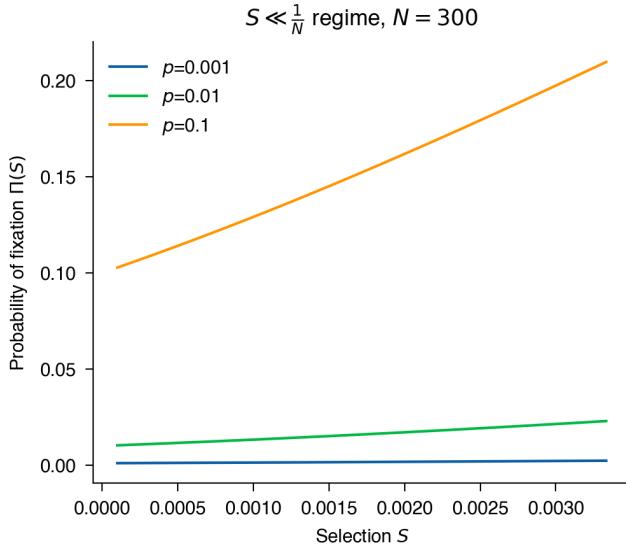
fig, ax = plt.subplots(1,2)
fig.set_size_inches(8,3)

Ss = np.linspace(start=1e-4, stop=1/N, num=500)
ax[0].set_ylabel("Probability of fixation $\Pi(S)$")
ax[0].set_xlabel("Selection $S$")
ax[0].set_title(r"$S \ll \frac{1}{N}$ regime, $N=300$")
for p in ps:
    sns.lineplot(x=Ss,y=probability_of_fixation(N,Ss,p), ax=ax[0], label=f"${p}={p:.2g}$")
```

```

Ss = np.linspace(start=1e-4, stop=1, num=500)
ax[1].set_ylabel("Probability of fixation  $\Pi(S)$ ")
ax[1].set_xlabel("Selection  $S$ ")
ax[1].set_title(r"$S \ll \frac{1}{N} \text{ regime, } N=300$")
for p in ps:
    sns.lineplot(x=Ss,y=probability_of_fixation(N,Ss,p), ax=ax[1], label=f"$p={p:.2g}$")

```



## 1.2 Problem 1 b

```

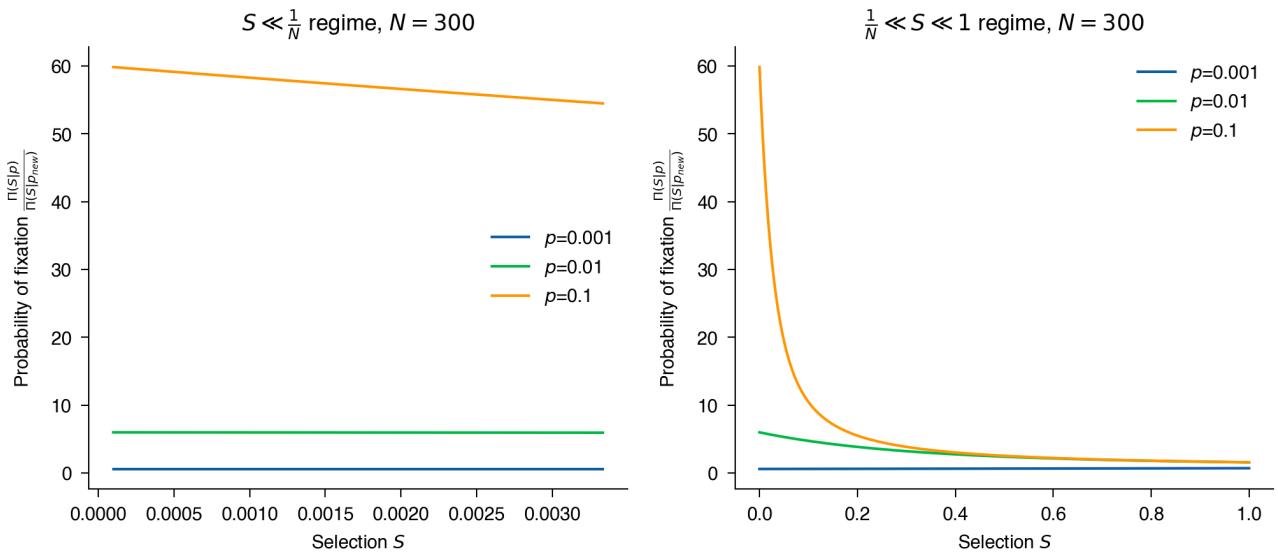
fig, ax = plt.subplots(1,2)
fig.set_size_inches(8,3)

N = 300
p_new = 1/(2*N)
ps = [0.001, 0.01, 0.1]

Ss = np.linspace(start=1e-4, stop=1/N, num=500)
ax[0].set_ylabel(r"Probability of fixation  $\frac{\Pi(S|p)}{\Pi(S|p_{\text{new}})}$ ")
ax[0].set_xlabel("Selection  $S$ ")
ax[0].set_title(r"$S \ll \frac{1}{N} \text{ regime, } N=300$")
for p in ps:
    sns.lineplot(x=Ss,y=probability_of_fixation(N,Ss,p)/probability_of_fixation(N,Ss,p_new), ax=ax[0])

Ss = np.linspace(start=1e-4, stop=1, num=500)
ax[1].set_ylabel(r"Probability of fixation  $\frac{\Pi(S|p)}{\Pi(S|p_{\text{new}})}$ ")
ax[1].set_xlabel("Selection  $S$ ")
ax[1].set_title(r"$\frac{1}{N} \ll S \ll 1 \text{ regime, } N=300$")
for p in ps:
    sns.lineplot(x=Ss,y=probability_of_fixation(N,Ss,p)/probability_of_fixation(N,Ss,p_new), ax=ax[1])

```



### 1.3 Problem 1 c

$$\begin{aligned}\Pi(p) &= C_1 e^{-2NSp} + C_2 \\ \Pi(f) &= 1 \quad \Pi(0) = 0\end{aligned}$$

$$\begin{aligned}\Pi(0) &= 0 = C_1 + C_2 \implies C_2 = -C_1 \\ \Pi(f) &= 1 = C_1 e^{-2NSf} + C_2 \implies C_2 = 1 - C_1 e^{-2NSf}\end{aligned}$$

$$1 - C_1 e^{-2NSf} = -C_1 \implies C_1 = \frac{1}{e^{-2NSf} - 1}$$

$$\begin{aligned}\Pi(p) &= C_1 e^{-2NSp} - C_1 = \frac{e^{-2NSp} - 1}{e^{-2NSf} - 1} \\ \Pi(p) &= \frac{1 - e^{-2NSp}}{1 - e^{-2NSf}}\end{aligned}$$

$$p = -\frac{1}{2NS} \ln [1 - \Pi(p) (1 - e^{-2NSf})]$$

```
def initial_freq_near_fixation(N,S,f,p_fixation):
    return -1/(2*N*S)*np.log(1-p_fixation*(1-np.exp(-2*N*S*f)))

fig, ax = plt.subplots(1,2)
fig.set_size_inches(8,3)

N = np.arange(300,5e4)
S = 0.001
f = 0.90

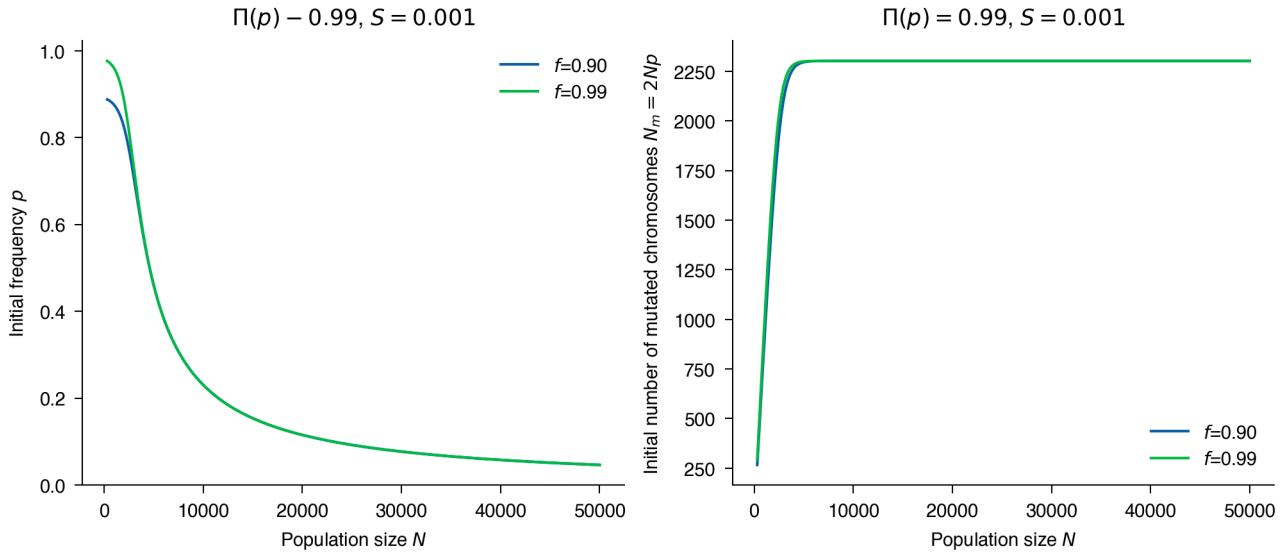
for f in [0.90,0.99]:
    p_fixation = 0.99
    ax[0].set_ylabel(r"Initial frequency $p$")
```

```

ax[0].set_xlabel("Population size $N$")
ax[0].set_title(r"$\Pi(p)=0.99$, $S=0.001$")
sns.lineplot(x=N,y=initial_freq_near_fixation(N,S,f,p_fixation),ax=ax[0] ,
label=f"${f}={f:.2f}$")

ax[1].set_ylabel(r"Initial number of mutated chromosomes $N_m=2Np$")
ax[1].set_xlabel("Population size $N$")
ax[1].set_title(r"$\Pi(p)=0.99$, $S=0.001$")
sns.lineplot(x=N,y=N*initial_freq_near_fixation(N,S,f,p_fixation),ax=ax[1] ,
label=f"${f}={f:.2f}$")

```



The actual number of mutated chromosomes  $N_m = 2Np$

$$N_m = Np = -\frac{1}{S} \ln[1 - \Pi(p)(1 - e^{-2NSf})]$$

In the limit of large  $N$ , the exponent term  $e^{-2NSf} \rightarrow 0$ , and the actual number of mutated chromosomes will not depend on the population size.

$$\lim_{N \rightarrow \infty} N_m = -\frac{1}{S} \ln[1 - \Pi(p)]$$

The initial frequency for near-fixation decreases with population size. For large populations, mutations that exceed a constant threshold  $N_m$  are fixed with high (99%) probability.

## 2 Problem 2

### 2.1 Problem 2 a

```

import pandas as pd
import numpy as np
from scipy.stats import linregress
import seaborn as sns
import matplotlib.pyplot as plt

```

```
df = pd.read_csv("./pset_2_assets/times.csv", index_col=0)
df["Parent_Mid"] = (df["Parent_1"]+df["Parent_2"])/2
```

Maternal and paternal genotypes are independent. For this section of the question, we are interested in the effects of genotype only, ignore covariance of maternal-offspring environment and the covariance of offspring genotype-environment. Assume no dominance, such that the covariance in the allele Cov( $M, M'$ ) is zero.

$$\text{Cov}(M, O) = \underline{\text{Cov}(X_P, X_M)} + \text{Cov}(X_M, X_M) + \underline{\text{Cov}(X_P, X_{M'})} + \text{Cov}(X_M, X_{M'}) + \text{Cov}(X_O, E_O) + \text{Cov}(E_M, E_O)$$

$$\text{Cov}(M, O) = \text{Cov}(X_M, X_M) = \text{Var}(X_M) = \frac{V_A}{2}$$

$$\text{Var}(M) = \text{Var}(P) = \text{Var}(O) = V_{\text{Phenotype}}$$

$$\text{CorrCoef}(M, O) = \frac{\text{Cov}(M, O)}{\sqrt{\text{Var}(M)\text{Var}(O)}} = \frac{V_A/2}{V_{\text{Phenotype}}} = \frac{h^2}{2}$$

$$X_{\text{Mid}} = \frac{X_P + X_M}{2}$$

$$\text{Var}(\text{Mid}) = \frac{2\text{Var}(X)}{4} = \frac{V_{\text{Phenotype}}}{2}$$

$$\text{CorrCoef}(M, \text{Mid}) = \frac{\text{Cov}(M, O)}{\sqrt{\text{Var}(\text{Mid})\text{Var}(O)}} = \frac{V_A/2}{V_{\text{Phenotype}}/\sqrt{2}} = \frac{h^2}{\sqrt{2}}$$

```
def reg(x, y, factor, **kwargs):
    """https://stackoverflow.com/questions/67268096
    how-to-display-pearsonr-squared-and-regression-equation-on-a-pairplot
    """
    ax = plt.gca()
    slope, intercept, r_value, p_value, std_err = linregress(x=x, y=y)
    # r=((x-x.mean())*(y-y.mean())).sum()/np.sqrt(((x-x.mean())**2).sum()*((y-y.mean())**2))
    ax.annotate(f'r ={r_value:.2f}\nhat y={slope:.2f}x{intercept:+.2f}' +
               f'\n^2={factor*r_value:.2f}', xy=(.05, .95), xycoords=ax.transAxes, fontsize=8,
               color='black', ha='left', va='top')

g = sns.pairplot(df, x_vars=["Parent_1", "Parent_2"],
                  y_vars=["Full_sibling_1", "Full_sibling_2"],
                  kind="reg",
                  plot_kws={'line_kws':{'color':'red'},
                            'scatter_kws': {'alpha': 0.2}})
g.map(lambda x, y, **kwargs: reg(x, y, 2, **kwargs));

g = sns.pairplot(df, x_vars=["Parent_Mid"],
                  y_vars=["Full_sibling_1", "Full_sibling_2"],
                  kind="reg",
```

```

plot_kws={'line_kws':{'color':'red'},
          'scatter_kws': {'alpha': 0.2}})
g.map(lambda x, y, **kwargs: reg(x, y, np.sqrt(2), **kwargs));

```

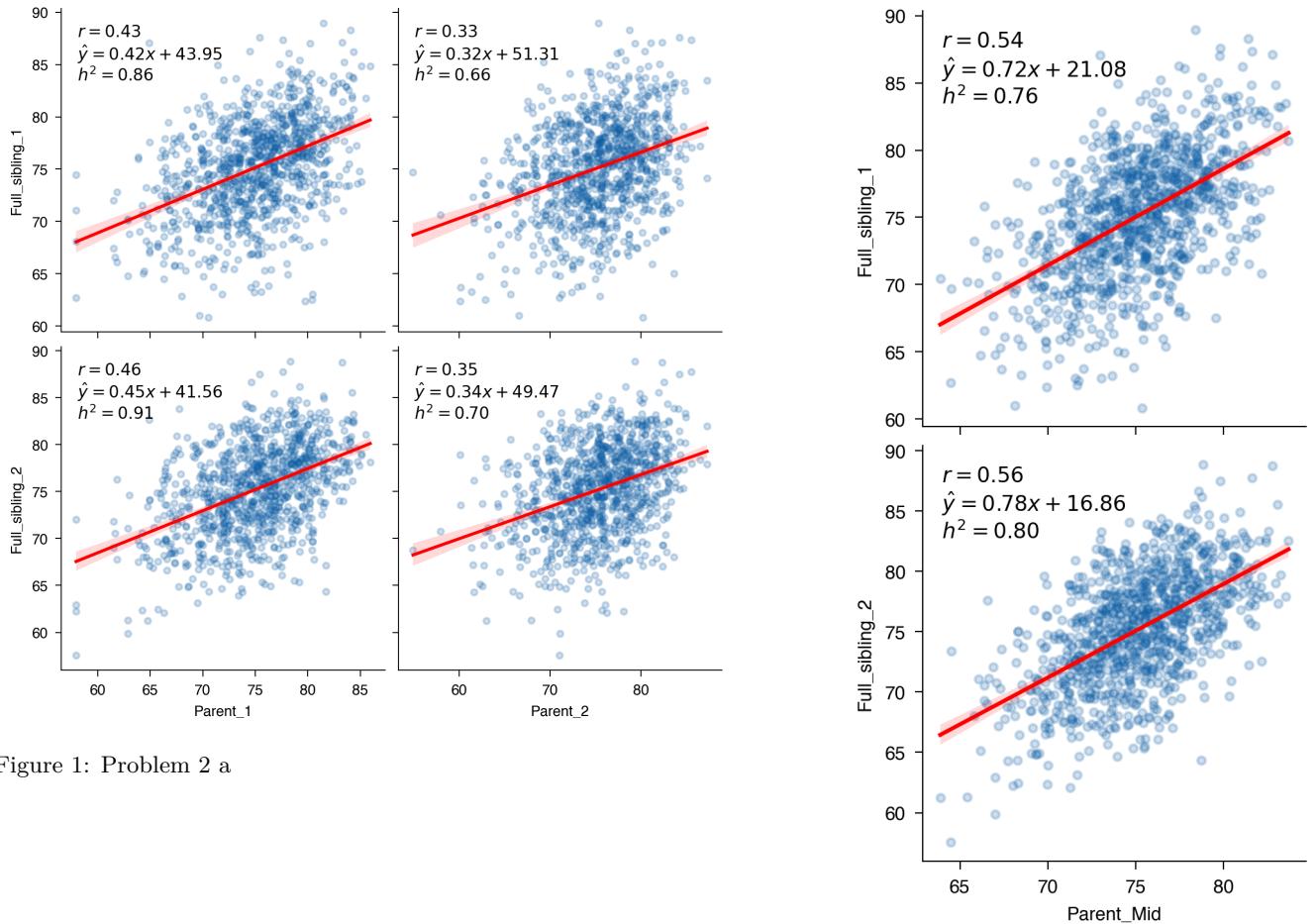


Figure 1: Problem 2 a

## 2.2 Problem 2 b

Assuming no dominance and independent parental genotypes. Not ignoring environmental variance:

$$\text{Cov}(M, O) = \text{Var}(X_M) + \text{Cov}(X_O, E_O) + \text{Cov}(E_M, E_O)$$

$$\text{Var}(X_M) = \frac{V_A}{2}$$

$$h_E^2 = \frac{V_A}{V_{\text{Phenotype}}} = \frac{2\text{Cov}(M, O)}{\sqrt{\text{Var}(M)\text{Var}(O)}} - \frac{2(\text{Cov}(X_O, E_O) + \text{Cov}(E_M, E_O))}{\sqrt{\text{Var}(M)\text{Var}(O)}} < h_{\text{No } E}^2$$

In the presence of environmental variance, there is an environmental contribution to the covariance of the dataset, decreasing the genotype variance estimated from the dataset, resulting in a decrease in the heritability.

### Case E1: Simulating $E_{M/P} = E_{O_1/O_2}$

```

mu = 0
std = 5
df_case_E1 = df+np.random.normal(mu, std, df.shape)

g = sns.pairplot(df_case_E1,x_vars=["Parent_1","Parent_2"],
                  y_vars=["Full_sibling_1","Full_sibling_2"],
                  kind="reg",
                  plot_kws={'line_kws':{'color':'red'},
                             'scatter_kws': {'alpha': 0.2}})
g.map(lambda x, y, **kwargs: reg(x, y, 2, **kwargs));

g = sns.pairplot(df_case_E1,x_vars=["Parent_Mid"],
                  y_vars=["Full_sibling_1","Full_sibling_2"],
                  kind="reg",
                  plot_kws={'line_kws':{'color':'red'},
                             'scatter_kws': {'alpha': 0.2}})
g.map(lambda x, y, **kwargs: reg(x, y, np.sqrt(2), **kwargs));

```

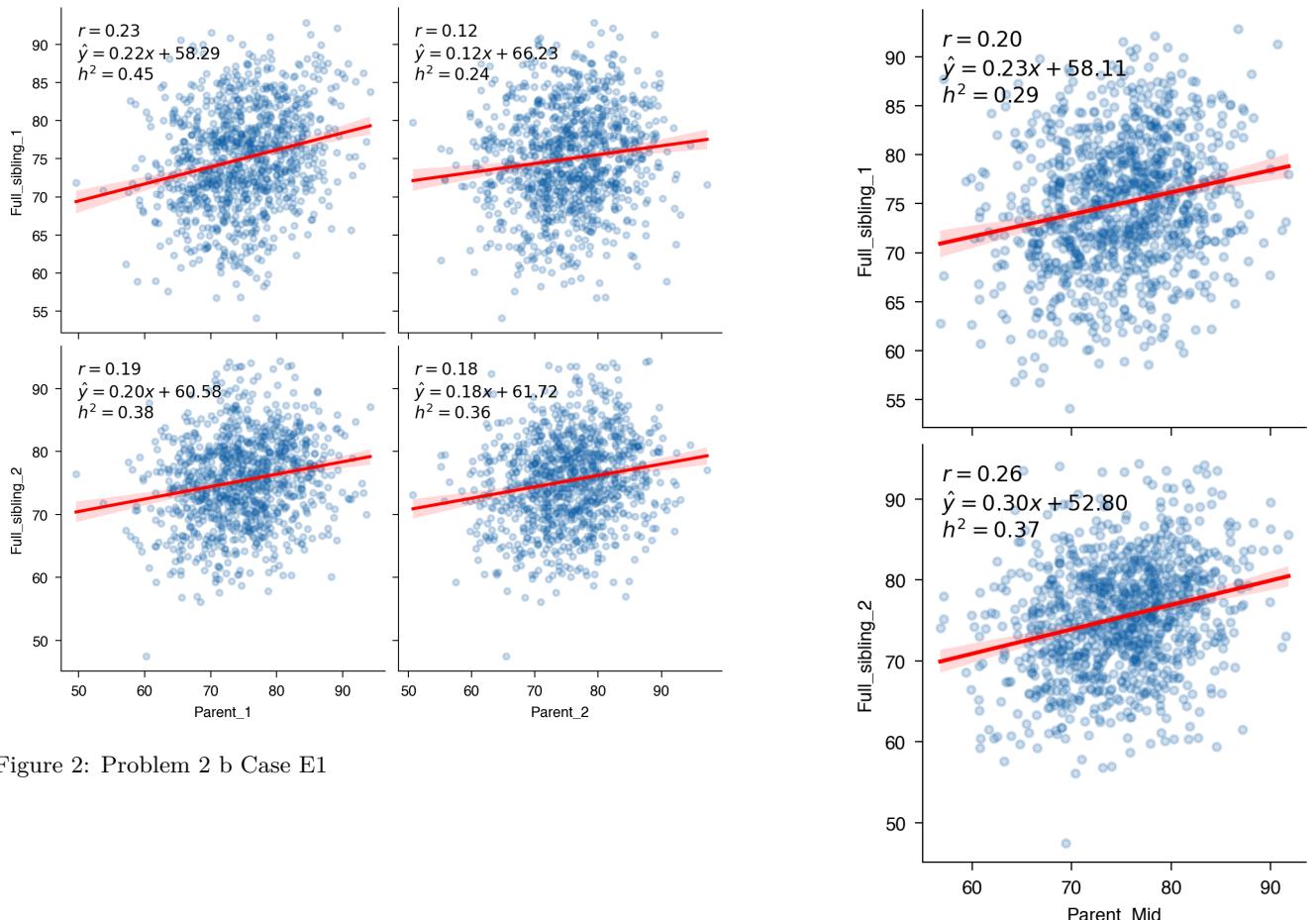


Figure 2: Problem 2 b Case E1

The heritability decreases

### Case E2: Simulating $E_{M/P} > E_{O_1/O_2}$

```
def noise_P0(df, std_P, std_0):
    for column in df.columns:
        if column.startswith("Parent"):
            mu = 0
            std = std_P
            df[column] += np.random.normal(mu, std, df.shape[0])
        elif column.startswith("Full_sibling"):
            mu = 0
            std = std_0
            df[column] += np.random.normal(mu, std, df.shape[0])

g = sns.pairplot(df, x_vars=["Parent_1", "Parent_2"],
                  y_vars=["Full_sibling_1", "Full_sibling_2"],
                  kind="reg",
                  plot_kws={'line_kws': {'color': 'red'},
                             'scatter_kws': {'alpha': 0.2}})
g.map(lambda x, y, **kwargs: reg(x, y, 2, **kwargs));

g = sns.pairplot(df, x_vars=["Parent_Mid"],
                  y_vars=["Full_sibling_1", "Full_sibling_2"],
                  kind="reg",
                  plot_kws={'line_kws': {'color': 'red'},
                             'scatter_kws': {'alpha': 0.2}})
g.map(lambda x, y, **kwargs: reg(x, y, np.sqrt(2), **kwargs));

noise_P0(df.copy(), 7.5, 2.5)
```

### Case E3: Simulating $E_{M/P} < E_{O_1/O_2}$

```
noise_P0(df.copy(), 2.5, 7.5)
```

### Case E4: Simulating $E_{O_1} > E_{O_2}$

```
def noise_0102(df, std_01, std_02):
    for column in df.columns:
        if column.startswith("Full_sibling_1"):
            mu = 0
            std = std_01
            df[column] += np.random.normal(mu, std, df.shape[0])
        elif column.startswith("Full_sibling_2"):
            mu = 0
            std = std_02
            df[column] += np.random.normal(mu, std, df.shape[0])

g = sns.pairplot(df, x_vars=["Parent_1", "Parent_2"],
                  y_vars=["Full_sibling_1", "Full_sibling_2"],
```

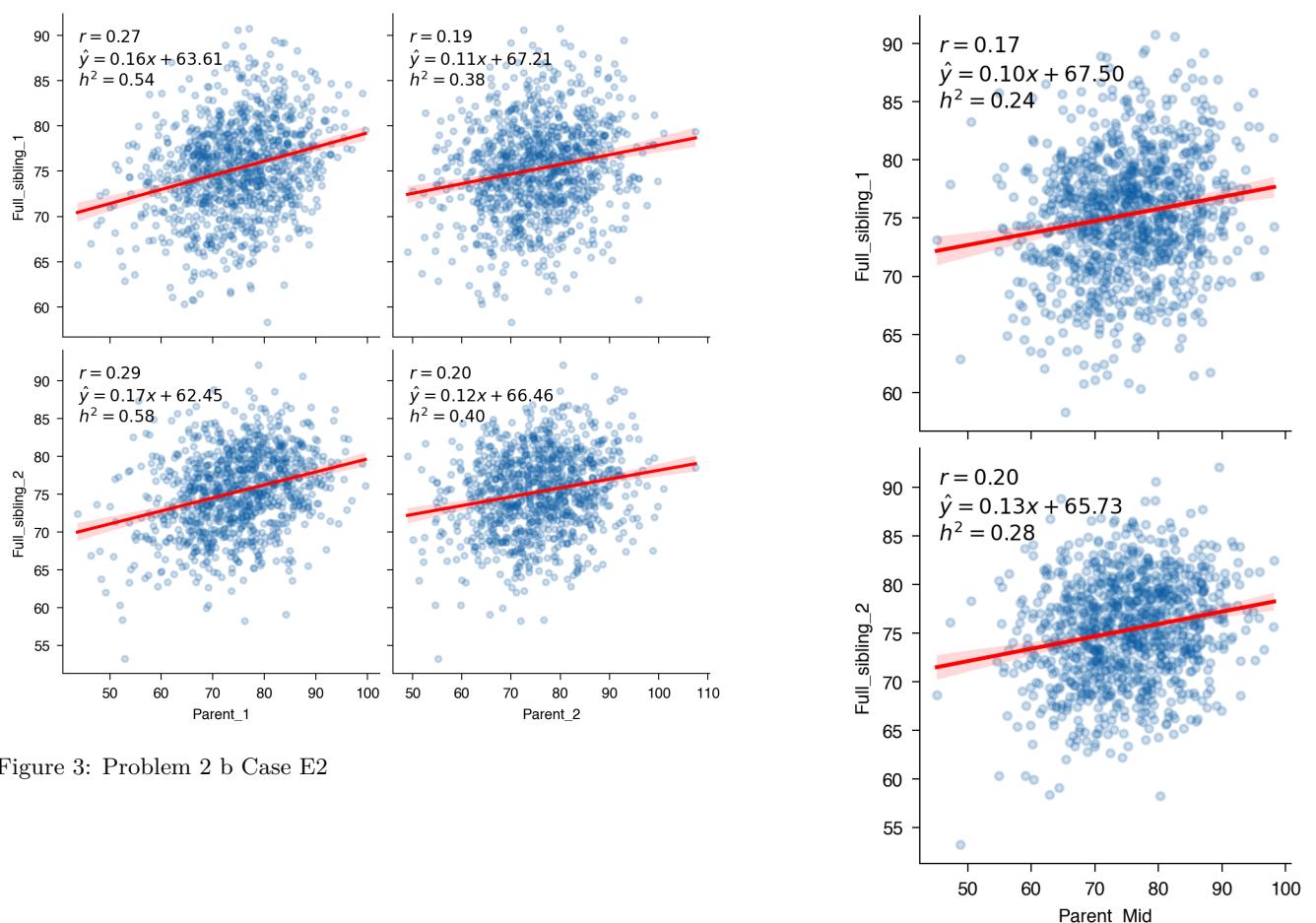


Figure 3: Problem 2 b Case E2

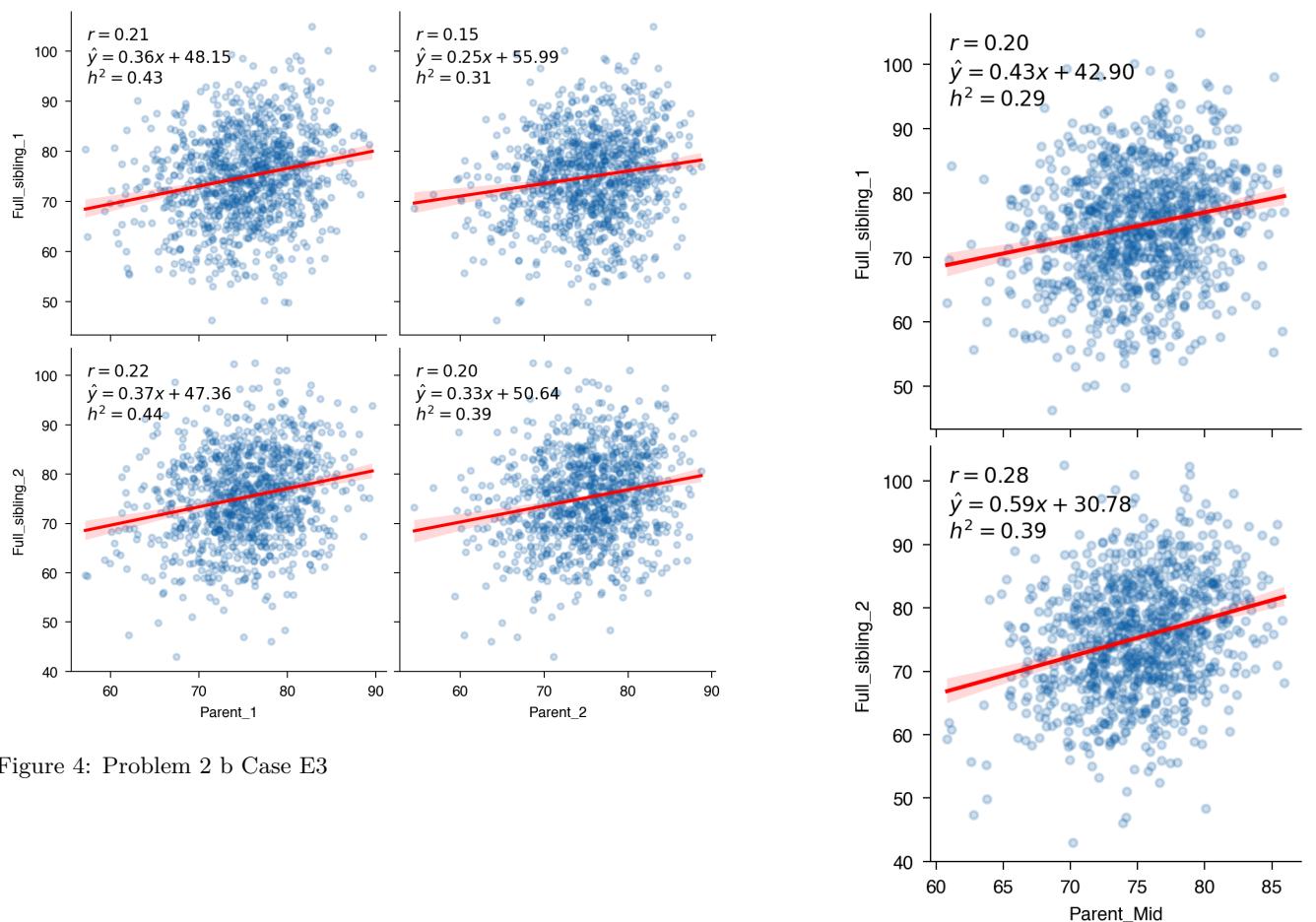


Figure 4: Problem 2 b Case E3

```

        kind="reg",
        plot_kws={'line_kws':{'color':'red'},
                   'scatter_kws': {'alpha': 0.2}})
g.map(lambda x, y, **kwargs: reg(x, y, 2, **kwargs))
g.fig.set_figheight(4)

g = sns.pairplot(df,x_vars=["Parent_Mid"],
                  y_vars=["Full_sibling_1","Full_sibling_2"],
                  kind="reg",
                  plot_kws={'line_kws':{'color':'red'},
                             'scatter_kws': {'alpha': 0.2}})
g.map(lambda x, y, **kwargs: reg(x, y, np.sqrt(2), **kwargs))
g.fig.set_figheight(4);

```

`noise_0102(df.copy(), 7.5, 2.5)`

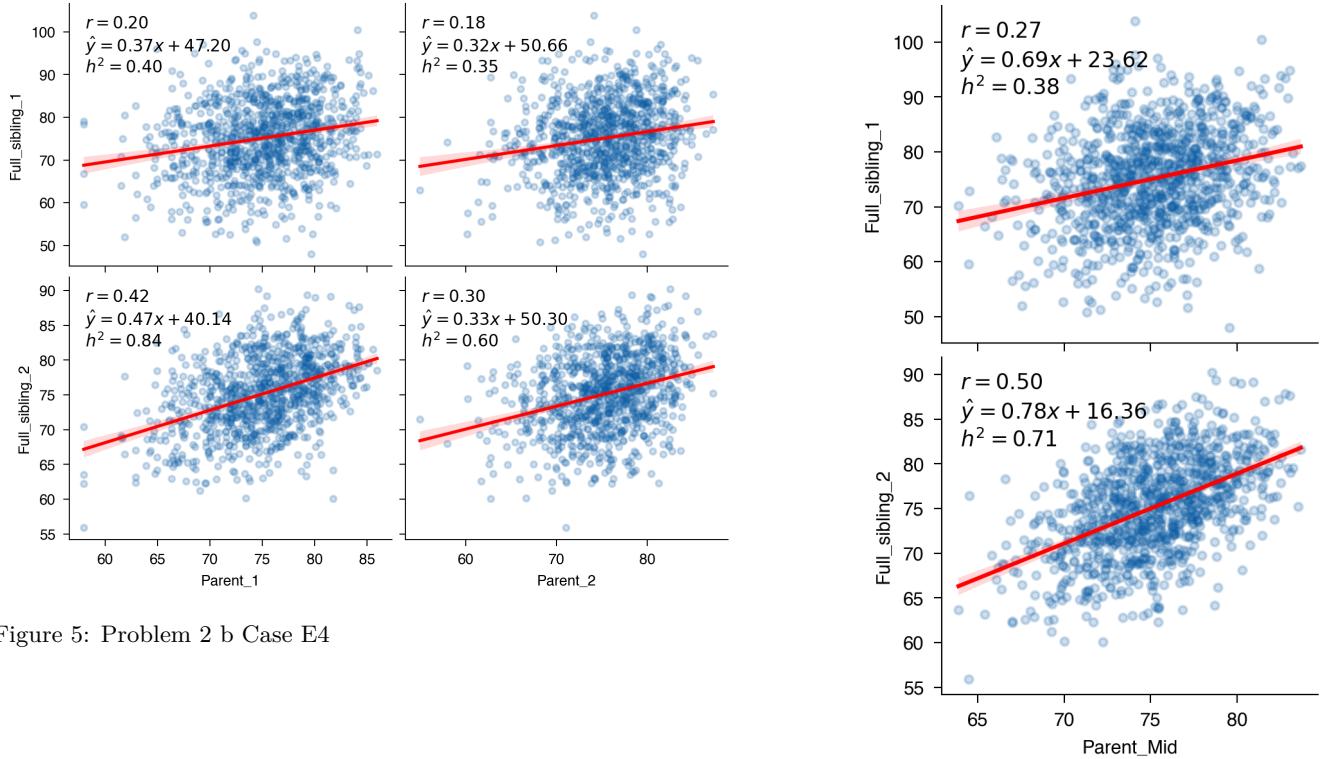


Figure 5: Problem 2 b Case E4

### Case E5: Simulating $E_{O_1} < E_{O_2}$

`noise_0102(df.copy(), 2.5, 7.5)`

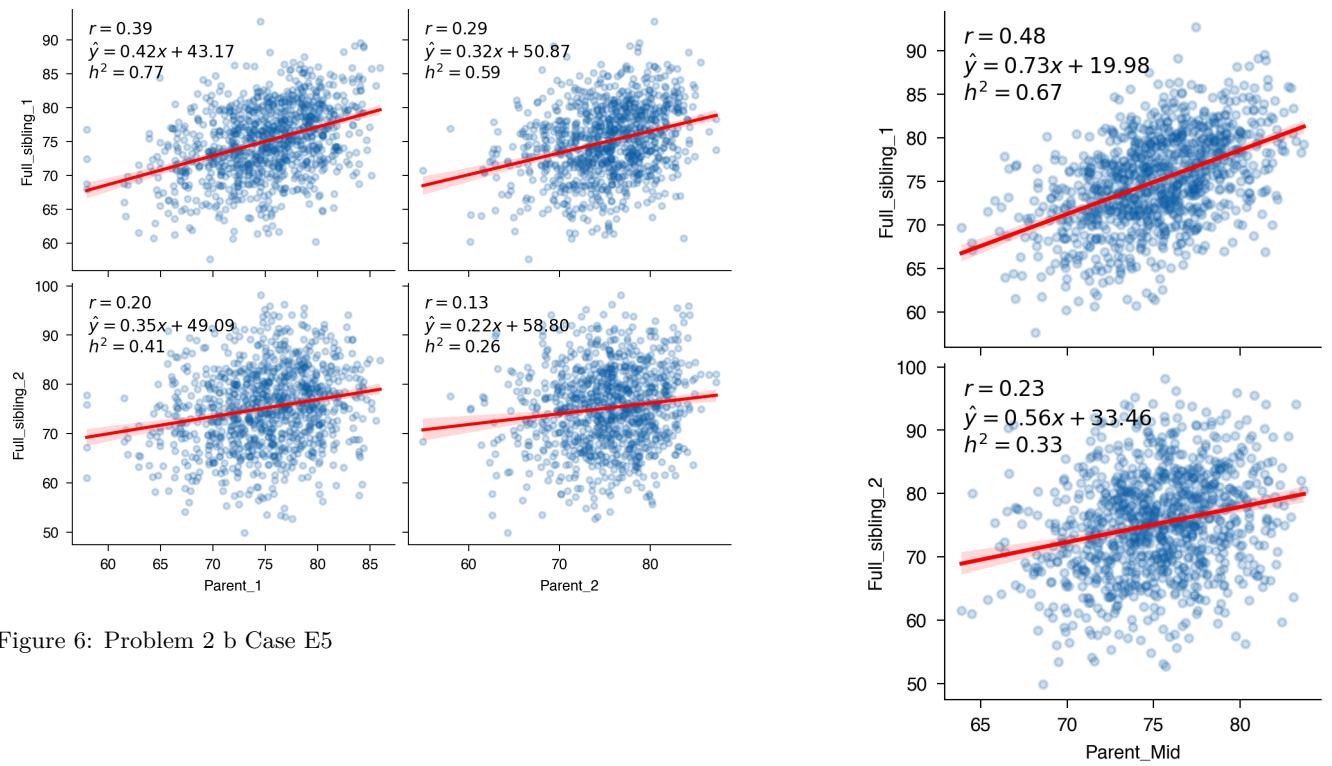


Figure 6: Problem 2 b Case E5