



# Hypothesis Testing With Python

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*True Difference or Noise?*

0.7196

**0.7552**

**Which is better?**

# Noise?

**That's a question.**

# Mosky

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- Python Charmer at Pinkoi.
- Has spoken at: PyCons in TW, MY, KR, JP, SG, HK, COSCUPs, and TEDx, etc.
- Countless hours on teaching Python.
- Own the Python packages: ZIPCodeTW, MoSQL, Clime, etc.
- <http://mosky.tw/>

# Outline

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- Introduction
- Welch's t-test
- Chi-squared test
- Power analysis
- More tests
- Complete steps
- Theory
  - P-value &  $\alpha$
  - Raw effect size,  
 $\beta$ , sample Size
  - Actual negative rate,  
inverse  $\alpha$ , inverse  $\beta$

# The PDF, Notebooks, and Packages

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- The PDF and notebooks are available on <https://github.com/moskytw/hypothesis-testing-with-python> .
- The packages:
  - \$ pip3 install jupyter numpy scipy sympy matplotlib ipython pandas seaborn statsmodels scikit-learn
- Or:
  - > conda install jupyter numpy scipy sympy matplotlib ipython pandas seaborn statsmodels scikit-learn

# To buy, or not to buy

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- Going to buy a **bulb** on an online store.
- If see 10/100 bad reviews? Hmm ...
- If see 5/100 bad reviews? **Good to buy.**
- If see 1/100 bad reviews? **Good to buy.**

- Going to buy a **notebook computer** on an online store.
- If see 10/100 bad reviews? Hmm ...
- If see 5/100 bad reviews? Hmm ...
- If see 1/100 bad reviews? **Maybe good enough.**
- **Context matters.**

# Build our “bad reviews” in statistics

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- Build a statistical model by **a hypothesis**.
  - “The means of two populations are equal.”
  - $\equiv E[X] - E[Y] = 0$
- Put the data into the model, get a probability, **p-value**.
  - “Given the model, the probability to observe the data.”
- If see *p-value* = 0.10?
- If see *p-value* = 0.05?
- If see *p-value* = 0.01?
- Decide by your context.

- If the hypothesis contains “equal”:
  - Can build a model directly, like the previous slide.
  - Called a **null hypothesis**.
- If the hypothesis contains “not equal”:
  - Can build a model by negating it.
    - $\neg$  “not equal”  $\equiv$  “equal”
  - Called an **alternative hypothesis**.
- P-value: given a **null**, the probability to observe the data.

- The  $\alpha$  is the significance level.
  - The value is decided by your context.
- If  $p\text{-value} < \alpha$ :
  - Can reject the null (equal).
  - Can accept the alternative (not equal).
- If  $p\text{-value} \geq \alpha$ :
  - Can't make any definite statement.
  - Can't reject the null  $\neq$  can accept the null.
    - If  $P(data | equal) = 6\% \geq \alpha = 5\%$ , will you accept equal?
    - We may just need more data.

# Suggested formatting

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p-value & $\alpha$	Wording	Summary
$p\text{-value} < 0.001$	Very significant	***
$p\text{-value} < 0.01$	Very significant	**
$p\text{-value} < 0.05$	Significant	*
$p\text{-value} \geq 0.05$	Not significant	ns

- Many researchers also suggest to report **without** formatting.
  - Since the largely misunderstandings like we just explain.
- Misunderstandings of p-values – Wikipedia
- Scientists rise up against statistical significance – Natural
  - “We are not calling for a ban on P values. Nor are we saying they cannot be used as a decision criterion in certain specialized applications.”
  - “We are calling for a stop to the use of P values in the conventional, dichotomous way — to decide whether a result refutes or supports a scientific hypothesis.”

# Define assumptions

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- The hypothesis testing:
- Suitable to answer a yes–no question:
  - “**Means** or medians of two populations are equal?”
  - E.g., “The order counts of A and B are equal?”
  - “**Proportions** of two populations are equal?”
  - E.g., “The conversion rates of A and B are equal?”

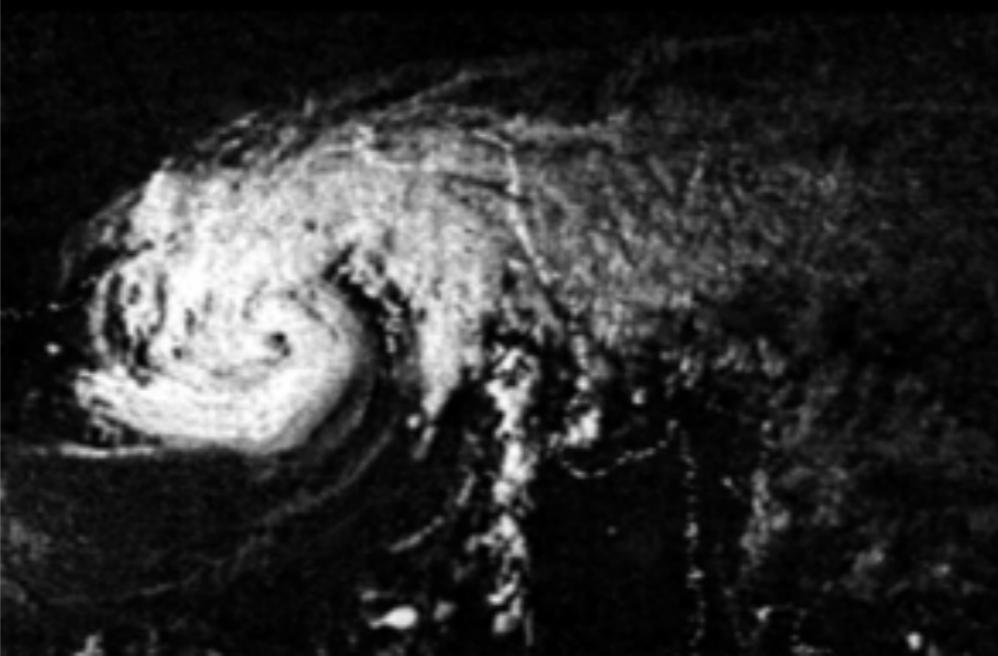
- “Poor or non-poor marriage has different affair times?”
- “Occupations have different affair times?”
- “Poor or non-poor marriage has different affair proportion?”
- “Occupations have different affair proportion?”

# Validate assumptions

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- Collect data ...
- The “Fair” dataset:
  - Fair, Ray. 1978. “A Theory of Extramarital Affairs,” Journal of Political Economy, February, 45-61.
  - A dataset from 1970s.
  - Rows: 6,366
  - Columns: (next slide)
- The full version of the analysis steps:  
<http://bit.ly/analysis-steps> .

1. *rate\_marriage*: 1~5; very poor, poor, fair, good, very good.
2. *age*
3. *yrs\_married*
4. *children*: number of children.
5. *religious*: 1~4; not, mildly, fairly, strongly.
6. *educ*: 9, 12, 14, 16, 17, 20; grade school, some college, college graduate, some graduate school, advanced degree.
7. *occupation*: 1, 2, 3, 4, 5, 6; student, farming-like, white-collar, teacher-like, business-like, professional with advanced degree.
8. *occupation\_husb*
9. *affairs*: n times of extramarital affairs per year since marriage.

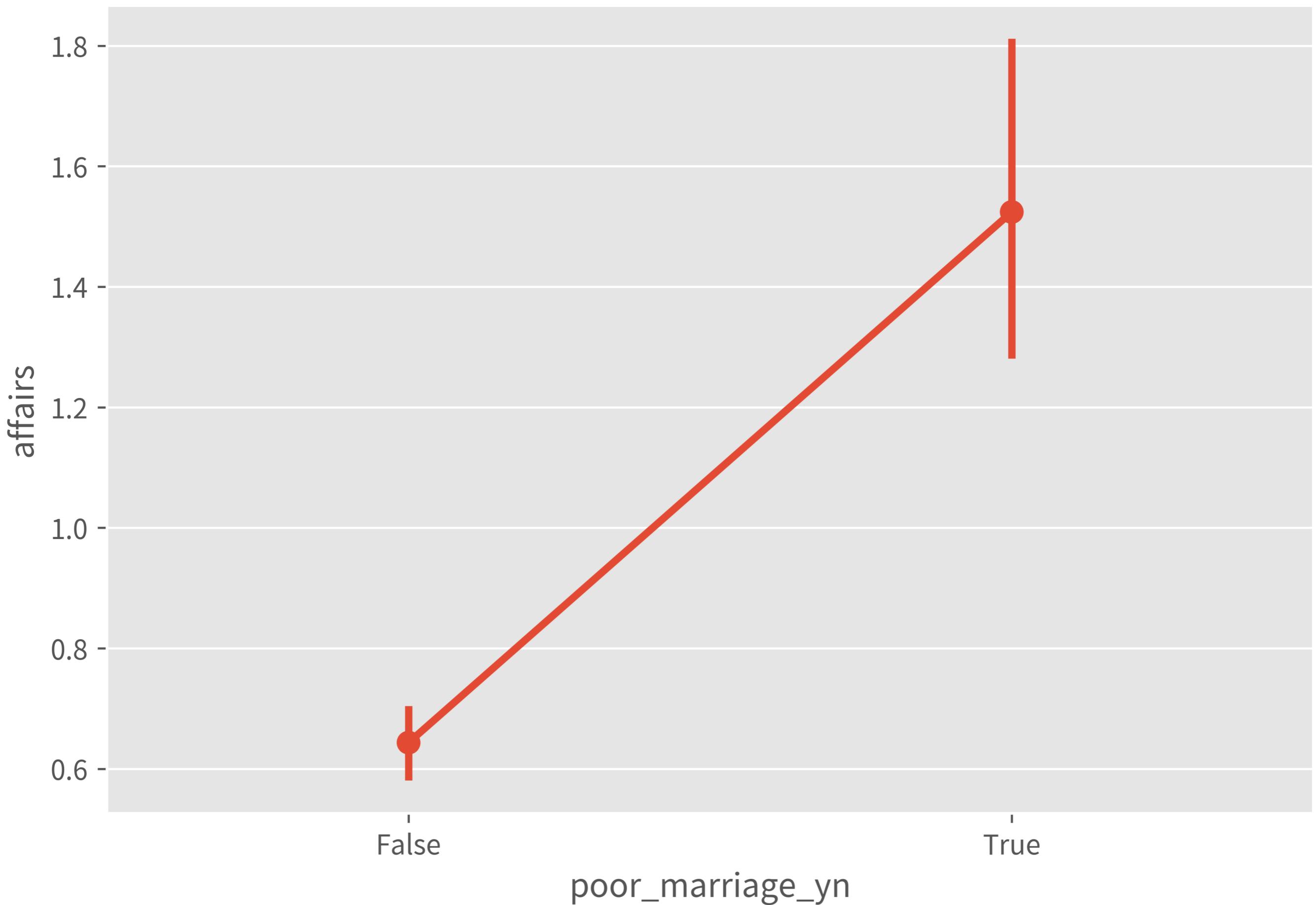


# Welch's t-test #1

---

	count	mean	std
<b>poor_marriage_yn</b>			
<b>False</b>	5919.0	0.643549	2.116982
<b>True</b>	447.0	1.524038	3.015937
p-value: 2.7446844166802127e-09			

- Preprocess:
  - Group into poor or not.
- Describe.
- Test:
  - Assume the affair times are equal, the probability to observe it: **super low**.
  - So, we **reject the means are equal** at 1% significance level:
    - Non-poor: 0.64
    - Poor: 1.52



```
import scipy as sp
import statsmodels.api as sm
import seaborn as sns

print(sm.datasets.fair.SOURCE,
      sm.datasets.fair.NOTE)

# -> Pandas's Dataframe
df_fair = sm.datasets.fair.load_pandas().data

df = df_fair
# 2: poor
# 3: fair
df = df.assign(poor_marriage_yn
                  =(df.rate_marriage <= 2))
df_fair_1 = df
```

```
df = df_fair_1

display(df
        .groupby('poor_marriage_yn')
        .affairs
        .describe())

a = df[df.poor_marriage_yn].affairs
b = df[~df.poor_marriage_yn].affairs

# ttest_ind(...) === Student's t-test
# ttest_ind(..., equal_var=False) === Welch's t-test
print('p-value:',
      sp.stats.ttest_ind(a, b, equal_var=False)[1])
```

```
df = df_fair_1  
sns.pointplot(x=df.poor_marriage_yn,  
               y=df.affairs)
```

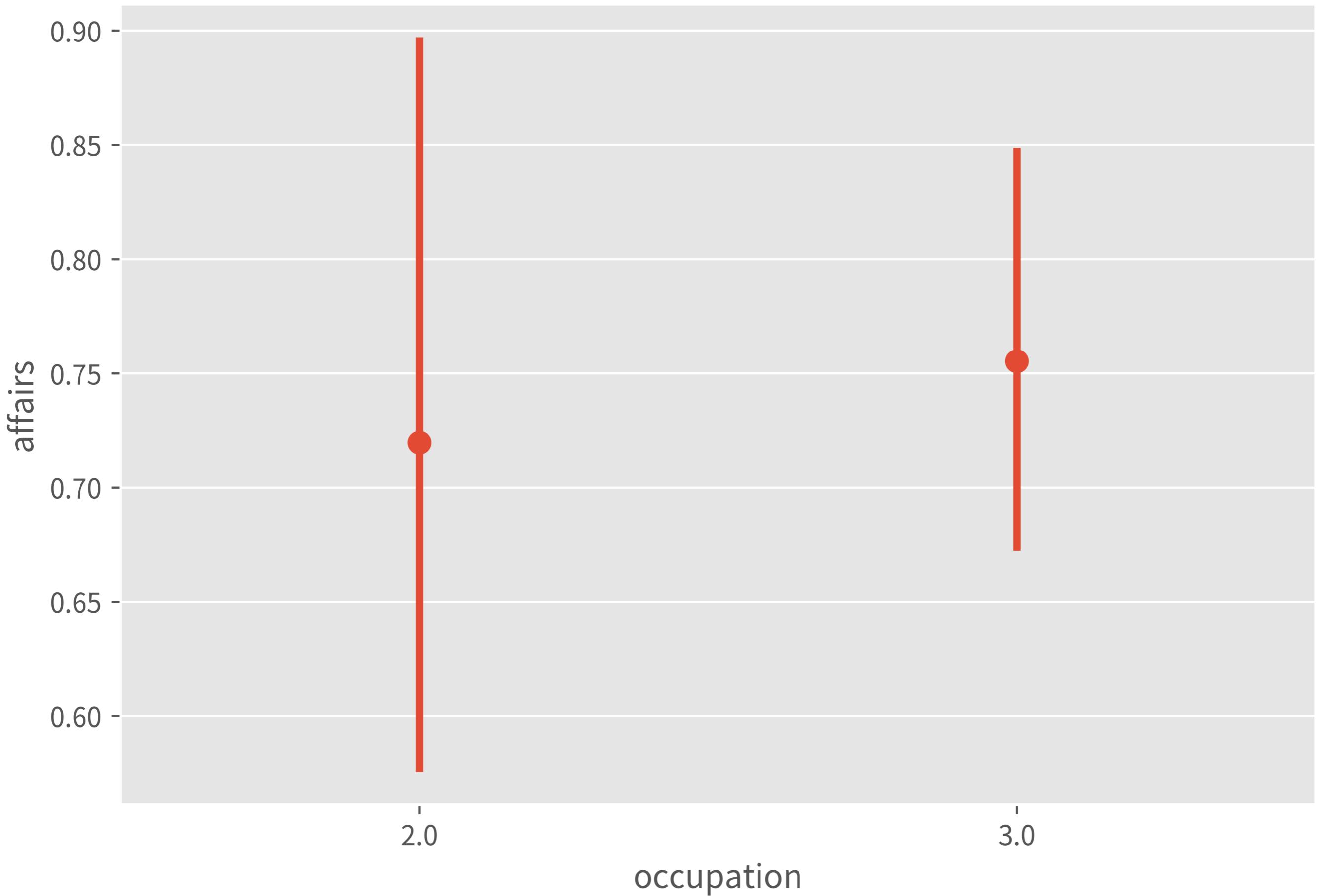
# Welch's t-test #2

---

occupation	count	mean	std
2.0	859.0	0.719556	2.375644
3.0	2783.0	0.755248	2.305594

p-value: 0.698381462473247

- Preprocess:
  - Select the two occupations.
  - Group by occupations.
- Describe.
- Test:
  - Assume the affair times are equal, the probability to observe it: 70%.
- So, we can't reject the means are equal at 1% significance level.
  - Farming-like: 0.72
  - White-colloar: 0.76



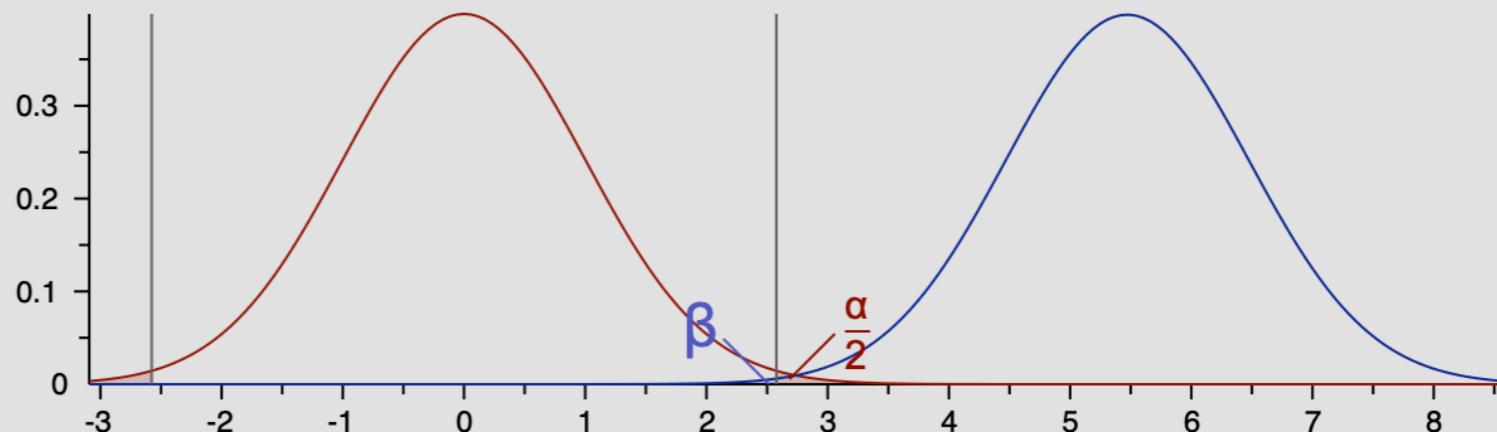
# If there is a true difference, can we detect it?

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- To detect  $\geq 0.5$  times difference at 1% significance level:
  - *raw effect size* = 0.5
  - $\alpha = 0.01$
- Use G\*Power or StatsModels:
  - *power* = 0.9981
- If there is a 0.5 times difference and the given significance level, we can detect it 99.81% of the time. It's good.
- If *power* is low, relax *effect size*,  $\alpha$ , or collect a larger sample.

Central and noncentral distributions

Protocol of power analyses

critical  $t = 2.5772$ 

Test family

t tests

Statistical test

Means: Difference between two independent means (two groups)

  $n_1 \neq n_2$ 

Mean group 1

0

Mean group 2

1

SD  $\sigma$  within each group

0.5

  $n_1 = n_2$ 

Mean group 1

0.719556

Mean group 2

1.219557

SD  $\sigma$  group 1

2.375644

SD  $\sigma$  group 2

2.305594

Calculate

Effect

0.2135952

Calculate and transfer to main window

Close effect size drawer

Input parameters

Determine

Tail(s) Two

Effect size d 0.2135952

 $\alpha$  err prob 0.01

Sample size group 1 859

Sample size group 2 2783

Output parameters

Noncentrality parameter  $\delta$  5.4723605

Critical t 2.5771807

Df 3640

Power (1- $\beta$  err prob) 0.9980984

X-Y plot for a range of values

Calculate

# $\alpha$ , power, confidence level, $\beta$

---

don't reject null

reject null

null

*confidence level*

$$\begin{aligned} &= P(\text{don't reject null} \mid \text{null}) \\ &= 1 - \alpha \end{aligned}$$

$\alpha$

$$\begin{aligned} &= P(\text{reject null} \mid \text{null}) \\ &= 1 - \text{confidence level} \end{aligned}$$

alter  
 $= \text{null} + \text{effect size}$

$\beta$

$$\begin{aligned} &= P(\text{don't accept alter} \mid \text{alter}) \\ &= 1 - \text{power} \end{aligned}$$

*power*

$$\begin{aligned} &= P(\text{reject null} \mid \text{alter}) \\ &= 1 - \beta \end{aligned}$$

# Power analysis

---

- $f(a, \text{raw effect size}, \beta) = \text{sample size}$
- Before collecting data,
  - Define  $a, \text{raw effect size}, \beta$  to calculate required sample size.
- After test,
  - If  $p\text{-value} < a$ , good to say there is a difference.
  - If  $p\text{-value} \geq a$ , or closes to  $a$ , may investigate the  $\beta$ .
- The  $a, \text{raw effect size}, \beta$  here are “to-achieve”, not “observed”.
- $2 \times 2$  chi-squared test ≡ two-proportion z-test. [ref]
  - The power analysis of two-proportion z-test is much easier.

```
df = df_fair
# 2: farming-like
# 3: white-colloar
df = df[df.occupation.isin([2, 3])]
df_fair_2 = df

df = df_fair_2

display(df
        .groupby('occupation')
        .affairs
        .describe())

a = df[df.occupation == 2].affairs
b = df[df.occupation == 3].affairs

print('p-value: ',
      sp.stats.ttest_ind(a, b, equal_var=False)[1])
```

```
df = df_fair_2
sns.pointplot(x=df.occupation,
               y=df.affairs,
               join=False)
```

```
print('p-value: ',
      sp.stats.ttest_ind([1, 2, 3, 4, 5, 6],
                          [1, 2, 3, 4, 5, 60],
                          equal_var=False)[1])
```

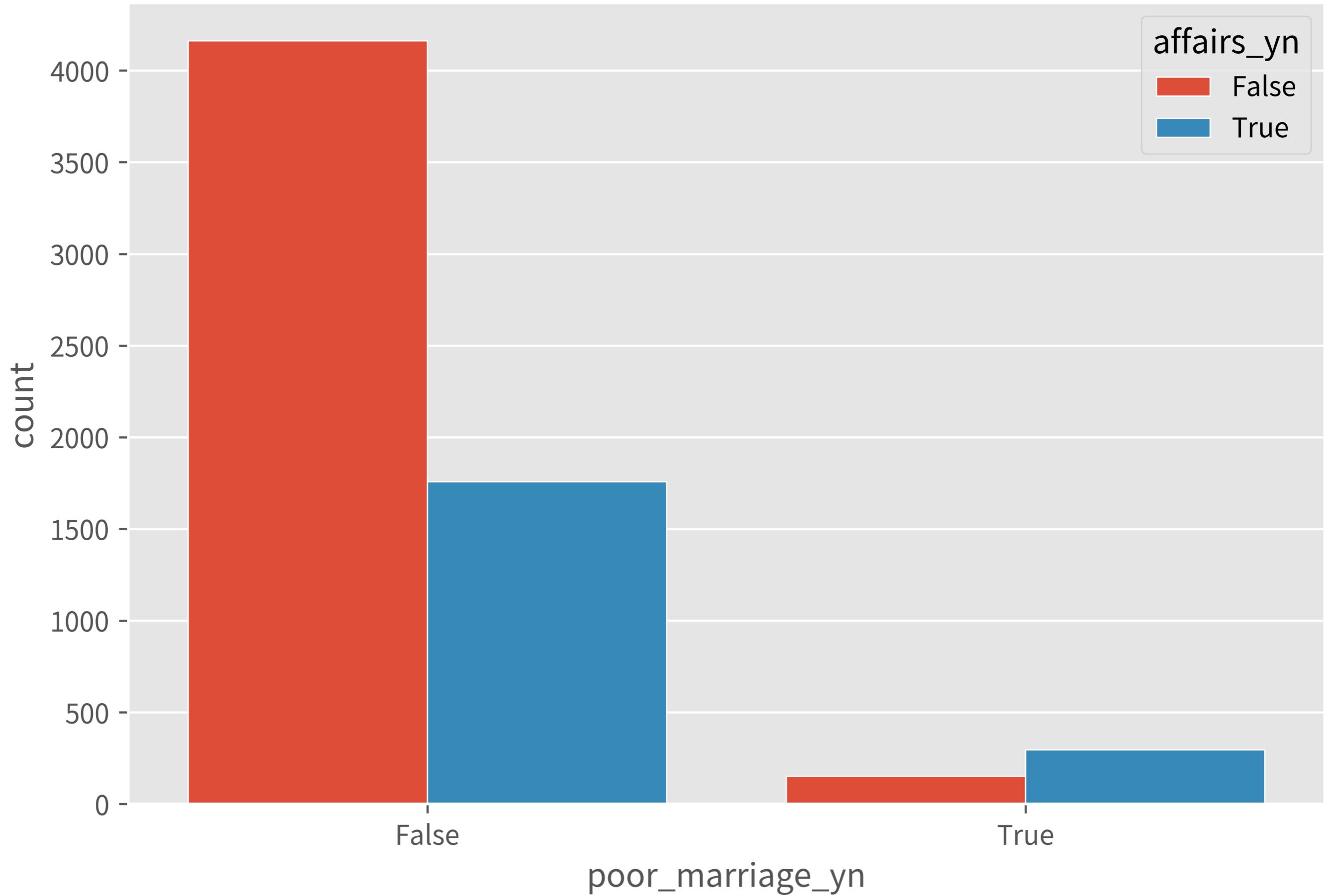
# Chi-squared test #1

---

	<b>affairs_yn</b>	<b>False</b>	<b>True</b>
<b>poor_marriage_yn</b>			
<b>False</b>	4161	1758	
<b>True</b>	152	295	
	<b>affairs_yn</b>	<b>False</b>	<b>True</b>
<b>poor_marriage_yn</b>			
<b>False</b>	0.702990	0.297010	
<b>True</b>	0.340045	0.659955	

**p-value:** 1.9460298519537103e-56

- Preprocess:
  - Add “affairs > 0” as true.
  - Group into poor or not.
- Describe.
- Test:
  - Assume equal, the probability to observe it: **super low**.
  - So, we **reject the proportions are equal** at 1% significance level:
  - Non-poor: **30%**; Poor: **66%**



```
df = df_fair
# 2: poor
# 3: fair
df = df.assign(poor_marriage_yn
                =(df.rate_marriage <= 2),
                affairs_yn=(df.affairs > 0))
df_fair_3 = df
```

```
df = df_fair_3

df = (df
      .groupby(['poor_marriage_yn', 'affairs_yn'])
      [['affairs']]
      .count()
      .unstack()
      .droplevel(axis=1, level=0))

df_pct = df.apply(axis=1, func=lambda r: r/r.sum())

display(df, df_pct)

print('p-value:',
      sp.stats.chi2_contingency(
          df,
          correction=False
      )[1])
```

```
df = df_fair_3
sns.countplot(data=df,
               x='poor_marriage_yn', hue='affairs_yn',
               saturation=0.95, edgecolor='white')
```

## Chi-squared test #2

.....

<b>affairs_yn</b>	<b>False</b>	<b>True</b>
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<b>occupation</b>		
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<b>2.0</b>	607	252
<b>3.0</b>	1818	965

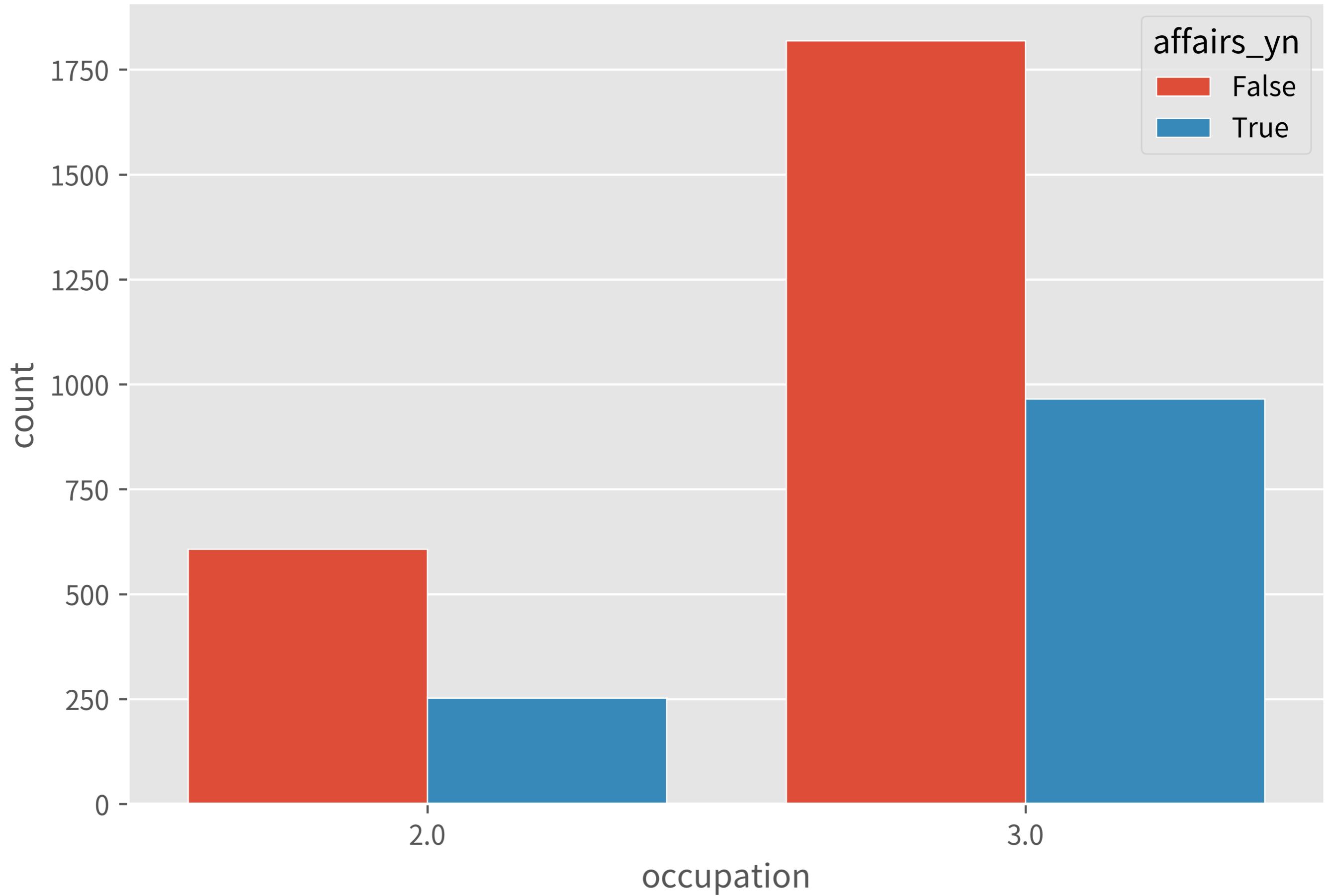
<b>affairs_yn</b>	<b>False</b>	<b>True</b>
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<b>occupation</b>		
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<b>2.0</b>	0.706636	0.293364
<b>3.0</b>	0.653252	0.346748

**p-value:** 0.0037369587127306517

- Preprocess:
  - Add “affairs > 0” as true.
  - Select the two occupations.
  - Group by occupation.
- Describe.
- Test:
  - Assume equal, the probability to observe it: 0.4%.
  - So, we **reject the proportions are equal** at 1% significance level:
    - Farming-like: 29%
    - White-colloar: 35%



```
df = df_fair_3
# 2: farming-like
# 3: white-colloar
df = df[df.occupation.isin([2, 3])]
df_fair_4 = df
```

```
df = df_fair_4

df = (df
      .groupby(['occupation', 'affairs_yn'])
      [['affairs']]
      .count()
      .unstack()
      .droplevel(axis=1, level=0))

df_pct = df.apply(axis=1, func=lambda r: r/r.sum())

display(df, df_pct)

print('p-value: ',
      sp.stats.chi2_contingency(
          df,
          correction=False
      )[1])
```

```
df = df_fair_4
sns.countplot(data=df,
               x='occupation', hue='affairs_yn',
               saturation=0.95, edgecolor='white')
```

```
print('p-value:',
      sp.stats.chi2_contingency(
          [[607, 252],
           [1818, 965]],
          correction=False
      )[1])
```

# Summary of our study

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	Times	Prop.	Uplift	P-value
Non-poor	0.64			
Poor	1.52		+138%	< 0.001 ***
		30%		
		66%	+120%	< 0.001 ***
Farming-like	0.72			
White-colloar	0.76		+6%	0.698 ns
		29%		
		35%	+21%	0.004 **

# The mini cheat sheet

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- If testing **means**, Welch's t-test.
- If testing medians, Mann–Whitney U test.
- If testing **proportions**, chi-squared test.

# The cheat sheet

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- If testing homogeneity:
  - If total sample size < 1000, or more than 20% of cells have expected frequencies < 5, Fisher's exact test.
  - Else, chi-squared test, or  $2 \times 2$  chi-squared test ≡ two-proportion z-test.
- If testing equality:
  - If median is better, don't want to trim outliers, variable is ordinal, or any group size  $\leq 20$ :
    - If groups are paired, Wilcoxon signed-rank test.
    - If groups are independent, Mann–Whitney U test.
  - Else:
    - If groups are paired, Paired Student's t-test.
    - If groups are independent, Welch's t-test, not Student's.

# Why Welch's t-test, not Student's t-test?

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- Student's t-test assumed the two populations have the same variance, which may not be true in most cases.
- Welch's t-test relaxed this assumption without side effects.
- So, just use Welch's t-test directly. [ref]

- More cheat sheets:
  - Selecting Commonly Used Statistical Tests – Bates College
  - Choosing a statistical test – HBS
- References:
  - Fisher's exact test of independence – HBS
  - Statistical notes for clinical researchers – Restor Dent Endod
  - Nonparametric Test and Parametric Test – Minitab
  - Dependent t-test for paired samples – Student's t-test – Wikipedia

# Complete steps

---

1. Decide what test.
2. Decide  $\alpha$ , raw effect size,  $\beta$  to achieve.
3. Calculate sample size.
4. Still collect a sample as large as possible.
5. Test.
6. Investigate  $\beta$  if need.
7. Report fully, not only significant or not.
  - Means, confidence intervals, p-values, research design, etc.

# Keep learning

---

- Seeing Theory
- Statistics – SciPy Tutorial
- StatsModels
- Biological Statistics
- Research Design

# Recap

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- The **null hypothesis** is the one states “equal”.
- The **p-value** is:
  - Given null, the probability to observe the data.
  - “How compatible the null hypothesis and the data are.”
- The **Welch's t-test** and **chi-squared test**.
- The power analysis to calculate sample size or power.
- Report fully, not only significant or not.
- Let's identify the true difference or noise efficiently! 

# P-value & $\alpha$

---

*Theory*

# Seeing is believing

---

- $p\text{-value} = 0.0027 (< 0.01)$ 
  - 
- $p\text{-value} = 0.0271 (0.01\text{--}0.05)$ 
  -  ?  ? ? ? ?
- $p\text{-value} = 0.2718 (\geq 0.05)$ 
  - ? ? ? ? ? ?
- *appendices/theory\_01\_how\_tests\_work.ipynb*

# Confusion matrix, where $A = 00_2 = C[0, 0]$

---

		predicted negative AC	predicted positive BD
actual negative AB	true negative A	false positive B	
actual positive CD	false negative C	true positive D	

**False positive rate =  $P(BD|AB) = B/AB = 4/(96+4) = 4/100$**

.....

		predicted negative AC	predicted positive BD
actual negative AB	96 A	4 B	
	9 C	41 D	

$$\alpha = P(\text{accept alter} | \text{null}) = P(\text{predicted positive} | \text{actual negative})$$

.....

		predicted negative	predicted positive
actual negative	AB	AC	BD
	true negative	A	false positive
actual positive	CD	C	true positive
	false negative	D	

# Predefined acceptable confusion matrix

---

	predicted negative AC	predicted positive BD
actual negative AB	true negative A	false positive B
actual positive CD	false negative C	true positive D

# False positive, p-value, and $\alpha$

---

false positive rate

Calculated  
with the actual answer.

p-value

Calculated false positive rate  
by a null hypothesis.

$\alpha$

Predefined acceptable  
false positive rate.

# Raw effect size, $\beta$ , sample size

---

*Theory*

# The elements of a complete test

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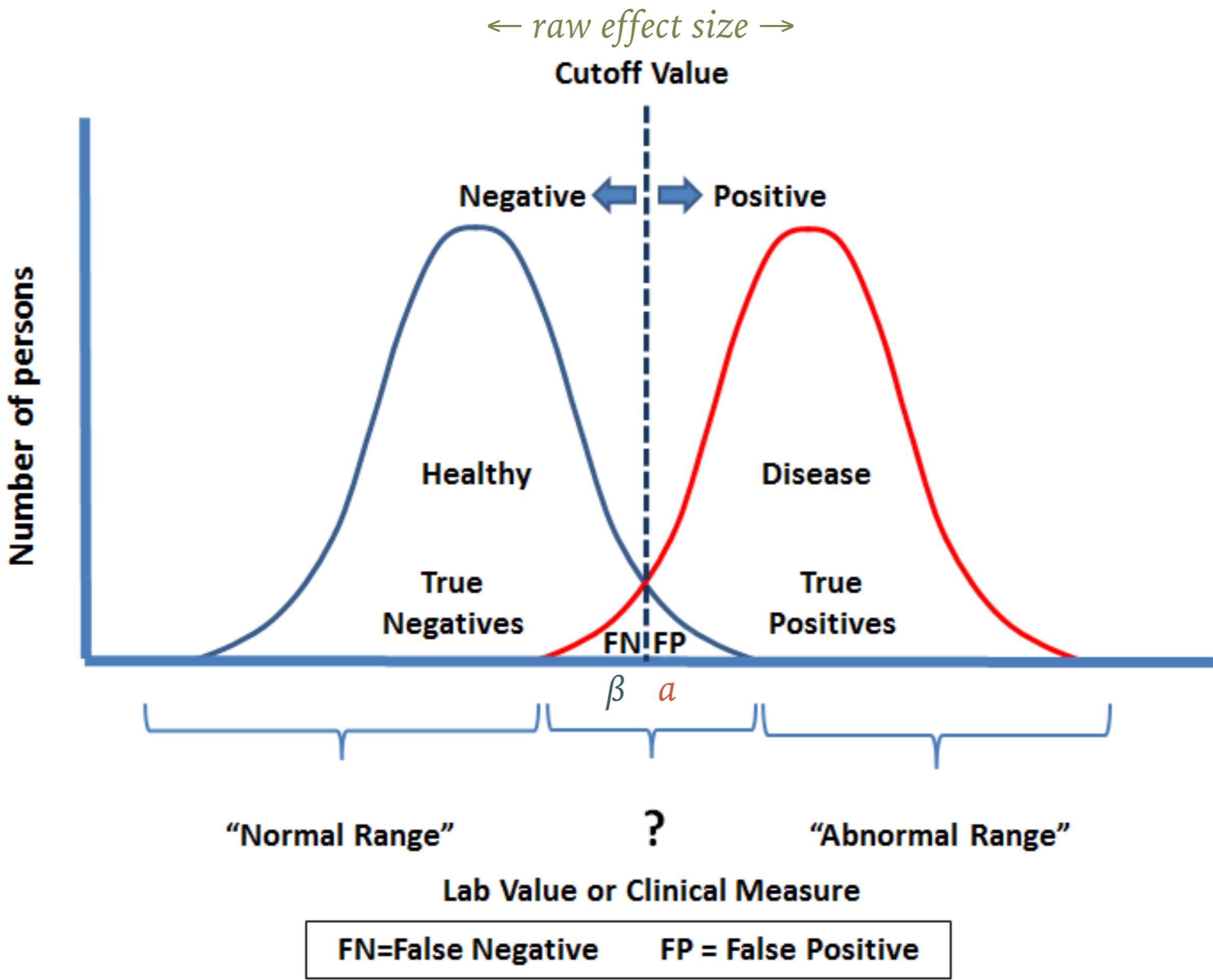
1. The null hypothesis, data, p-value,  $\alpha$ .
  2. The raw effect size,  $\beta$ , sample size.
  3. The false negative rate, inverse  $\alpha$ , inverse  $\beta$ .
- Will introduce them by the confusion matrix.

# Raw effect size, and $\beta$

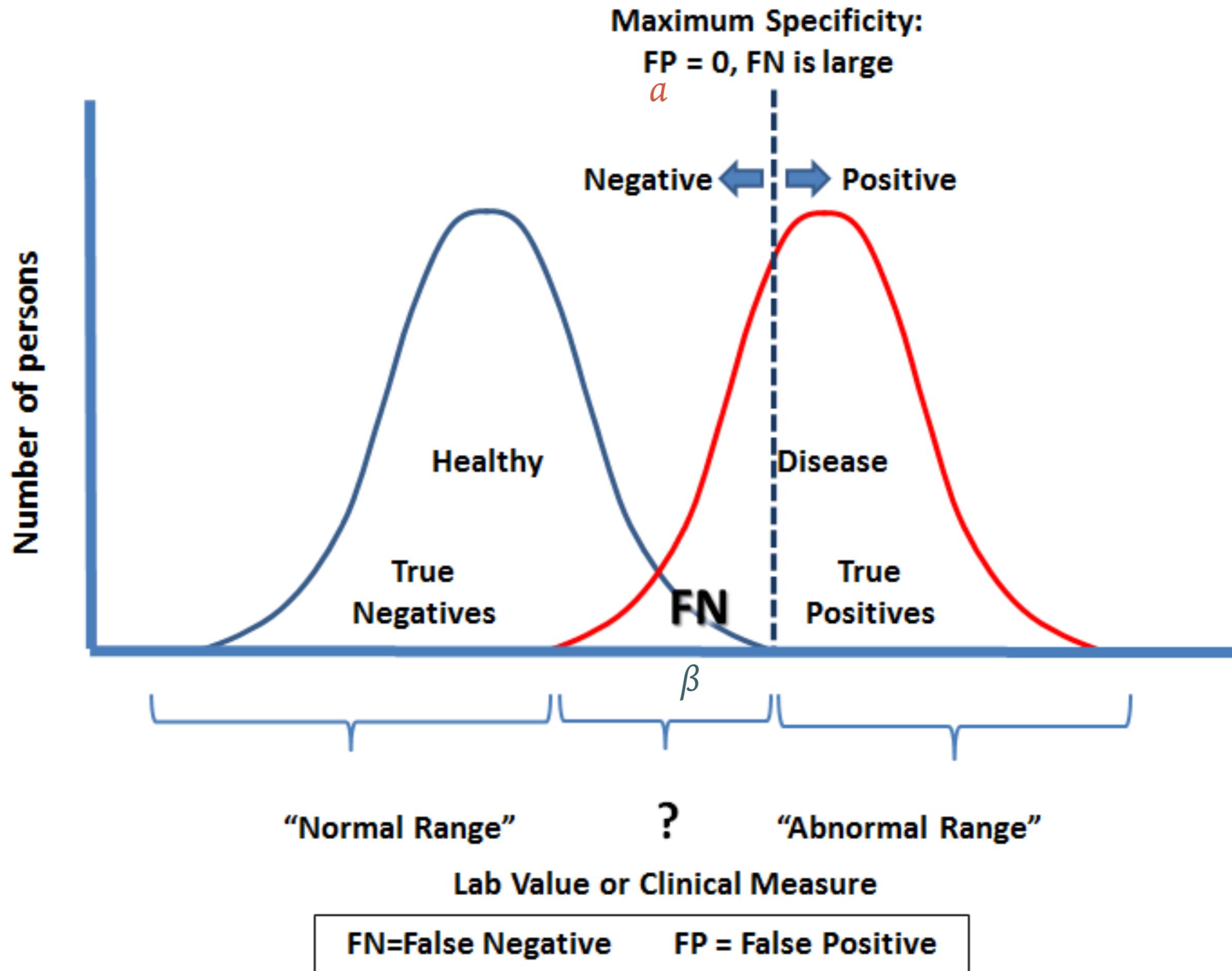
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- DSM5: The case for double standards – James Coplan, M.D.
  - The figures explain  $a$ , *raw effect size*, and  $\beta$  perfectly.
  - “FP”:  $a$
  - “The distance between the means”: *raw effect size*
  - “FN”:  $\beta$

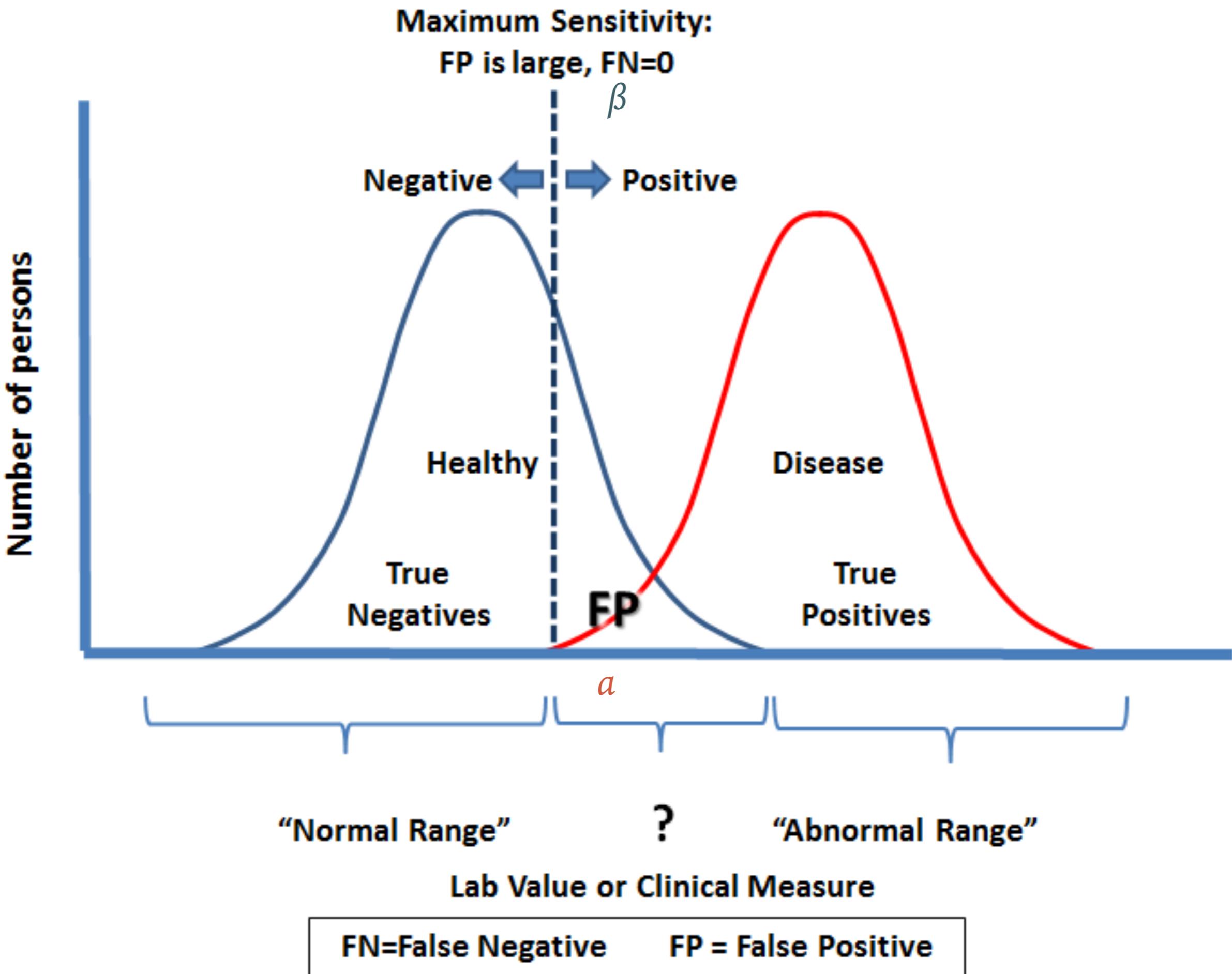
B.



C.



D.



*sample size ↑*

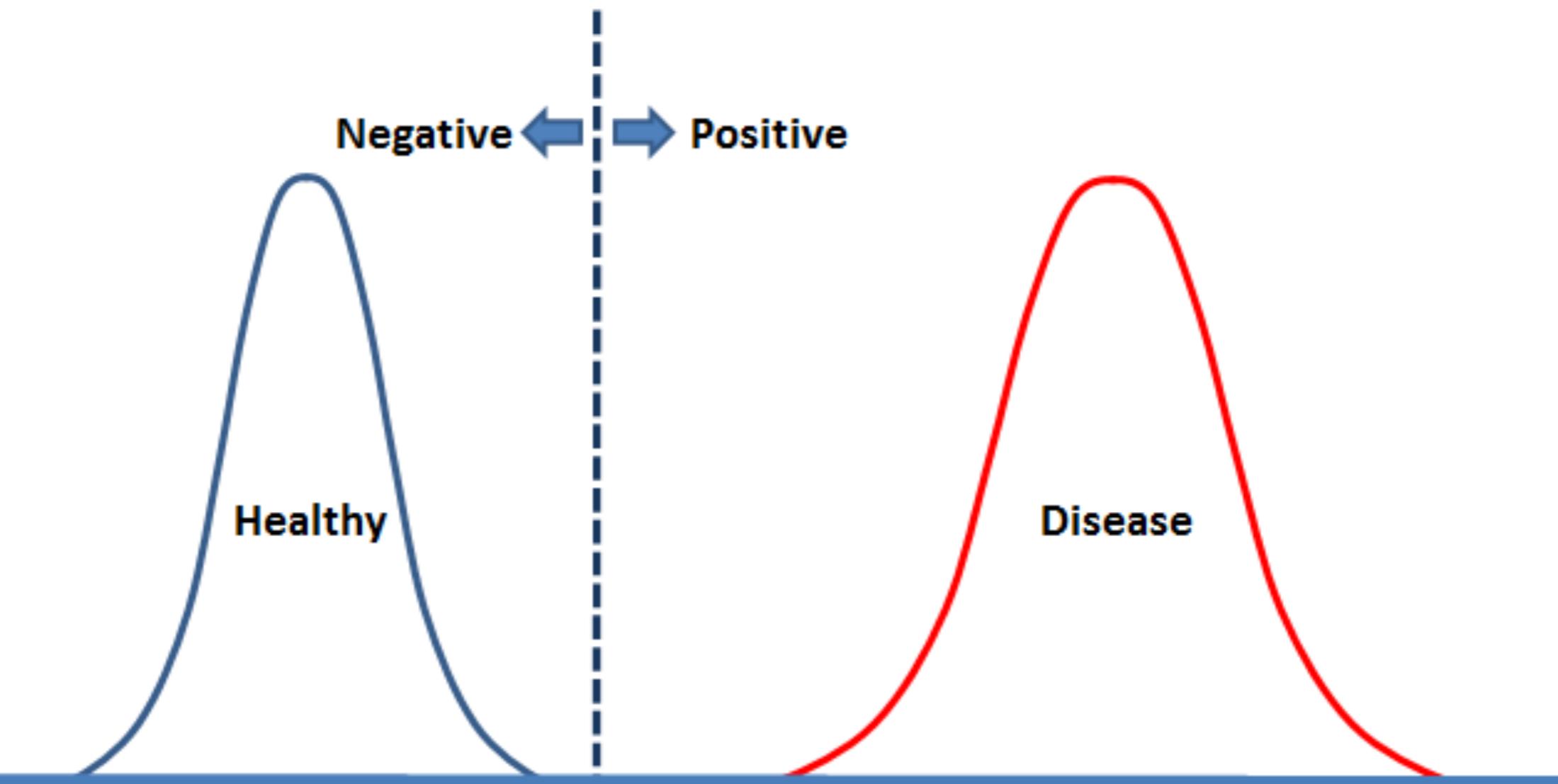
**Cutoff Value**

**Negative** ← → **Positive**

Number of persons

**Healthy**

**Disease**



**“Normal Range”**

**“Abnormal Range”**

**Lab Value or Clinical Measure**

**A.**

$$\beta = P(AC|CD) = C/CD$$

.....

		predicted negative AC	predicted positive BD
actual negative AB	true negative A	false positive B	
	false negative C	true positive D	
actual positive CD			

- Given  $\alpha$ , raw effect size,  $\beta$ , get the sample size.
- Given  $\alpha$ , raw effect size, sample size, get the  $\beta$ .
- Increase sample size to decrease  $\alpha$ ,  $\beta$ , or raw effect size.

Actual negative rate,  
inverse  $\alpha$ , inverse  $\beta$

---

*Theory*

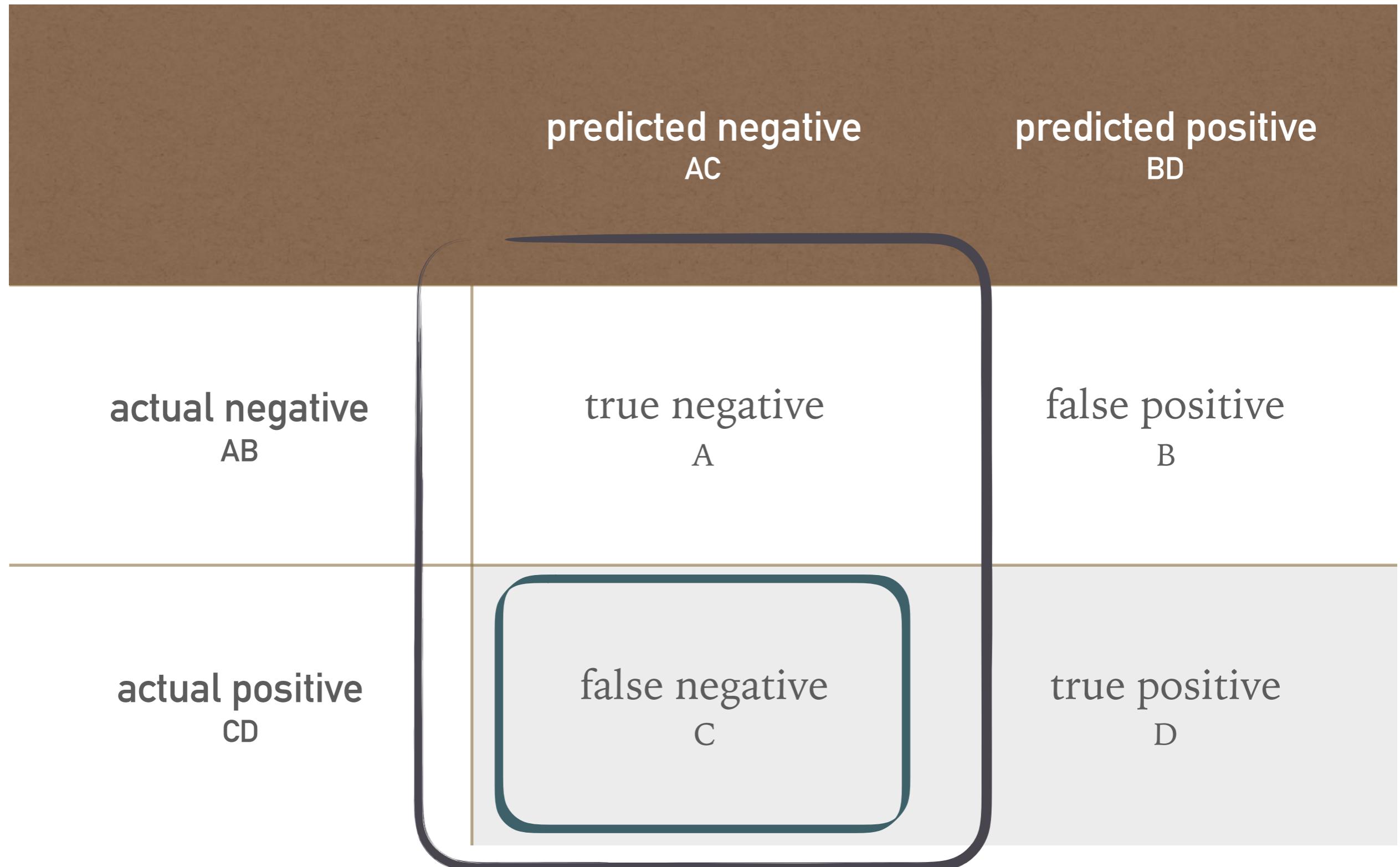
$$\text{Inverse } a = P(AB|BD) = B/BD$$

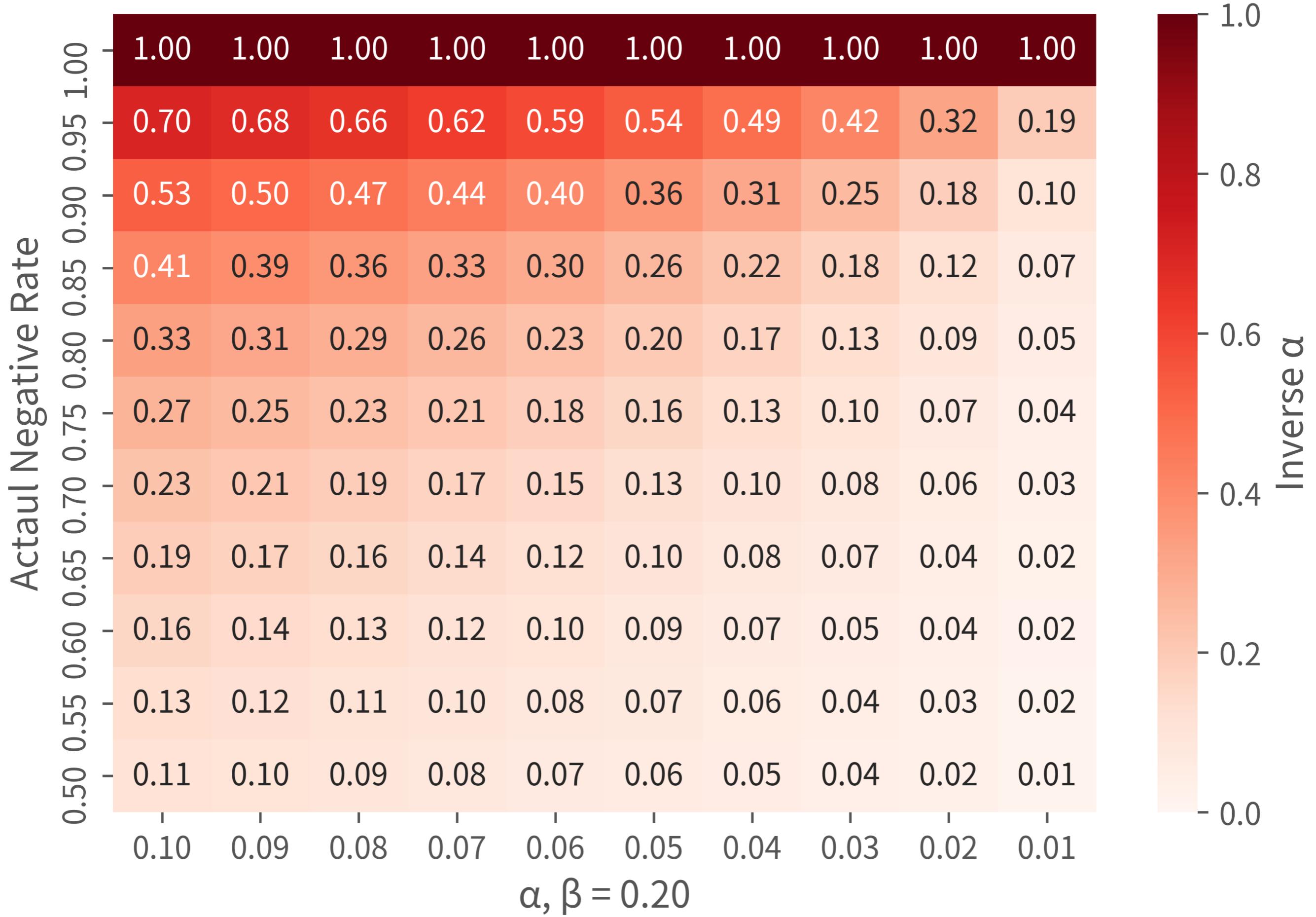
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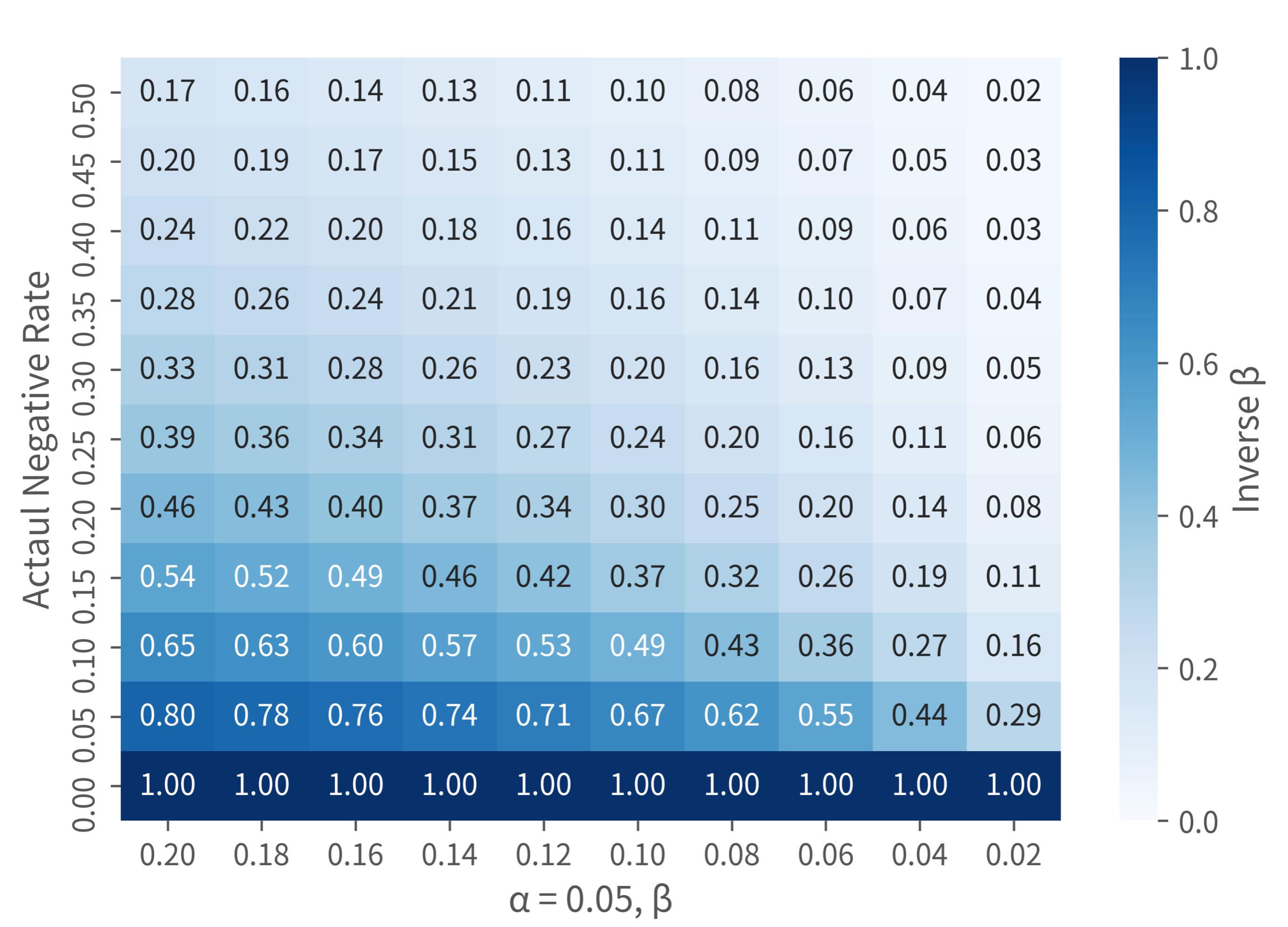
	predicted negative AC	predicted positive BD
actual negative AB	true negative A	false positive B
actual positive CD	false negative C	true positive D

$$\text{Inverse } \beta = P(CD|AC) = C/AC$$

.....







# Rates in predefined acceptable confusion matrix

= = = predefined

a	B/AB	significance level type I error rate	false positive rate
$\beta$	C/CD	type II error rate	false negative rate
inverse a	B/BD		false discovery rate
inverse $\beta$	C/AC		false omission rate
confidence level	A/AB	1-a	specificity
power	D/CD	1- $\beta$	sensitivity recall

# Rates in confusion matrix

---

	=	=	= observed
false positive rate	B/AB		$\alpha$
false negative rate	C/CD		$\beta$
false discovery rate	B/BD		inverse $\alpha$
false omission rate	C/AC		inverse $\beta$
actual negative rate	AB/ABCD		
sensitivity	D/CD	recall	power
specificity	A/AB		confidence level
precision	D/BD		inverse power
recall	D/CD	sensitivity	power

- *appendices/theory\_02\_complete\_a\_test.ipynb*
- *appendices/theory\_03\_figures.ipynb*
- That's all. 