

4V001 - Workshops in molecular and cellular biology Applied biostatistics

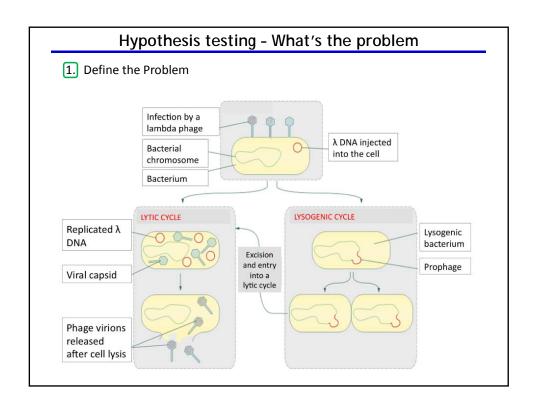
Martin LARSEN

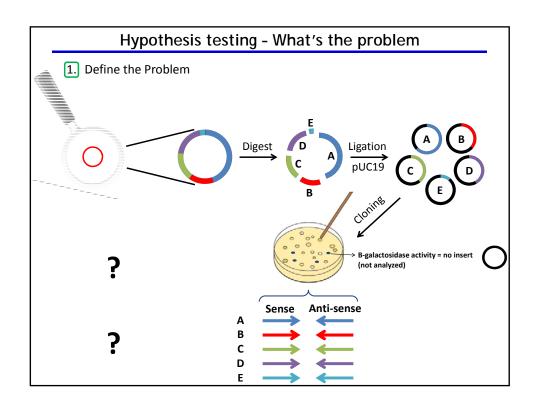
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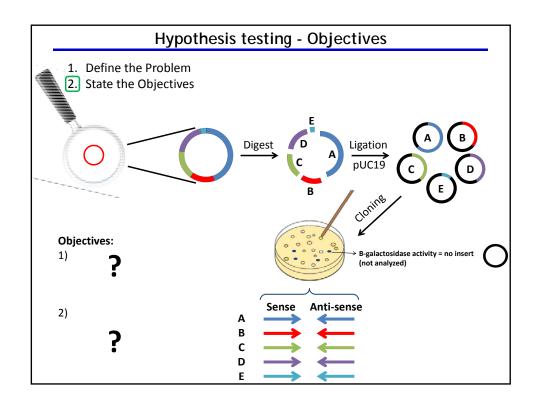
INSERM U1135, CHU Pitié-Salpetrière, Paris, France

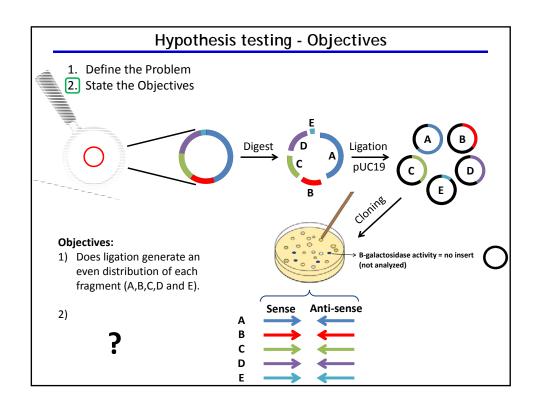
Hypothesis testing Step-by-step

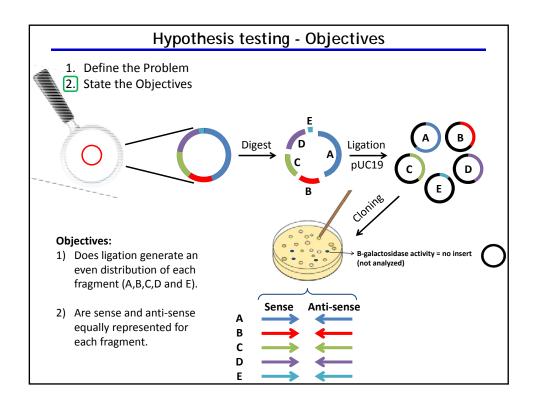
- 1. Define the Problem
- 2. State the Objectives
- 3. State the Null Hypothesis (H₀)
- 4. State the Alternative Hypothesis (H₁)
- 5. Select the appropriate statistical test
- 6. Decide if the Hypothesis testing will be left-tailed, right-tailed, or two tailed test.
- 7. State the alpha-risk (α) level
- 8. State the beta-risk (1-β) level
- 9. State or Establish (require prior knowledge) the Effect Size
- 10. Create Sampling Plan, determine sample size
- 11. Gather samples
- 12. Collect and pre-analyse data
- 13. Calculate the test statistic
- 14. Determine critical test value and p-value
 - If p-value < α, reject H₀
 - If p-value > α , fail to reject H₀
- 15. Post hoc analysis











Hypothesis testing - State hypothesis

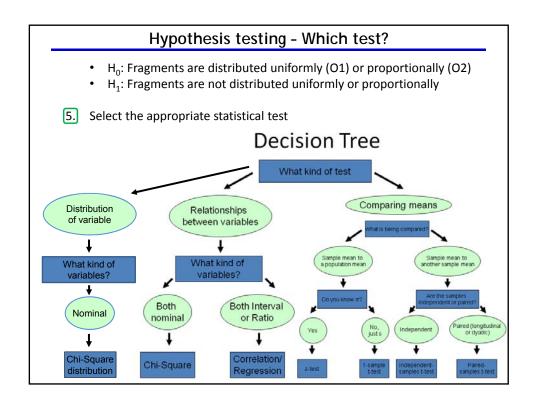
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 - Is sense and anti-sense equally represented for each fragment.
- 3. State the Null Hypothesis (H_0)
 - H₀: Fragments are distributed
 - Obj. 1: ?
 - Obj. 2: ?
- 4. State the Alternative Hypothesis (H₁)
 - H₁: Fragments are not distributed
 - Obj. 1:?
 - Obj. 2: ?

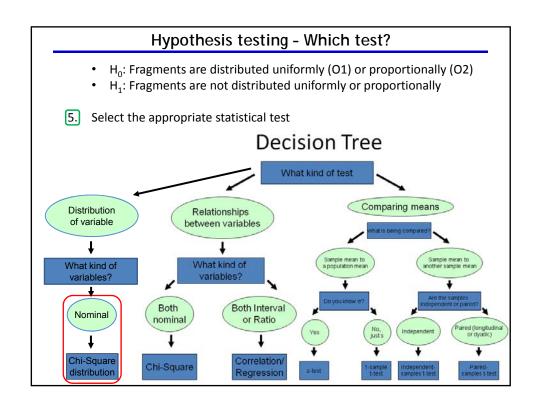
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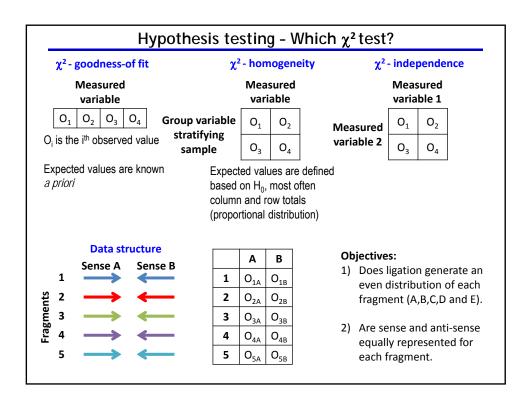
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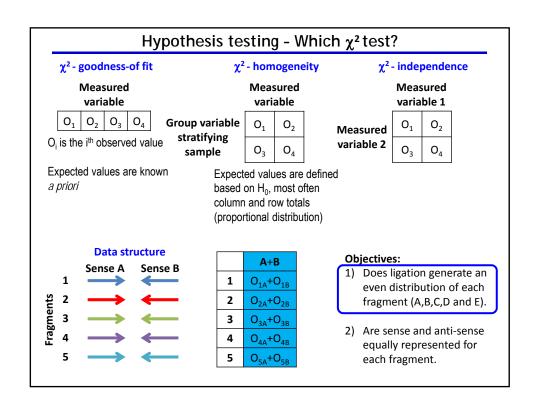
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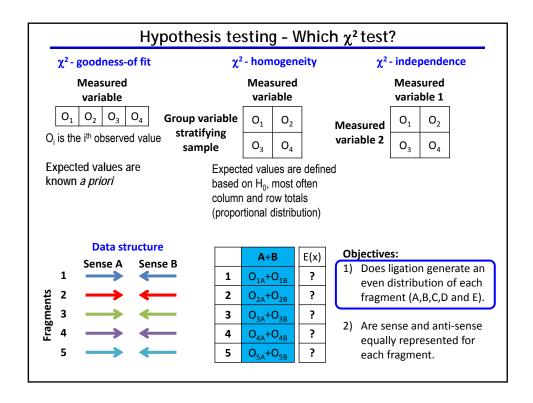
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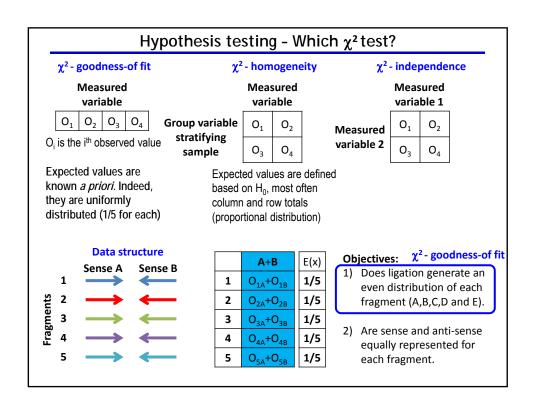


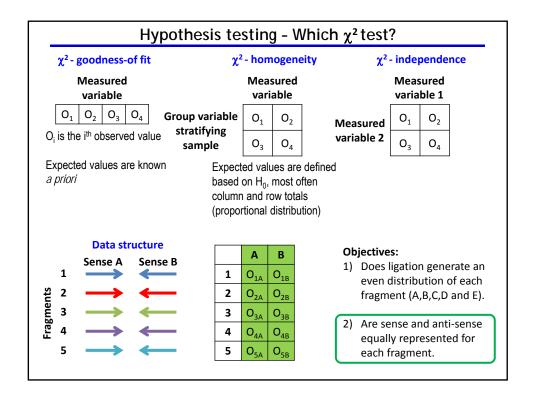


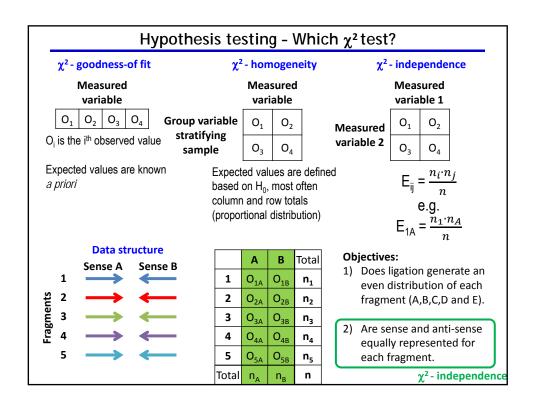


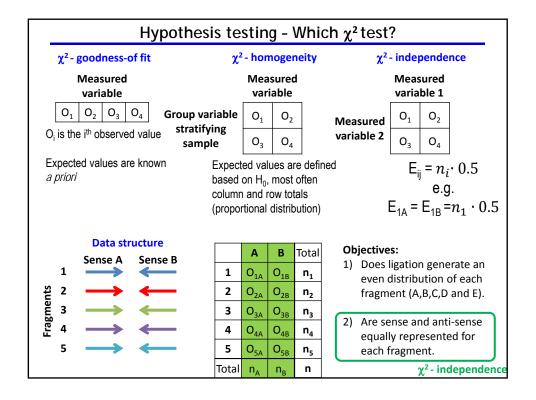


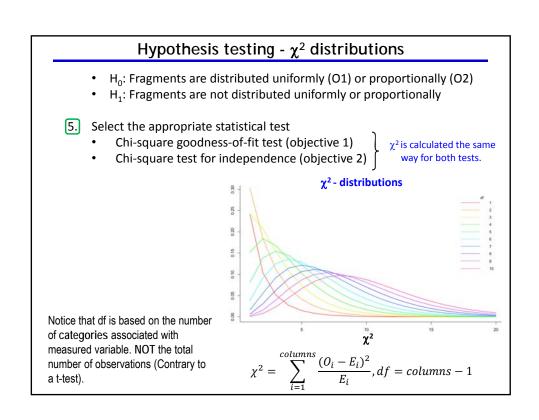




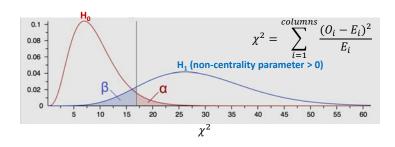






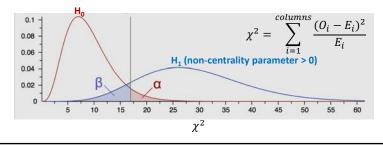


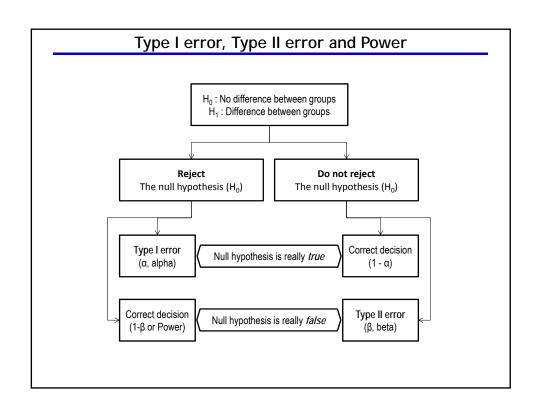
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- 5. Select the appropriate statistical test
 - Chi-square goodness-of-fit test
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 - By definition right-tailed for goodness-of-fit. (χ^2 increases for each error)

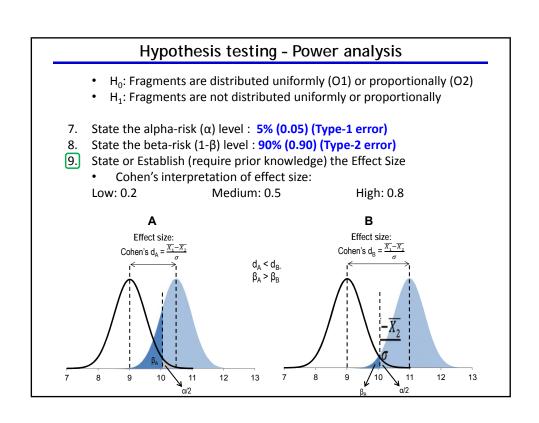


Hypothesis testing - Power analysis

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- 7. State the alpha-risk (α) level : 5% (0.05) (Type-1 error)
- 8. State the beta-risk (1-β) level : 90% (0.90) (Type-2 error)





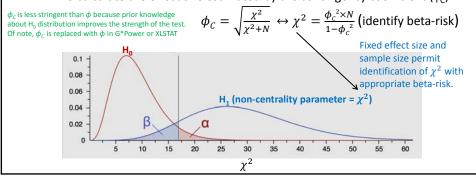


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- 9. State or Establish (require prior knowledge) the Effect Size
 - Interpretation of effect size (depends on df):

Low: 0.1 Medium: 0.3

• To calculate the effect size estimated by the contingency coefficient (ϕ_c) :

High: 0.5

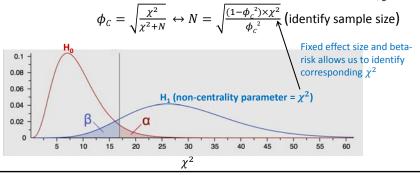


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Low: 0.1 Medium: 0.3

High: 0.5

To calculate the effect size estimated by the contingency coefficient (ϕ_c):

$$\phi_{\it C} = \sqrt{\frac{\chi^2}{\chi^2 + N}} \leftrightarrow N = \sqrt{\frac{(1 - \phi_{\it C}^2) \times \chi^2}{\phi_{\it C}^2}}$$
 (identify sample size)

Standardize to φ_{Max} to avoid effect from altering df.

$$\phi_{\it Max} = \sqrt{rac{r-1}{r}}$$
 , (r=rows, r x 1 contingency table)

$$\phi_{Max} = \sqrt[4]{rac{r-1}{r} imes rac{c-1}{c}}$$
 (r=rows, c=columns, r x c contingency table)

 $\phi_{Standardized} = \frac{\phi_{c}}{\phi_{Max}}$, ([0,1]=[Independence, Dependence] – interpret like r correlation coefficient)

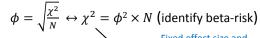
Hypothesis testing - Power analysis

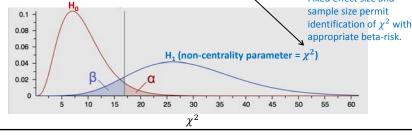
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- State or Establish (require prior knowledge) the Effect Size
 - Interpretation of effect size (depends on df):

Medium: 0.3 Low: 0.1

High: 0.5

To calculate the effect size estimated by $phi(\phi)$:





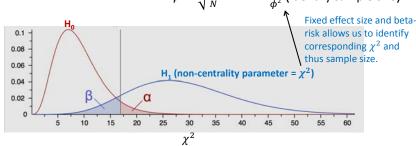
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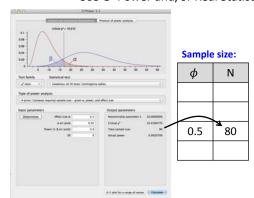
• To calculate the effect size estimated by phi (ϕ):

$$\phi = \sqrt{\frac{\chi^2}{N}} \leftrightarrow N = \frac{\chi^2}{\phi^2}$$
 (identify sample size)



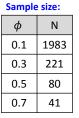
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- 10. Create Sampling Plan, determine sample size
 - Use G*Power and/or Real Statistics (free software)



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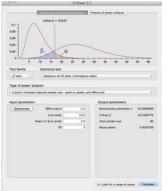


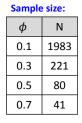


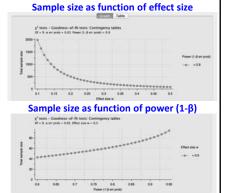


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Hypothesis testing - Cohort and data collection

- H₀: Fragments are distributed uniformly (O1) or proportionally (O2)
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- 7. State the alpha-risk (α) level : 5% (0.05) (Type-1 error)
- 8. State the beta-risk (1-β) level: 90% (0.90) (Type-2 error)
- 9. State or Establish (require prior knowledge) the Effect Size : $\phi = 0.5$
- 10. Create Sampling Plan, determine sample size: N = 80
- 11. Gather samples
- 12. Collect and pre-analyse data

Hypothesis testing - χ^2 test objective 1

- H₀: Fragments are distributed uniformly (O1) or proportionally (O2)
- H₁: Fragments are not distributed uniformly or proportionally
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- 12. Collect and pre-analyse data
- 13. Calculate the test statistic
 - Obj. 1: Does ligation generate an even distribution of each fragment.

Data from 2016

	Α	В	H ₀
			$\sum_{i=1}^{o.1} (O_i - E_i)^2$
1	3	0	$\chi^2 = \sum_{i=1}^{\infty} \frac{(O_i - E_i)}{F_i}$
2	12	6	0.06 $\frac{1}{i}$ H ₁ (non-centrality parameter > 0)
3	6	9	0.04
4	15	0	0.02
5	0	2	5 10 15 20 25 30 35 40 45 50 55 60
			χ^2

Hypothesis testing - χ^2 test objective 1

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Data from 2016				
	Α	В		
1	3	0	R	
2	12	6	R S	
3	6	9		
4	15	0		
5	0	2		

	_		-		
	Obse	rved		Expe	ected
		0			Ε
ow	1	3		1	53/5
um	2	18		2	53/5
→	3	15		3	53/5
	4	15		4	53/5
	5	2		5	53/5
	N=53				

$$\chi^{2} = \sum_{i=1}^{columns} \frac{(O_{i} - E_{i})^{2}}{E_{i}} = \frac{(3-10.6)^{2}}{10.6} + \frac{(18-10.6)^{2}}{10.6} + \frac{(15-10.6)^{2}}{10.6} + \frac{(15-10.6)^{2}}{10.6} + \frac{(2-10.6)^{2}}{10.6} = 21.25$$

Degrees of freedom (df) = 5-1 = 4

Hypothesis testing - χ^2 test objective 1

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- 12. Collect and pre-analyse data
- 13. Calculate the test statistic
 - Obj. 1: Does ligation generate an even distribution of each fragment.

	alpha			
df	0.05	0.01		
1	3.84	6.64		
2	5.99	9.21		
3	7.82	11.34		
4	9.49	13.28		
5	11.07	15.09		
6	12.59	16.81		
7	14.07	18.48		
8	15.51	20.09		
9	16.92	21.67		
10	18.31	23.21		

Observed				Ехре	cted
		0			Ε
	1	3		1	53/5
	2	18		2	53/5
	3	15		3	53/5
	4	15		4	53/5
	5	2		5	53/5
N=53					

bse	rved		Expe	ected	$\chi^2 = 21.25$
	0			Е	Degrees of freedom (df) = $5-1 = 4$
1	3		1	53/5	$\chi_{Critical}^{2} = 9.49 < 21.25$
2	18		2	53/5	Statistical Conclusion:
3	15		3	53/5	Reject H ₀ hypothesis. Samples do not deri
4	15		4	53/5	from a uniform distribution. Biological Conclusion:
		ı			Diological Coliciusion.

 $\boldsymbol{\lambda}$ Phage DNA fragments are not cloned into pUC19 in equal proportions.

Hypothesis testing - objective 1 post hoc

 Add-on question: The fragments are not cloned at equal proportions, but which fragments are significantly different from the uniform distribution?

Hypothesis testing - objective 1 post hoc

- Add-on question: The fragments are not cloned at equal proportions, but which fragments are significantly different from the uniform distribution?
- This question can be answered with post-hoc (Latin, meaning "after this") methods.
- Many post-hoc methods are available. The most simple is the repetitive analysis of all possible combinations corrected for Type-I error using Bonferroni correction (dividing alpha with the number of combinations tested).
- For objective 1 we could compare each of the fragments with all the other fragments combined (using multiple Chi-square tests).
- An alternative is to consider the observations as a normal distributed random variable and transform them to adjusted residuals following the standardized normal distribution (N(0,1)).
- The latter approach will be scrutinized here.

χ^2 -squared - post hoc analysis

- Suppose, X is a standard normal random variable (mean = 0 and variance = 1). X
- A sample drawn randomly from X is normally distributed.
- The residuals of the sample will equally be normally distributed this time with a
 - $\begin{array}{ll} \text{mean of 0. Of note, the variance will differ for each } O_{ij}. \\ \bullet \quad \text{The variance is inversely correlated with } p_i \text{ and } p_j. \\ \text{The more frequent an} \end{array}$ observation is for a given measured variable the less variance. We can therefore correct by dividing the residual with $\sqrt{(1-p_i)}$. For frequent observations the adjusted residual will increase more than for infrequent observations.
- The adjusted residuals can be compared to a critical Z-score
 - in excel for two-tailed analysis = NORM.INV(α /2, 0, 1) = NORM.INV(0.025, 0, 1) = 1.96
 - Make correction for multiple comparisons. Bonferroni: $\alpha_{corr} = \alpha/n_{comparisons}$

$$E_i = p_i \cdot n$$
 (Expected) and $p_i = \frac{1}{5}$

Residual:
$$r_i = \frac{O_i - E_i}{\sqrt{E_i}}$$

$$\text{Adjusted residual} = \frac{O_i - E_i}{\sqrt{E_i(1 - p_i)}}$$

Hypothesis testing - objective 1 post hoc

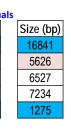
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$$E_i = p_i \cdot n$$
 (Expected) and $p_i = \frac{1}{5}$

Residual:
$$\mathbf{r}_{i} = \frac{O_{i} - E_{i}}{\sqrt{E_{i}}}$$

$$\text{Adjusted residual} = \frac{O_i - E_i}{\sqrt{E_i (1 - p_i)}}$$

bse	rved	Adj	usted	resi
	O _i			rac
1	3		1	-2.6
2	18		2	2.5
3	15		3	1.5
4	15		4	1.5
5	2		5	-2.9
	n-53			



 $\alpha = 0.05$ **Conclusion:**

Tests = 5 $\alpha_{bonferroni} = 0.05/5 = 0.01$ N(0.01/2,0,1)=2.58

Hypothesis testing - objective 1 post hoc

 Add-on question: The fragments are not cloned at equal proportions, but which fragments are significantly different from the uniform distribution?

 $E_i = p_i \cdot n$ (Expected) and $p_i = \frac{1}{5}$

Residual: $r_i = \frac{O_i - E_i}{\sqrt{E_i}}$

Adjusted residual = $\frac{O_i - E_i}{\sqrt{E_i(1 - p_i)}}$

Observed			
	O _i		
1	3		
2	18		
3	15		
4	15		
5	2		
	n=53		

Adjusted residuals

wj	ujusteu residuais					
		r _{adi}		Size (bp)		
	1	-2.61		16841		
	2	2.54		5626		
	3	1.51		6527		
	4	1.51		7234		
	5	-2.95		1275		

 $\alpha = 0.05$ Tests = 5

 $\alpha_{bonferroni} = 0.05/5 = 0.01$ N(0.01/2,0,1)=2.58

Conclusion:

Fragment 2 show a tendency of being overrepresented, whereas fragment 1 and 5 are significantly underrepresented.

Why? Find potential causes for your observations

- 1) Large fragment: ?
- 2) Small fragment: ?

Hypothesis testing - objective 1 post hoc

• Add-on question: The fragments are not cloned at equal proportions, but which fragments are significantly different from the uniform distribution?

 $E_i = p_i \cdot n$ (Expected) and $p_i = \frac{1}{5}$

Residual: $r_i = \frac{O_i - E_i}{\sqrt{E_i}}$

 $\label{eq:Adjusted residual} \mbox{Adjusted residual} = \frac{O_i - E_i}{\sqrt{E_i (1 - p_i)}}$

Obse	Observed			
	O _i			
1	3			
2	18			
3	15			
4	15			
5	2			
n=53				

ib	Size (bp)
31	16841
4	5626
1	6527
1	7234
95	1275

 $\alpha = 0.05$ Tests = 5

> $\alpha_{bonferroni} = 0.05/5 = 0.01$ N(0.01/2,0,1)=2.58

Conclusion:

Fragment 2 show a tendency of being overrepresented, whereas fragment 1 and 5 are significantly underrepresented.

Why? Find potential causes for your observations

- 1) Large fragment: Transfection efficiency
- 2) Small fragment: DNA purification

Hypothesis testing - objective 1

· Apply to your own samples!

$$\chi^2 = \sum_{i=1}^{columns} \frac{(O_i - E_i)^2}{E_i}$$

 $E_i = p_i \cdot n$ (Expected) and $p_i = \frac{1}{5}$

Residual: $\mathbf{r}_i = \frac{O_i - E_i}{\sqrt{E_i}}$

Adjusted residual = $\frac{O_i - E_i}{\sqrt{E_i(1 - p_i)}}$

Obse	rved	 Expe	cted
	0		Ε
1	O ₁	1	E ₁
2	02	2	E ₂
3	O ₃	3	E ₃
4	04	4	E ₄
5	05	5	E ₅

Hypothesis testing - χ^2 test objective 2

- H₀: Fragments are distributed uniformly (O1) or proportionally (O2)
- H₁: Fragments are not distributed uniformly or proportionally
- 7. State the alpha-risk (α) level: 5% (0.05) (Type-1 error)
- 8. State the beta-risk $(1-\beta)$ level: 90% (0.90) (Type-2 error)
- 9. State or Establish (require prior knowledge) the Effect Size : $\phi = 0.5$
- 10. Create Sampling Plan, determine sample size : N = 80
- 11. Gather samples
- 12. Collect and pre-analyse data
- 13. Calculate the test statistic
 - Obj. 2: Are sense and anti-sense equally represented for each fragment.

Observations							
	A B Total						
1	3	0	3				
2	12	6	18				
3	6	9	15				
4	15	0	15				
5	0	2	2				
Total	36	17	53				
	50:50?						

Expected				
	Α	В		
1	E _{1A}	E _{1B}		
2	E _{2A}	E _{2B}		
3	E _{3A}	E _{3B}		
4	E _{4A}	E _{4B}		
5	E _{5A}	E _{5B}		
50:50				

$$E_{ij} = n_i \cdot 0.5$$

$$\chi^2 = \sum_{j=1}^{rows} \sum_{i=1}^{columns} \frac{(O_{ij} - E_{ij})^2}{E_{ij}}$$

Hypothesis testing - χ^2 test objective 2

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Α	В	Total
3	0	З
12	6	18
6	9	15
15	0	15
0	2	2
36	17	53
50:	50?	
	12 6 15 0 36	3 0 12 6 6 9 15 0 0 2

Expected				
	Α			

	Α	В		
1	1.5	1.5		
2	9	9		
3	7.5	7.5		
4	7.5	7.5		
5	1	1		
50:50				

$$E_{ii} = n_i \cdot 0.5$$

$$\chi^{2} = \sum_{j=1}^{rows} \sum_{i=1}^{columns} \frac{(O_{ij} - E_{ij})^{2}}{E_{ij}} = 22.6$$

Hypothesis testing - χ^2 test objective 2

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Observations

	Α	В	Total		
1+5	3	2	5		
2	12	6	18		
3	6	9	15		
4	15	0	15		
Total	36	17	53		
50:50?					

	Α	В		
1+5	2.5	2.5		
2	9	9		
3	7.5	7.5		
4	7.5	7.5		
50:50				
25% E _{ii} <5				

$$E_{ij} = n_i \cdot 0.5$$

$$\chi^{2} = \sum_{j=1}^{rows} \sum_{i=1}^{columns} \frac{(O_{ij} - E_{ij})^{2}}{E_{ij}} = 17.8$$

Hypothesis testing - χ^2 test objective 2

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m	bs	0	n	12	tı	0	n	

Obsci vations					
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Total	36	17	53		
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50:50					
25% E _{ij} <5					

 $E_{ij} = n_i \cdot 0.5$

$$\chi^{2} = \sum_{j=1}^{rows} \sum_{i=1}^{columns} \frac{(O_{ij} - E_{ij})^{2}}{E_{ij}} = 17.8$$

Degré de libérté (df) = (ligne-1)*(colonne-1) =

$$\chi^2_{Critical} = 7.82 < 17.8 => \text{Reject H}_0$$

χ^2 -squared - objective 2 post hoc

- Suppose, X is a standard normal random variable (mean = 0 and variance = 1). X ~ N(0,1).
- A sample drawn randomly from X is normally distributed.
- The residuals of the sample will equally be normally distributed this time with a mean of 0. Of note, the variance will differ for each O_{ij}.
 - The variance is inversely correlated with p_i and p_i . The more frequent an observation is for a given measured variable the less variance. We can therefore correct by dividing the residual with $\sqrt{(1-p_i)(1-p_i)}$. For frequent observations the adjusted residual will increase more than for infrequent observations.
- The adjusted residuals can be compared to the critical Z-score
 - in excel for two-tailed analysis = NORM.INV(α /2, 0, 1) = NORM.INV(0.025, 0, 1) = 1.96
 - Make correction for multiple comparisons. Bonferroni: $\alpha_{corr} = \alpha/n_{comparisons}$

$$\mathsf{E}_{\mathsf{i}\mathsf{j}} = \mathsf{n}_{\mathsf{i}} \cdot p j$$
 (Expected) and $\mathsf{p}_{\mathsf{i}} = \frac{n_{\mathsf{i}}}{n}$, $\mathsf{p}_{\mathsf{j}} = 0.5$

Residual:
$$r_{ij} = \frac{O_{ij} - E_{ij}}{\sqrt{E_{ij}}}$$

$$\text{Adjusted residual} = \frac{o_{ii} - E_{ii}}{\sqrt{E_{ij}(1 - p_i)(1 - p_j)}}$$

		M_{j}		
		j=1	j=2	
NA	i=1	O _{ij}	O _{ij}	n _{i=1}
Mi	i=2	O _{ij}	O _{ij}	n _{i=2}
		n _{j=1}	n _{j=2}	N

M = Measure (variable)

O = Observation

n = Row, column or total sums

Hypothesis testing - objective 2 post hoc

 Add-on question: Which fragment has a skewed sense/anti-sense distribution?

 $E_{ij} = n_i \cdot pj$ (Expected) and $p_i = \frac{n_i}{n}$, $p_j = 0.5$

Residual:
$$r_{ij} = \frac{O_{ij} - E_{ij}}{\sqrt{E_{ij}}}$$

$$\text{Adjusted residual} = \frac{o_{ii} - E i_i}{\sqrt{E_{ij} (1 - p_i) (1 - p_j)}}$$

Conclusion:

Observed

Α B Total 3 0 3 12 18 6 3 6 9 15 4 15 0 15 5 0 2 2 Total 36 17 53

Adjusted residuals

Aujusteu residu		
	Α	В
1	1.78	-1.78
2	1.74	-1.74
3	-0.91	0.91
4	4.57	-4.57
5	-1.44	1.44

 $\alpha = 0.05$ Tests = 10

 $\begin{array}{l} \alpha_{bonferroni}\!=\!0.05/10\!=\!0.005 \\ N(0.005/2,0,1)\!=\!2.81 \end{array}$

Hypothesis testing - objective 2 post hoc

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Observed

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Conclusion:

Fragment 4 is significantly more represented in the sense direction (sense A) compared to the antisense.

Why? Find a cause for your finding. 1)

Hypothesis testing - objective 2 post hoc

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Conclusion:

Fragment 4 is significantly more represented in the sense direction (sense A) compared to the antisense.

Why? Find a cause for your finding.

1) Toxicity

Hypothesis testing - objective 2

Apply to your own samples!

$$\chi^2 = \sum_{j=1}^{rows} \sum_{i=1}^{columns} \frac{(O_{ij} - E_{ij})^2}{E_{ij}}$$

 $E_{ij} = n_i \cdot p_j$ (expected) and $p_i = \frac{n_i}{n}$, p_j =0.5

Residual:
$$r_{ij} = \frac{O_{ij} - E_{ij}}{\sqrt{E_{ij}}}$$

$$\text{Adjusted residual} = \frac{o_{ii} - E_{ii}}{\sqrt{E_{ij}(1 - p_i)(1 - p_j)}}$$

Observed

	Α	В	Tota
1	O_{1A}	O _{1B}	n ₁
2	O_{2A}	O_{2B}	n ₂
3	O_{3A}	O _{3B}	n_3
4	O_{4A}	O_{4B}	n ₄
5	O_{5A}	O_{5B}	n ₅
Total	n _A	n _B	n

Estimated

	Α	В
1	E _{1A}	E _{1B}
2	E _{2A}	E _{2B}
3	E _{3A}	E _{3B}
4	E _{4A}	E_{4B}
5	E _{5A}	E _{5B}