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Computing the inter-annotator agreement

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Exercice

Use the data from the gene renaming annotation campaign to:

1. compute the metrics:
   - S
   - κ
   - π
2. what do you notice?

Reminder of the formulas

		Annotator A		
		Yes	No	Total
Annotator B	Yes	24	8	32
	No	14	24	38
	Total	38	32	70

- Observed agreement: $A_o = \frac{24+24}{70} = 0,68$
- Expected agreement:
  1. $A_e^S = \frac{1}{2} = 0,5$
  2. $A_e^\pi = \frac{(\frac{(38+32)}{2})^2+(\frac{(32+38)}{2})^2}{70^2} = 0,5$
  3. $A_e^\kappa = \frac{\frac{(32\times 38)}{70}+\frac{(38\times 32)}{70}}{70} = 0,49$
- Results:
  1. $S = \frac{0.68-0.5}{1-0.5} = 0,36$
  2. $\pi = \frac{0.68-0.5}{1-0.5} = 0,36$
  3. $\kappa = \frac{0.68-0.49}{1-0.49} = 0,37$

Gene renaming example

"*The yppB:cat and ypbC:cat null alleles rendered cells sensitive to DNA-damaging agents, impaired plasmid transformation (25- and 100-fold), and moderately affected chromosomal transformation when present in an otherwise Rec+ B. subtilis strain. The yppB gene complemented the defect of the recG40 strain. <**former-name1 id="1"**>**yppB**</**former-name1**> and <**former-name2 id="2"**>**ypbC**</**former-name2**> and their respective null alleles were termed "<**new-name1 id="1"**>**recU**</**new-name1**>" and "recU1" (recU:cat) and "<**new-name2 id="2"**>**recS**</**new-name2**>" and "recS1" (recS:cat), respectively. The recU and recS mutations were introduced into rec-deficient strains representative of the alpha (recF), beta (addA5 addB72), gamma (recH342), and epsilon (recG40) epistatic groups.* "

Gene renaming data

		A1			
		Former	New	Nothing	Total
A2	Former	71	13	23	107
	New	8	69	15	92
	Nothing	7	8	18 840	18 855
	Total	86	90	18 878	19 054

Changing perspectives

		A1			
		Former	New	Nothing	Gene names
A2	Former	71	13	23	107
	New	8	69	15	92
	Nothing	7	8	951	966
	Gene names	86	90	989	1 165