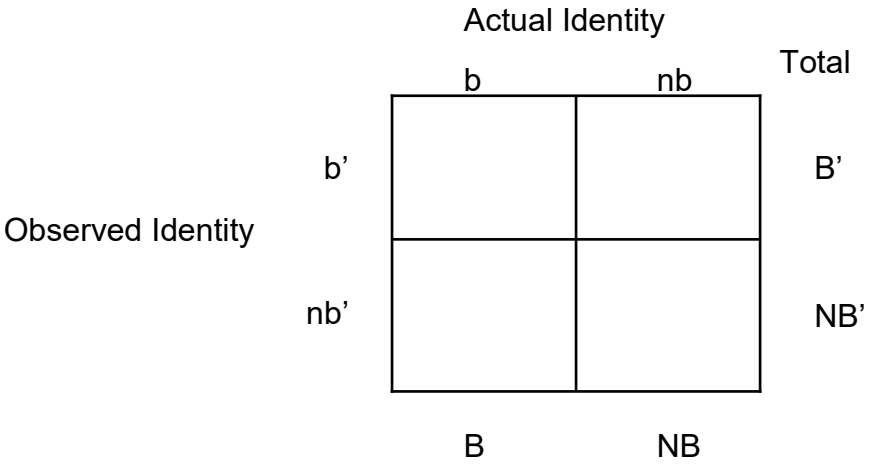
7.003 Spring 2022
Day 22 In-Lab Questions

1) When using the colony counts from your plates today to calculate the total number of EBY100 or L7.5.1 cells in your final bead selections, how will you know which quadrant of colony counts to use for each plate if you want to have the most accurate data? Explain your reasoning.

2) A confusion matrix is a table that can be used to visualize the success of a classification system at categorizing items into two different groups. Some examples of classification systems might be a diagnostic test (e.g. classifying patients as healthy vs diseased), an AI-recognition software (e.g. classifying an image as a human face vs not human face), or in our case for 7.003, a yeast display magnetic bead selection (classifying yeast cells as either binders to a target or non-binders). A confusion matrix for a bead selection is shown below (b = binder and nb = non-binder).



A) In your bead selection system, each individual yeast cell will have both an actual identity (either b or nb) and an observed identity (either b' or nb'). Define what is meant by a cell's actual identity and observed identity.

The lowercase letters (e.g. b or nb) indicate an individual cell, while the uppercase letters (e.g. B or NB) represent total values (cell numbers). Each yeast cell that goes through the bead selection system will end up in one of the four boxes of the confusion matrix, resulting in the final total values of B, NB, B', and NB'.

B) Fill in True Positive (TP), True Negative (TN), False Positive (FP), and False Negative (FN) in the four boxes of the confusion matrix. What do each of these four values represent?

C) Which values (B, NB, B', NB', TP, TN, FP, or FN) did you already know before you even started the bead selection?

D) Which values (B, NB, B', NB', TP, TN, FP, or FN) can you directly determine straight from the YPD and SC-Trp plate colony counts?

E) For the remaining values that you don't already know from Part C and Part D, how would you calculate those remaining values?

3) Using your confusion matrix values (B, NB, B', NB', TP, TN, FP, or FN), write out the formulas for calculating sensitivity, specificity, and accuracy (see lab manual page 130).

4) Discuss and compare your group's bead selection results with the other lab groups in your TA section. Which lab group had the highest sensitivity or highest specificity? How do you think their particular protocol modifications led to that result?

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