

Bachelor's Degree in Bioinformatics  
Statistical Models & Stochastic processes  
Academic year 2023-2024 1st Quarter

Practical 2. Likelihood ratio test (LRT)

Hand-in date: 25/10/2023

Resolve the following exercise in groups of two students. Write your solution in a Word, Latex or Markdown document and generate a pdf file with your solution. Upload the pdf file with your solution to the corresponding task at the Moodle environment of the course, no later than the hand-in date.

Many well-known standard statistical tests are actually LRT tests. We do some exercises with data sets where we apply these LRT tests.

1. (10p) Likelihood ratio test for Hardy-Weinberg equilibrium. In a genetic association study, the genotypes of a single nucleotide polymorphism have been determined for a sample of individuals. The genotype data file `snp.txt` contains the genotyping results.
  - a) (1p) Load the data in the R environment, and make a table of the different genotypes. Report the table. What is the sample size of the study?
  - b) (1p) How many alleles does this SNP have? How many genotypes could it theoretically have? Estimate all relative genotype frequencies by maximum likelihood (ML). Report the values of the ML estimators.
  - c) (2p) Count the number of alleles of each type in the sample. Estimate the relative allele frequencies by ML. Report the values of the ML estimators.
  - d) (1p) Which allele is the minor (least common) allele?
  - e) (1p) Do a likelihood ratio test (LRT) for Hardy-Weinberg equilibrium using the `HWLratio` function of the R-package `HardyWeinberg`. Report the likelihood ratio statistic and the p-value.
  - f) (1p) State your conclusion of the LRT.
  - g) (1p) State the distribution the LR statistic for this problem.
  - h) (1p) Calculate the p-value "by hand" using the value observed for the LR statistic and its distribution. Show your computations. Do you obtain the same result as the `HWLratio` function?
  - i) (1p) Calculate the expected genotype counts under the assumption of Hardy-Weinberg equilibrium. Compare them with the observed counts. What do you observe?
2. (10p) Comparison of regression models.

The outcome or response variable is `seize` and the explanatory variables or predictors are `trt`, `base` and `age`. Subject contains an ID for every individual.

The dataset `seizures_visit4.xls` contains the measures performed at visit 4 in a clinical trial.

The Clinical trial was conducted in  $m = 59$  subjects suffering from simple or partial seizures.

- Patients were randomized to the anti-epileptic drug progabide or placebo (0= Placebo, 1=Progabide; variable `trt`).
- A baseline measure of each subject's propensity for seizures was recorded, namely, the number of seizures suffered in the 8 weeks leading up to the start of the study (variable `base`).
- Each subject's age at the start of assigned treatment was also recorded (variable `age`).
- After initiation of assigned treatment, the number of seizures experienced by each subject in  $n = 4$  consecutive two-week periods was recorded, so that the response is a count measured at week 8 of follow up (variable `seize`).

The variable `seize` is used as the response variable in a multiple regression with the available variables as predictors.

- a. (0p) Load the data into the R environment. Do a summary of the data set.
- b. (2p) Fit a full model by the regression of `seize` on all predictors available in the data set. Report the adjusted  $R^2$  statistic of this model. Which variables are not significant? (use  $\alpha = 0.05$ ).
- c. (2p) Fit a reduced model, eliminating all insignificant predictors from the regression equation in a stepwise fashion (use  $\alpha = 0.05$ ). Report the adjusted  $R^2$  statistic of this reduced model. Does this model have a better or worse fit, according to this statistic?
- d. (2p) Do a likelihood ratio test (F-test) to see whether the full or reduced model fits the data better. Report the F statistic, its reference distribution and the p-value, and state your conclusion.
- e. (2p) Do simple linear regressions of `seize` on the predictors that you eliminated from the model. Do these regressions confirm that the eliminated predictors do not explain `seize`? State your findings and conclusions.
- f. (2p) Are regression coefficients you found in the different regressions consistent with each other? Comment on your findings.