Teaching statistics to biologists: the `R`-library `asbio`

Ken A. Aho

Idaho State University

An understanding of statistical concepts can be enhanced through computer programming and graphical applications. The `R`-library `asbio` "applied statistics for biologists" (Aho 2010) uses these capabilities to demonstrate introductory statistical concepts often poorly understood by biological scientists. In this presentation I describe how the teaching of four important statistical ideas can be enhanced with `asbio`. These topics are: 1) probability density functions, 2) parameter estimation, 3) likelihood, and 4) recognition of sampling and experimental designs. First, the theory underlying classical probability can be addressed with function `Venn`, derivation of probability for continuous probability density functions is addressed with `shade`, and demonstrations of sampling distributions for descriptive and test statistics are provided by the function `samp.dist`. Second, least square and maximum likelihood parameter estimation can be visually demonstrated using a number of `asbio` functions including `ls.plot` and `loglik.plot`. Third, concepts underlying likelihood (e.g. the influence of sample size the shape of the likelihood function) and REML are explained with the functions `loglik.plot` and `reml.plot`. Fourth, a large number of sampling and experimental designs are graphically depicted with the functions `runSampDesign` and `runExpDesign`. Randomization in these designs can be demonstrated by repeatedly creating plots using these functions. I will also address the practical applications of `asbio` in biological research including survivorship models for species using transition matrices, relevé table summaries, models for environmental engineering in vegetation reclamation, pruning analysis of multivariate community classifications, and the tracking animal trajectories in the context of habitat patches.