Kohn(x,a,b)

Eggert(x,a,b)

Chessel(x,a,b)

Kohn.gr(a,b,x)

Eggert.gr(a,b,x)

Chessel.gr(a,b,x)

cumunique(x)

Returns the cumulative number of unique values in a vector.x = vector with numbers.

get.ini.mm(x, y=NULL, iniMethod=c(”grouped”,”nls”,”rlm”,”lm”))

Generate start values for nls. x = samples, y = genotypes. Internal function called by acc.curve.

acc.fit(x, y, nS, IC=TRUE, iniMethod=c(”grouped”,”nls”,”rlm”,”lm”))

x = samples, y = genotypes, nS = length(samples), IC=returns a table with model selection parameters (AICc, Akaike weights) if IC=TRUE, iniMethod=which method to use for generation of start values. Internal function called by acc.curve.

acc.curve(samples, genotypes, shuffle=TRUE, iniMethod c(”grouped”,”nls”,”rlm”,”lm”), Log=FALSE)

Main function for fitting a single data set. shuffle = TRUE shuffles the data set once before analysis. iniMethod = method for generation of start values. Log = TRUE uses log(cumulative number of individuals) when fitting curves.

plot.acc.curve(obj, plot.type=c(“extended”,"normal"), xlim=NULL, addPoints=TRUE)

resampl.data(samples, genotypes, resamplings, replace=FALSE, Log=FALSE)

acc.curve.resamp(input.data, iniMethod="nls", IC=TRUE, distmom=FALSE)

acc.curve.mixed(input.data)

plot.curve(obj, model, ylim=NULL)

plot.hist(obj, model, breaks=30, plot.type=c(“density”,"histogram"), drawN=TRUE)

plot.est.comp(obj)

plot.par.cor(obj, …)

skew(x)

kurtosis(x)

chao.est(capt.freq)

genToFreq(z)

FreqTogen(n ,freq)

SIMULATIONS

sim.gen.data()

sim.run.data()

sim.summary()

sim.plot()