

HKA.test

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R Markdown

This is an R Markdown document. Markdown is a simple formatting syntax for authoring HTML, PDF, and MS Word documents. For more details on using R Markdown see <http://rmarkdown.rstudio.com>.

When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document. You can embed an R code chunk like this:

Input Data File Format:

Line 1 - a line of text. If desired, up to 10 extra lines of commentary can be added following line 1

line 2 - the number of loci = numloci

line 3 - the names of the two species, species 1 and species 2

the next numloci lines each have the following items

locus identifier

inheritance scalar (1.0 for autosomal 0.75 for X linked 0.25 for extrachromosomal or Y)

mean sequence length for species 1

mean sequence length species 2

mean sequence length in comparisons between species

of sequences for species 1

of sequences for species 2

of polymorphic sites species1

of polymorphic sites species2

mean pairwise divergence between species

Tajima D for species 1 (Tajima, 1989)

Tajima D for species 2 (Tajima, 1989)

Fu & Li D (rooted) for species 1 (Fu and Li, 1993)

Fu & Li D (rooted) for species 2 (Fu and Li, 1993)

Thus the basic format is of a table. With K loci the table would have K rows. Each row begins with a l

If one species has only a single sequence at one, at one or any of the loci, then that data set should

Inclusion of Tajima's and Fu&Li's statistics is optional and they need not be included. However if they

If tests of D statistics are desired, but the values for some loci are not known or are not calculable,

Including Plots

You can also embed plots, for example: