Distance sampling analysis using R
stratify.hazard <- ddf(dsmodel=~cds(key="hr", formula=~1, adj=TRUE, meta.data=list(width=1.94, control=list(mono=TRUE, m=60), hazard.aic <- stratify.hazard$criterion
    halfnorm.aic <- stratify.reanalyse$criterion

library(Distance)
stratify.hazard <- ds(key="hr", formula=~1, adj=TRUE, meta.data=list(width=1.94, control=list(mono=TRUE, m=60), hazard.aic <- stratify.hazard$criterion
    halfnorm.aic <- stratify.reanalyse$criterion

ama.hn.mas <- run_analysis(amakihi.proj$m13 - HIM
ama.data.std <- amakihi.proj$m13 - HN MAS w82.5
ama.data.std$SMAS.std <- ama.data.std$MAS/sd(ama.data.std$SMAS.std

Detection probability

Distance
Three elements needed to begin analysis using R

- Assume you have installed R ([www.cran.r-project.org](http://www.cran.r-project.org)) and also R-Studio ([www.rstudio.com](http://www.rstudio.com))
- Beyond this, you will need the package Distance available from CRAN
- Deeper understanding of distance sampling survey data organisation
Survey data in Distance

Data Layers

Global  Stratum  Sample  Observation

CREEM
Centre for Research into Ecological and Environmental Modelling

University of St Andrews
Distance for windows data tab

Comma separated values file of same data
Exercises accompanying analysis using R

- Duck nests
  - Conventional distance sampling analysis
  - Also used in Chapter 1 of online workshop

- Amakihi songbirds
  - Point transects
  - Multiple covariate distance sampling analysis
  - Also used in Chapter 5 of online workshops

- Scottish Crossbills
  - Detection function derived from a separate survey
  - Detection probability applied to data from main survey
  - Uncertainty derived using bootstrapping technique

- Multi-species songbird survey
  - Techniques for filtering species-specific data from multi-species data
  - Challenge is to ensure survey effort is correctly recorded
  - Introducing programming to modularise analyses