# MCDS.exe Testing

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## Things outstanding in mrds

In addition to the notes throughout this document the following also needs further work or investigations:

- **FIXED** Issue 83 in mrds relating to factor ordering differences between mrds and MCDS (https://github.com/DistanceDevelopment/mrds/issues/83)
- **Now seems to spot and display warnings and errors from MCDS** Reading in and processing the warnings and / or errors in the log file generated by MCDS - What do we do about cases where mcds.exe fits with negative pdf? E.g. https://github.com/DistanceDevelopment/Distance/issues/160
- Do the monotonicity constraints get passed to MCDS correctly? **YES**
- Check the passing of parameter starting values to MCDS - also potential issues here regarding factor ordering! **Now passing parameter start values - no problems with factor ordering as this is dealt with by the reordering of the factor names passed to MCDS**
- **Made errors into non fatal warnings and messages**
- Check the passing of parameter bound to MCDS. Note this can only be done via mrds NOT via Distance. Low priority - not done
- Could do with more tests of the case of uniform only models to check that abundance estimates are correctly calculated.

## Capercaillie Data

Various warnings and errors that want further investigation:

```
# MCDS warning - does this want removed?
# ** Warning: One or more cluster sizes are coded as -1. Distance assumes -1 to mean a cluster of undet
```

```
data("capercaillie")

ds.fit <- ds(capercaillie,
             key = "hn",
             adjustment = "herm",
             nadj = 2,
             optimizer = "MCDS")

model.compare <- test.models(capercaillie,
                             truncation = max(capercaillie$distance),
                             transect = "line",
                             convert.units = 10)

save(model.compare, file = "results/capercaillie.ROBJ")
```

Table 1: Comparison of R and MCDS model fits for Capercaillie data. key - key function, adj - type of adjustment term, nadj - number of adjustments, lnl_R - likelihood value for R optimiser, lnl_MCDS - likelihood value for MCDS optimiser, optimizer - the selected optimiser, p_R the estimated average probability of detection for the R optimised model, p_MCDS the estimated average probability of detection for the MCDS optimised model, Nhat_R - estimated abundance in covered region from R optimised model, Nhat_MCDS - estimated abundance in covered region from MCDS optimised model.

| key | adj | nadj | lnl_R | lnl_MCDS | optimizer | p_R | p_MCDS | Nhat_R | Nhat_MCDS |
|---|---|---|---|---|---|---|---|---|---|
| unif | cos | 0 | -490.7870 | -490.7870 | mrds (nlminb) | 1.00 | 1.00 | 112.00 | 112.00 |
| unif | cos | 1 | -478.1321 | -478.1321 | mrds (nlminb) | 0.59 | 0.59 | 188.93 | 188.93 |
| unif | cos | 2 | -477.0771 | -477.0765 | MCDS.exe | 0.68 | 0.68 | 164.27 | 164.21 |
| unif | cos | 3 | -477.0723 | -477.0713 | MCDS.exe | 0.68 | 0.68 | 165.59 | 165.57 |
| hn | cos | 0 | -477.9525 | -477.9525 | mrds (nlminb) | 0.61 | 0.61 | 182.76 | 182.76 |
| hn | cos | 1 | -477.2076 | -477.2057 | MCDS.exe | 0.66 | 0.66 | 169.09 | 169.04 |
| hn | cos | 2 | -477.0673 | -477.0672 | MCDS.exe | 0.69 | 0.69 | 162.03 | 162.04 |
| hn | herm | 0 | -477.9525 | -477.9525 | mrds (nlminb) | 0.61 | 0.61 | 182.76 | 182.76 |
| hn | herm | 1 | -477.2173 | -477.2162 | MCDS.exe | 0.67 | 0.67 | 166.20 | 166.15 |
| hn | herm | 2 | -477.2205 | NA | mrds (nlminb) | 0.67 | NA | 166.04 | NA |
| hr | poly | 0 | -476.9369 | -476.9369 | mrds (nlminb) | 0.70 | 0.70 | 159.40 | 159.45 |
| hr | poly | 1 | -476.9394 | -476.9395 | mrds (nlminb) | 0.70 | 0.70 | 159.56 | 159.46 |
| hr | poly | 2 | -476.8707 | -476.7331 | MCDS.exe | 0.71 | 0.68 | 157.86 | 164.52 |

## Cue Counting Data

Things that might want further investigation:

- Nhat for the hn herm 1 model is ~14% higher for the MCDS optimised model than the R optimised model
- Why is the lnl_R value for the hr poly 2 model negative? This has now changed!

Various warnings and errors that want further investigation:

```
# Fitting hazard-rate key function with simple polynomial(4,6) adjustments
# ** Warning: One or more cluster sizes are coded as -1. Distance assumes -1 to mean a cluster of undet
# Warning: Detection function is not strictly monotonic!Warning: Detection function is less than 0 at s
# Warning: Detection function is less than 0 at some distancesAIC= -0.103
# Fitting half-normal key function with Hermite(4,6) adjustments
# ** Warning: One or more cluster sizes are coded as -1. Distance assumes -1 to mean a cluster of undet
# ** Warning: convergence failure **
# Warning in check.mono(result, n.pts = control$mono.points) :
#   Detection function is not strictly monotonic!
# Warning in check.mono(result, n.pts = control$mono.points) :
#   Detection function is not strictly monotonic!
# AIC= -1.752
# Warning in mrds::check.mono(model, n.pts = 20) :
#   Detection function is not strictly monotonic!
# No survey area information supplied, only estimating detection function.
#
# Fitting half-normal key function with Hermite(4,6) adjustments
# ** Warning: One or more cluster sizes are coded as -1. Distance assumes -1 to mean a cluster of undet
# ** Warning: convergence failure **
# Warning in check.mono(result, n.pts = control$mono.points) :
#   Detection function is not strictly monotonic!
# AIC= 1.966
# No survey area information supplied, only estimating detection function.
```

```
data("CueCountingExample")

model.compare <- test.models(CueCountingExample,
                             truncation = max(CueCountingExample$distance, na.rm = TRUE),
                             transect = "point")

save(model.compare, file = "results/cue_counting.ROBJ")
```

Table 2: Comparison of R and MCDS model fits for cue counting data. key - key function, adj - type of adjustment term, nadj - number of adjustments, lnl_R - likelihood value for R optimiser, lnl_MCDS - likelihood value for MCDS optimiser, optimizer - the selected optimiser, p_R the estimated average probability of detection for the R optimised model, p_MCDS the estimated average probability of detection for the MCDS optimised model, Nhat_R - estimated abundance in covered region from R optimised model, Nhat_MCDS - estimated abundance in covered region from MCDS optimised model.

| key | adj | nadj | lnl_R | lnl_MCDS | optimizer | p_R | p_MCDS | Nhat_R | Nhat_MCDS |
|---|---|---|---|---|---|---|---|---|---|
| unif | cos | 0 | -18.110662 | -18.110662 | mrds (nlminb) | 1.00 | 1.00 | 40.00 | 40.00 |
| unif | cos | 1 | 1.933002 | 1.933002 | MCDS.exe | 0.31 | 0.31 | 128.30 | 128.30 |
| unif | cos | 2 | 2.377847 | 2.377847 | MCDS.exe | 0.25 | 0.25 | 160.47 | 160.45 |
| unif | cos | 3 | 2.569996 | 2.661115 | mrds (nlminb) | 0.32 | 0.30 | 124.64 | 132.36 |
| hn | cos | 0 | 1.916333 | 1.916332 | MCDS.exe | 0.24 | 0.24 | 167.61 | 167.61 |
| hn | cos | 1 | 2.109706 | 2.109790 | mrds (nlminb) | 0.30 | 0.30 | 132.40 | 132.27 |
| hn | cos | 2 | 2.132097 | 2.132096 | MCDS.exe | 0.28 | 0.28 | 144.42 | 144.34 |
| hn | herm | 0 | 1.916333 | 1.916332 | MCDS.exe | 0.24 | 0.24 | 167.61 | 167.61 |
| hn | herm | 1 | 2.016928 | 1.925329 | MCDS.exe | 0.28 | 0.24 | 145.05 | 165.77 |
| hn | herm | 2 | 2.016971 | 3.876089 | mrds (nlminb) | 0.28 | 0.28 | 145.06 | 142.45 |
| hr | poly | 0 | 1.381404 | 1.381404 | MCDS.exe | 0.28 | 0.28 | 142.27 | 142.26 |
| hr | poly | 1 | 1.701666 | 1.701666 | MCDS.exe | 0.27 | 0.27 | 145.94 | 145.92 |
| hr | poly | 2 | NA | 4.051256 | mrds (nlminb) | NA | 0.29 | NA | 138.47 |

## Ducknest Data

Things that might want further investigation:

- p_MCDS is 1 for a few of these models and when it is, it is estimating Nhat much lower than the R optimiser.

```
# Fitting half-normal key function with Hermite(4,6) adjustments
# Warning: First partial hessian is singular and second-partial hessian is NULL, no hessian
# AIC= 932.07
# No hessian, possible numerical problems; only estimating detection function.
```

```
data("ducknest")

model.compare <- test.models(ducknest,
                             truncation = max(ducknest$distance, na.rm = TRUE),
                             transect = "line")

save(model.compare, file = "results/ducknest.ROBJ")
```

Table 3: Comparison of R and MCDS model fits for Ducknest data. key - key function, adj - type of adjustment term, nadj - number of adjustments, lnl_R - likelihood value for R optimiser, lnl_MCDS - likelihood value for MCDS optimiser, optimizer - the selected optimiser, p_R the estimated average probability of detection for the R optimised model, p_MCDS the estimated average probability of detection for the MCDS optimised model, Nhat_R - estimated abundance in covered region from R optimised model, Nhat_MCDS - estimated abundance in covered region from MCDS optimised model.

| key | adj | nadj | lnl_R | lnl_MCDS | optimizer | p_R | p_MCDS | Nhat_R | Nhat_MCDS |
|---|---|---:|---:|---:|---|---:|---:|---:|---:|
| unif | cos | 0 | -467.5003 | -467.5003 | mrds (nlminb) | 1.00 | 1.00 | 534.00 | 534.00 |
| unif | cos | 1 | -463.2398 | -463.2398 | MCDS.exe | 0.85 | 0.85 | 630.88 | 630.88 |
| unif | cos | 2 | -462.6916 | -462.6908 | MCDS.exe | 0.88 | 0.88 | 607.05 | 606.98 |
| unif | cos | 3 | -462.6444 | -462.6443 | MCDS.exe | 0.89 | 0.89 | 599.64 | 599.63 |
| hn | cos | 0 | -463.0669 | -467.4962 | mrds (nlminb) | 0.87 | 1.00 | 614.25 | 534.04 |
| hn | cos | 1 | -462.9360 | -462.9358 | MCDS.exe | 0.89 | 0.89 | 599.84 | 599.78 |
| hn | cos | 2 | -462.9327 | -462.9326 | MCDS.exe | 0.89 | 0.89 | 597.68 | 597.66 |
| hn | herm | 0 | -463.0669 | -467.4962 | mrds (nlminb) | 0.87 | 1.00 | 614.25 | 534.04 |
| hn | herm | 1 | -463.0601 | -463.0592 | MCDS.exe | 0.87 | 0.87 | 615.35 | 614.76 |
| hn | herm | 2 | -463.0417 | -463.0352 | MCDS.exe | 0.86 | 0.86 | 619.58 | 620.01 |
| hr | poly | 0 | -462.8967 | -462.8967 | mrds (nlminb) | 0.89 | 0.89 | 600.63 | 600.82 |
| hr | poly | 1 | -462.8996 | -462.9044 | mrds (nlminb) | 0.89 | 0.89 | 600.86 | 600.89 |
| hr | poly | 2 | -462.4992 | -462.1233 | MCDS.exe | 0.90 | 0.89 | 592.58 | 600.37 |

## DuikerCameraTraps

Things that might want further investigation: - Nhat values look to differ by around 20% between the two optimisers

```
# Fitting half-normal key function with Hermite(4,6) adjustments
# Warning: First partial hessian is singular; using second-partial hessian
# Warning: First partial hessian is singular; using second-partial hessian
# AIC= 25014.184
# Error in array(x, c(length(x), 1L), if (!is.null(names(x))) list(names(x),  :
#   'data' must be of a vector type, was 'NULL'
# Error in t(partial) %*% vcov :
#   requires numeric/complex matrix/vector arguments
```

```
data("DuikerCameraTraps")

model.compare <- test.models(DuikerCameraTraps,
                             truncation = list(left = 2, right = 15),
                             cutpoints = c(seq(2,8,1), 10, 12, 15),
                             transect = "point")

save(model.compare, file = "results/DuikerCameraTraps.ROBJ")
```

Table 4: Comparison of R and MCDS model fits for Duiker camera trap data. key - key function, adj - type of adjustment term, nadj - number of adjustments, lnl_R - likelihood value for R optimiser, lnl_MCDS - likelihood value for MCDS optimiser, optimizer - the selected optimiser, p_R the estimated average probability of detection for the R optimised model, p_MCDS the estimated average probability of detection for the MCDS optimised model, Nhat_R - estimated abundance in covered region from R optimised model, Nhat_MCDS - estimated abundance in covered region from MCDS optimised model.

| key | adj | nadj | lnl_R | lnl_MCDS | optimizer | p_R | p_MCDS | Nhat_R | Nhat_MCDS |
|---|---|---:|---:|---:|---|---:|---:|---:|---:|
| unif | cos | 0 | -14689.18 | -14689.18 | mrds (nlminb) | 0.98 | 0.98 | 5971.15 | 5971.15 |
| unif | cos | 1 | -12497.73 | -12497.73 | mrds (nlminb) | 0.30 | 0.30 | 19550.79 | 19550.13 |
| unif | cos | 2 | -12527.50 | -12495.90 | MCDS.exe | 0.35 | 0.32 | 16662.78 | 18517.00 |
| unif | cos | 3 | -12463.77 | -12463.65 | MCDS.exe | 0.34 | 0.34 | 17293.59 | 17283.16 |
| hn | cos | 0 | -12539.80 | -12539.80 | mrds (nlminb) | 0.26 | 0.26 | 22381.29 | 22380.94 |
| hn | cos | 1 | -12476.04 | -12475.87 | MCDS.exe | 0.33 | 0.33 | 17813.30 | 17796.84 |
| hn | cos | 2 | -12458.57 | -12458.56 | MCDS.exe | 0.37 | 0.37 | 15798.09 | 15799.97 |
| hn | herm | 0 | -12539.80 | -12539.80 | mrds (nlminb) | 0.26 | 0.26 | 22381.29 | 22380.94 |
| hn | herm | 1 | -12472.93 | -12510.95 | mrds (nlminb) | 0.34 | 0.29 | 17320.90 | 20043.80 |
| hn | herm | 2 | -12472.49 | -12504.09 | mrds (nlminb) | 0.34 | 0.29 | 17224.44 | 19894.14 |
| hr | poly | 0 | -12436.80 | -12436.80 | mrds (nlminb) | 0.40 | 0.40 | 14739.07 | 14738.80 |
| hr | poly | 1 | -12436.80 | -12436.81 | mrds (nlminb) | 0.40 | 0.40 | 14738.67 | 14742.50 |
| hr | poly | 2 | -12436.22 | -12434.54 | MCDS.exe | 0.39 | 0.38 | 14852.24 | 15326.45 |

## LTExercise Data

Things that might want further investigation: - - Why is is warning about “Warning in process.data(data, meta.data, check = FALSE) : no truncation distance specified; using largest observed distance”?

```
data("LTExercise")

model.compare <- test.models(LTExercise,
                             truncation = max(LTExercise$distance, na.rm = TRUE),
                             transect = "line")

save(model.compare, file = "results/LTExercise.ROBJ")
```

Table 5: Comparison of R and MCDS model fits for LTExercise data. key - key function, adj - type of adjustment term, nadj - number of adjustments, lnl_R - likelihood value for R optimiser, lnl_MCDS - likelihood value for MCDS optimiser, optimizer - the selected optimiser, p_R the estimated average probability of detection for the R optimised model, p_MCDS the estimated average probability of detection for the MCDS optimised model, Nhat_R - estimated abundance in covered region from R optimised model, Nhat_MCDS - estimated abundance in covered region from MCDS optimised model.

| key | adj | nadj | lnl_R | lnl_MCDS | optimizer | p_R | p_MCDS | Nhat_R | Nhat_MCDS |
|---|---|---:|---:|---:|---|---:|---:|---:|---:|
| unif | cos | 0 | -375.6845 | -375.6845 | mrds (nlminb) | 1.00 | 1.00 | 105.00 | 105.00 |
| unif | cos | 1 | -327.2768 | -327.2768 | mrds (nlminb) | 0.51 | 0.51 | 207.38 | 207.38 |
| unif | cos | 2 | -335.3956 | -315.8040 | MCDS.exe | 0.61 | 0.37 | 171.61 | 280.68 |
| unif | cos | 3 | -315.5099 | -315.3818 | MCDS.exe | 0.34 | 0.35 | 306.93 | 304.08 |
| hn | cos | 0 | -317.4681 | -317.4681 | mrds (nlminb) | 0.35 | 0.35 | 300.70 | 300.70 |
| hn | cos | 1 | -317.4680 | -317.4680 | MCDS.exe | 0.35 | 0.35 | 300.21 | 300.26 |
| hn | cos | 2 | -317.2043 | -317.2043 | MCDS.exe | 0.37 | 0.37 | 281.75 | 281.75 |
| hn | herm | 0 | -317.4681 | -317.4681 | mrds (nlminb) | 0.35 | 0.35 | 300.70 | 300.70 |
| hn | herm | 1 | -317.4610 | -317.4610 | mrds (nlminb) | 0.35 | 0.35 | 300.77 | 300.78 |
| hn | herm | 2 | -315.4484 | -315.4070 | MCDS.exe | 0.34 | 0.34 | 311.19 | 306.79 |
| hr | poly | 0 | -317.5457 | -317.5457 | mrds (nlminb) | 0.42 | 0.42 | 250.34 | 250.32 |
| hr | poly | 1 | -317.5458 | NA | mrds (nlminb) | 0.42 | NA | 250.30 | NA |
| hr | poly | 2 | -342.2048 | -316.4437 | MCDS.exe | 0.59 | 0.39 | 177.21 | 270.83 |

## PTExercise Data

Things that might want further investigation: - - Why is is warning about “Warning in process.data(data, meta.data, check = FALSE) : no truncation distance specified; using largest observed distance”?

```
data("PTExercise")

model.compare <- test.models(PTExercise,
                             truncation = max(PTExercise$distance, na.rm = TRUE),
                             transect = "point")

save(model.compare, file = "results/PTExercise.ROBJ")
```

Table 6: Comparison of R and MCDS model fits for PTExercise data. key - key function, adj - type of adjustment term, nadj - number of adjustments, lnl_R - likelihood value for R optimiser, lnl_MCDS - likelihood value for MCDS optimiser, optimizer - the selected optimiser, p_R the estimated average probability of detection for the R optimised model, p_MCDS the estimated average probability of detection for the MCDS optimised model, Nhat_R - estimated abundance in covered region from R optimised model, Nhat_MCDS - estimated abundance in covered region from MCDS optimised model.

| key | adj | nadj | lnl_R | lnl_MCDS | optimizer | p_R | p_MCDS | Nhat_R | Nhat_MCDS |
|---|---|---:|---:|---:|---|---:|---:|---:|---:|
| unif | cos | 0 | -576.5580 | -576.5580 | mrds (nlminb) | 1.00 | 1.00 | 144.00 | 144.00 |
| unif | cos | 1 | -472.1765 | -472.1765 | mrds (nlminb) | 0.30 | 0.30 | 479.26 | 479.26 |
| unif | cos | 2 | -471.3570 | -457.2211 | MCDS.exe | 0.29 | 0.18 | 489.04 | 814.73 |
| unif | cos | 3 | -467.8910 | -457.0976 | MCDS.exe | 0.32 | 0.19 | 446.72 | 764.10 |
| hn | cos | 0 | -458.5701 | -458.5701 | mrds (nlminb) | 0.16 | 0.16 | 875.75 | 875.75 |
| hn | cos | 1 | -457.8850 | -457.8850 | mrds (nlminb) | 0.20 | 0.20 | 726.49 | 726.28 |
| hn | cos | 2 | -457.8646 | -457.8646 | mrds (nlminb) | 0.21 | 0.21 | 700.66 | 700.37 |
| hn | herm | 0 | -458.5701 | -458.5701 | mrds (nlminb) | 0.16 | 0.16 | 875.75 | 875.75 |
| hn | herm | 1 | -458.1114 | -458.5393 | mrds (nlminb) | 0.19 | 0.17 | 750.89 | 866.98 |
| hn | herm | 2 | -458.1115 | NA | mrds (nlminb) | 0.19 | NA | 753.01 | NA |
| hr | poly | 0 | -458.8069 | -458.8069 | mrds (nlminb) | 0.26 | 0.26 | 549.29 | 549.27 |
| hr | poly | 1 | -458.7402 | -458.7402 | MCDS.exe | 0.26 | 0.26 | 557.15 | 557.16 |
| hr | poly | 2 | -585.5221 | -456.5765 | MCDS.exe | 0.24 | 0.22 | 610.24 | 643.09 |

### Savannah Sparrow 1980

```
# Fitting uniform key function with cosine(1,2,3) adjustments
# Warning in check.mono(result, n.pts = control$mono.points) :
#   Detection function is not strictly monotonic!
# Warning in check.mono(result, n.pts = control$mono.points) :
#   Detection function is not strictly monotonic!
# AIC= 2212.082
```

```
data("Savannah_sparrow_1980")

model.compare <- test.models(Savannah_sparrow_1980,
                             truncation = max(Savannah_sparrow_1980$distance, na.rm = TRUE),
                             transect = "point")

save(model.compare, file = "results/Savannah_sparrow_1980.ROBJ")
```

Table 7: Comparison of R and MCDS model fits for Savannah sparrow 1980 data. key - key function, adj - type of adjustment term, nadj - number of adjustments, lnl_R - likelihood value for R optimiser, lnl_MCDS - likelihood value for MCDS optimiser, optimizer - the selected optimiser, p_R the estimated average probability of detection for the R optimised model, p_MCDS the estimated average probability of detection for the MCDS optimised model, Nhat_R - estimated abundance in covered region from R optimised model, Nhat_MCDS - estimated abundance in covered region from MCDS optimised model.

| key | adj | nadj | lnl_R | lnl_MCDS | optimizer | p_R | p_MCDS | Nhat_R | Nhat_MCDS |
|---|---|---|---|---|---|---|---|---|---|
| unif | cos | 0 | -1352.103 | -1352.103 | mrds (nlminb) | 1.00 | 1.00 | 276.00 | 276.00 |
| unif | cos | 1 | -1140.331 | -1140.331 | mrds (nlminb) | 0.30 | 0.30 | 922.84 | 922.84 |
| unif | cos | 2 | -1103.437 | -1103.140 | MCDS.exe | 0.17 | 0.17 | 1589.95 | 1632.38 |
| unif | cos | 3 | -1134.781 | -1103.041 | MCDS.exe | 0.32 | 0.16 | 855.36 | 1696.16 |
| hn | cos | 0 | -1103.866 | -1103.866 | mrds (nlminb) | 0.15 | 0.15 | 1827.90 | 1827.80 |
| hn | cos | 1 | -1103.810 | -1103.810 | MCDS.exe | 0.15 | 0.15 | 1886.75 | 1887.79 |
| hn | cos | 2 | -1102.887 | -1102.887 | MCDS.exe | 0.13 | 0.13 | 2153.27 | 2152.34 |
| hn | herm | 0 | -1103.866 | -1103.866 | mrds (nlminb) | 0.15 | 0.15 | 1827.90 | 1827.80 |
| hn | herm | 1 | -1103.864 | -1103.864 | MCDS.exe | 0.15 | 0.15 | 1828.57 | 1828.97 |
| hn | herm | 2 | -1102.912 | -1102.593 | MCDS.exe | 0.16 | 0.16 | 1734.67 | 1694.40 |
| hr | poly | 0 | -1112.460 | -1112.460 | mrds (nlminb) | 0.20 | 0.20 | 1381.75 | 1381.48 |
| hr | poly | 1 | -1109.578 | -1109.578 | mrds (nlminb) | 0.19 | 0.19 | 1479.80 | 1479.61 |
| hr | poly | 2 | -1109.428 | -1102.601 | MCDS.exe | 0.19 | 0.15 | 1480.74 | 1843.54 |

## Savannah Sparrow 1981

Everything looks to run fine.

```
# Fitting uniform key function with cosine(1,2,3) adjustments
# ** Warning: convergence failure **
# Warning in check.mono(result, n.pts = control$mono.points) :
#   Detection function is not strictly monotonic!
# Warning in check.mono(result, n.pts = control$mono.points) :
#   Detection function is less than 0 at some distances
```

```
data("Savannah_sparrow_1981")

model.compare <- test.models(Savannah_sparrow_1981,
                             truncation = max(Savannah_sparrow_1981$distance, na.rm = TRUE),
                             transect = "point")

save(model.compare, file = "results/Savannah_sparrow_1981.ROBJ")
```

Table 8: Comparison of R and MCDS model fits for Savannah sparrow 1981 data. key - key function, adj - type of adjustment term, nadj - number of adjustments, lnl_R - likelihood value for R optimiser, lnl_MCDS - likelihood value for MCDS optimiser, optimizer - the selected optimiser, p_R the estimated average probability of detection for the R optimised model, p_MCDS the estimated average probability of detection for the MCDS optimised model, Nhat_R - estimated abundance in covered region from R optimised model, Nhat_MCDS - estimated abundance in covered region from MCDS optimised model.

| key | adj | nadj | lnl_R | lnl_MCDS | optimizer | p_R | p_MCDS | Nhat_R | Nhat_MCDS |
|---|---|---|---|---|---|---|---|---|---|
| unif | cos | 0 | -946.7393 | -946.7393 | mrds (nlminb) | 1.00 | 1.00 | 186.00 | 186.00 |
| unif | cos | 1 | -814.4403 | -814.4403 | mrds (nlminb) | 0.30 | 0.30 | 614.72 | 614.72 |
| unif | cos | 2 | -811.7519 | -789.8251 | MCDS.exe | 0.29 | 0.18 | 642.58 | 1052.40 |
| unif | cos | 3 | -788.2451 | -1146.4401 | mrds (nlminb) | 0.15 | 0.18 | 1276.63 | 1020.20 |
| hn | cos | 0 | -790.8846 | -790.8846 | mrds (nlminb) | 0.16 | 0.16 | 1153.99 | 1153.93 |
| hn | cos | 1 | -790.1360 | -790.1360 | mrds (nlminb) | 0.14 | 0.14 | 1336.80 | 1336.55 |
| hn | cos | 2 | -788.3169 | -788.3169 | mrds (nlminb) | 0.17 | 0.17 | 1083.33 | 1083.00 |
| hn | herm | 0 | -790.8846 | -790.8846 | mrds (nlminb) | 0.16 | 0.16 | 1153.99 | 1153.93 |
| hn | herm | 1 | -790.8620 | -790.8620 | mrds (nlminb) | 0.16 | 0.16 | 1154.83 | 1154.77 |
| hn | herm | 2 | -788.4557 | -788.4557 | mrds (nlminb) | 0.15 | 0.15 | 1258.17 | 1257.86 |
| hr | poly | 0 | -787.8818 | -787.8818 | mrds (nlminb) | 0.20 | 0.20 | 950.35 | 950.29 |
| hr | poly | 1 | -787.8781 | -787.8781 | mrds (nlminb) | 0.20 | 0.20 | 952.19 | 952.12 |
| hr | poly | 2 | -787.8423 | -787.5409 | MCDS.exe | 0.19 | 0.19 | 968.09 | 981.53 |

## Sika Deer

```
# Fitting hazard-rate key function with simple polynomial(4,6) adjustments
# Warning in ddf.ds(dsmodel = dsmodel, data = data, meta.data = meta.data,  :
#   Estimated hazard-rate scale parameter close to 0 (on log scale). Possible problem in data (e.g., sp
# Warning in check.mono(result, n.pts = control$mono.points) :
#   Detection function is not strictly monotonic!
# Warning in ddf.ds(dsmodel = dsmodel, data = data, meta.data = meta.data,  :
#   Estimated hazard-rate scale parameter close to 0 (on log scale). Possible problem in data (e.g., sp
# Warning in check.mono(result, n.pts = control$mono.points) :
#   Detection function is not strictly monotonic!
# AIC= 20204.647
```

```
data("sikadeer")

model.compare <- test.models(sikadeer,
                             truncation = max(sikadeer$distance, na.rm = TRUE),
                             transect = "line")

save(model.compare, file = "results/sikadeer.ROBJ")
```

Table 9: Comparison of R and MCDS model fits for sikadeer data. key - key function, adj - type of adjustment term, nadj - number of adjustments, lnl_R - likelihood value for R optimiser, lnl_MCDS - likelihood value for MCDS optimiser, optimizer - the selected optimiser, p_R the estimated average probability of detection for the R optimised model, p_MCDS the estimated average probability of detection for the MCDS optimised model, Nhat_R - estimated abundance in covered region from R optimised model, Nhat_MCDS - estimated abundance in covered region from MCDS optimised model.

| key | adj | nadj | lnl_R | lnl_MCDS | optimizer | p_R | p_MCDS | Nhat_R | Nhat_MCDS |
|---|---|---:|---:|---:|---|---:|---:|---:|---:|
| unif | cos | 0 | -10178.07 | -10178.07 | mrds (nlminb) | 1.00 | 1.00 | 1921.00 | 1921.00 |
| unif | cos | 1 | -10104.93 | -10104.93 | MCDS.exe | 0.73 | 0.73 | 2638.66 | 2638.72 |
| unif | cos | 2 | -10097.06 | -10096.96 | MCDS.exe | 0.66 | 0.66 | 2892.67 | 2900.70 |
| unif | cos | 3 | -10097.06 | -10096.95 | MCDS.exe | 0.66 | 0.67 | 2893.42 | 2887.48 |
| hn | cos | 0 | -10117.72 | -10117.72 | mrds (nlminb) | 0.77 | 0.77 | 2506.17 | 2506.17 |
| hn | cos | 1 | -10104.13 | -10104.13 | MCDS.exe | 0.65 | 0.65 | 2939.25 | 2939.16 |
| hn | cos | 2 | -10101.39 | -10101.15 | MCDS.exe | 0.69 | 0.69 | 2792.91 | 2796.22 |
| hn | herm | 0 | -10117.72 | -10117.72 | mrds (nlminb) | 0.77 | 0.77 | 2506.17 | 2506.17 |
| hn | herm | 1 | -10117.29 | -10117.29 | MCDS.exe | 0.77 | 0.77 | 2509.27 | 2509.21 |
| hn | herm | 2 | -10096.92 | -10096.82 | MCDS.exe | 0.67 | 0.66 | 2887.08 | 2905.58 |
| hr | poly | 0 | -10103.46 | -10103.46 | mrds (nlminb) | 0.68 | 0.68 | 2816.55 | 2815.37 |
| hr | poly | 1 | NA | -10098.33 | MCDS.exe | NA | 0.65 | NA | 2934.68 |
| hr | poly | 2 | -10100.86 | -10098.32 | MCDS.exe | 0.62 | 0.66 | 3086.04 | 2926.67 |

### Wren 5 minute count

Note that the following model fails to fit in R and gives warnings in MCDS but does return a result with a very poor likelihood.

```
# Fitting uniform key function with cosine(1,2,3) adjustments
# ** Warning: Maximum probability of detection is greater than one: invalid model fitted **
# ** Warning: Maximum probability of detection is greater than one: invalid model fitted **
# ** Warning: Maximum probability of detection is greater than one: invalid model fitted **
# Warning in check.mono(result, n.pts = control$mono.points) :
#   Detection function is less than 0 at some distances
# Warning in check.mono(result, n.pts = control$mono.points) :
#   Detection function is less than 0 at some distances
# AIC= 7796.69
```

```
data("wren_5min")

model.compare <- test.models(wren_5min,
                             truncation = max(wren_5min$distance, na.rm = TRUE),
                             transect = "point")

save(model.compare, file = "results/wren_5min.ROBJ")
```

Table 10: Comparison of R and MCDS model fits for wren_5min data. key - key function, adj - type of adjustment term, nadj - number of adjustments, lnl_R - likelihood value for R optimiser, lnl_MCDS - likelihood value for MCDS optimiser, optimizer - the selected optimiser, p_R the estimated average probability of detection for the R optimised model, p_MCDS the estimated average probability of detection for the MCDS optimised model, Nhat_R - estimated abundance in covered region from R optimised model, Nhat_MCDS - estimated abundance in covered region from MCDS optimised model.

| key | adj | nadj | lnl_R | lnl_MCDS | optimizer | p_R | p_MCDS | Nhat_R | Nhat_MCDS |
|---|---|---|---|---|---|---|---|---|---|
| unif | cos | 0 | -664.8902 | -664.8902 | mrds (nlminb) | 1.00 | 1.00 | 134.00 | 134.00 |
| unif | cos | 1 | -601.4723 | -601.4723 | mrds (nlminb) | 0.31 | 0.31 | 435.61 | 435.61 |
| unif | cos | 2 | -601.4600 | -601.4600 | mrds (nlminb) | 0.32 | 0.32 | 424.20 | 424.12 |
| unif | cos | 3 | NA | -3895.3448 | mrds (nlminb) | NA | 0.11 | NA | 1271.25 |
| hn | cos | 0 | -604.6857 | -604.6857 | mrds (nlminb) | 0.26 | 0.26 | 524.24 | 524.22 |
| hn | cos | 1 | -600.3846 | -600.3704 | MCDS.exe | 0.31 | 0.31 | 428.89 | 428.51 |
| hn | cos | 2 | -597.6245 | -597.5602 | MCDS.exe | 0.37 | 0.38 | 360.38 | 355.28 |
| hn | herm | 0 | -604.6857 | -604.6857 | mrds (nlminb) | 0.26 | 0.26 | 524.24 | 524.22 |
| hn | herm | 1 | -600.1696 | -603.7420 | mrds (nlminb) | 0.32 | 0.27 | 418.55 | 493.43 |
| hn | herm | 2 | -600.1190 | -600.0568 | MCDS.exe | 0.32 | 0.32 | 416.87 | 413.04 |
| hr | poly | 0 | -597.2705 | -597.2705 | mrds (nlminb) | 0.39 | 0.39 | 345.72 | 345.71 |
| hr | poly | 1 | -597.2698 | -597.2698 | MCDS.exe | 0.39 | 0.39 | 346.21 | 346.18 |
| hr | poly | 2 | -596.8258 | -594.3689 | MCDS.exe | 0.39 | 0.37 | 345.46 | 361.61 |

## Wren cue counting

This one brings up the warning 'Detection function is less than 0 at some distances' for quite a few of the models. This warning occurred for the last model where there is a substantial difference in abundance estimates.

```
data("wren_cuecount")

model.compare <- test.models(wren_cuecount,
                             truncation = max(wren_cuecount$distance, na.rm = TRUE),
                             transect = "point")

save(model.compare, file = "results/wren_cuecount.ROBJ")
```

Table 11: Comparison of R and MCDS model fits for wren_cuecount data. key - key function, adj - type of adjustment term, nadj - number of adjustments, lnl_R - likelihood value for R optimiser, lnl_MCDS - likelihood value for MCDS optimiser, optimizer - the selected optimiser, p_R the estimated average probability of detection for the R optimised model, p_MCDS the estimated average probability of detection for the MCDS optimised model, Nhat_R - estimated abundance in covered region from R optimised model, Nhat_MCDS - estimated abundance in covered region from MCDS optimised model.

| key | adj | nadj | lnl_R | lnl_MCDS | optimizer | p_R | p_MCDS | Nhat_R | Nhat_MCDS |
|---|---|---|---|---|---|---|---|---|---|
| unif | cos | 0 | -4245.327 | -4245.327 | mrds (nlminb) | 1.00 | 1.00 | 774.00 | 774.00 |
| unif | cos | 1 | -3591.352 | -3591.352 | MCDS.exe | 0.30 | 0.30 | 2594.48 | 2594.48 |
| unif | cos | 2 | -3437.363 | -3424.317 | MCDS.exe | 0.17 | 0.16 | 4518.35 | 4835.56 |
| unif | cos | 3 | -3430.144 | -35113.874 | mrds (nlminb) | 0.14 | 0.82 | 5525.55 | 946.66 |
| hn | cos | 0 | -3446.447 | -3446.447 | mrds (nlminb) | 0.13 | 0.13 | 5883.48 | 5883.13 |
| hn | cos | 1 | -3415.952 | -3415.825 | MCDS.exe | 0.17 | 0.17 | 4512.30 | 4504.66 |
| hn | cos | 2 | -3410.772 | -3410.746 | MCDS.exe | 0.19 | 0.19 | 4074.65 | 4072.11 |
| hn | herm | 0 | -3446.447 | -3446.447 | mrds (nlminb) | 0.13 | 0.13 | 5883.48 | 5883.13 |
| hn | herm | 1 | -3416.716 | -3497.836 | mrds (nlminb) | 0.17 | 0.15 | 4518.43 | 5224.07 |
| hn | herm | 2 | -3416.781 | -3435.901 | mrds (nlminb) | 0.17 | 0.15 | 4507.43 | 5128.45 |
| hr | poly | 0 | -3425.337 | -3425.337 | mrds (nlminb) | 0.23 | 0.23 | 3354.83 | 3354.43 |
| hr | poly | 1 | -3423.197 | -3423.197 | MCDS.exe | 0.22 | 0.22 | 3587.06 | 3586.67 |
| hr | poly | 2 | -4500.702 | -3409.010 | MCDS.exe | 0.26 | 0.20 | 3005.98 | 3908.23 |

### Wren line transect

```r
data("wren_lt")

model.compare <- test.models(wren_lt,
                             truncation = max(wren_lt$distance, na.rm = TRUE),
                             transect = "line")

save(model.compare, file = "results/wren_lt.ROBJ")
```

Table 12: Comparison of R and MCDS model fits for wren_lt data. key - key function, adj - type of adjustment term, nadj - number of adjustments, lnl_R - likelihood value for R optimiser, lnl_MCDS - likelihood value for MCDS optimiser, optimizer - the selected optimiser, p_R the estimated average probability of detection for the R optimised model, p_MCDS the estimated average probability of detection for the MCDS optimised model, Nhat_R - estimated abundance in covered region from R optimised model, Nhat_MCDS - estimated abundance in covered region from MCDS optimised model.

| key | adj | nadj | lnl_R | lnl_MCDS | optimizer | p_R | p_MCDS | Nhat_R | Nhat_MCDS |
|---|---|---|---|---|---|---|---|---|---|
| unif | cos | 0 | -718.4065 | -718.4065 | mrds (nlminb) | 1.00 | 1.00 | 156.00 | 156.00 |
| unif | cos | 1 | -709.8168 | -709.8168 | mrds (nlminb) | 0.66 | 0.66 | 235.41 | 235.41 |
| unif | cos | 2 | -706.9010 | -706.8959 | MCDS.exe | 0.71 | 0.71 | 218.95 | 218.90 |
| unif | cos | 3 | -705.2165 | -705.2152 | MCDS.exe | 0.76 | 0.76 | 206.18 | 205.97 |
| hn | cos | 0 | -708.0940 | -708.0940 | mrds (nlminb) | 0.69 | 0.69 | 227.72 | 227.73 |
| hn | cos | 1 | -706.8055 | -706.8016 | MCDS.exe | 0.72 | 0.72 | 216.36 | 216.31 |
| hn | cos | 2 | -705.8964 | -705.8591 | MCDS.exe | 0.76 | 0.76 | 206.22 | 205.41 |
| hn | herm | 0 | -708.0940 | -708.0940 | mrds (nlminb) | 0.69 | 0.69 | 227.72 | 227.73 |
| hn | herm | 1 | -706.1314 | -706.1162 | MCDS.exe | 0.73 | 0.73 | 213.46 | 212.84 |
| hn | herm | 2 | -706.0683 | -705.5404 | MCDS.exe | 0.73 | 0.74 | 212.74 | 210.18 |
| hr | poly | 0 | -704.0664 | -704.0674 | mrds (nlminb) | 0.84 | 0.84 | 184.83 | 184.65 |
| hr | poly | 1 | -703.7942 | -703.7942 | mrds (nlminb) | 0.81 | 0.81 | 191.89 | 191.89 |
| hr | poly | 2 | -703.5428 | -702.9242 | MCDS.exe | 0.81 | 0.75 | 193.26 | 208.62 |

## Wren snapshot

The below analysis is problematic in R but works in MCDS

```
data("wren_snapshot")
fit.test <- ds(wren_snapshot,
               key = "hn",
               adjustment = "herm",
               nadj = 1,
               truncation = max(wren_snapshot$distance, na.rm = TRUE),
               transect = "point",
               optimizer = "R")
```

```
## Fitting half-normal key function with Hermite(4) adjustments
```

```
## Warning in check.mono(result, n.pts = control$mono.points): Detection function
## is less than 0 at some distances
```

```
## AIC= 2e+24
```

```
## Warning in mrds::check.mono(model, n.pts = 20): Detection function is less than
## 0 at some distances
```

```
## Some variance-covariance matrix elements were NA, possible numerical problems; only estimating detect
```

```
data("wren_snapshot")

model.compare <- test.models(wren_snapshot,
                             truncation = max(wren_snapshot$distance, na.rm = TRUE),
                             transect = "point")

save(model.compare, file = "results/wren_snapshot.ROBJ")
```

Table 13: Comparison of R and MCDS model fits for wren_snapshot data. key - key function, adj - type of adjustment term, nadj - number of adjustments, lnl_R - likelihood value for R optimiser, lnl_MCDS - likelihood value for MCDS optimiser, optimizer - the selected optimiser, p_R the estimated average probability of detection for the R optimised model, p_MCDS the estimated average probability of detection for the MCDS optimised model, Nhat_R - estimated abundance in covered region from R optimised model, Nhat_MCDS - estimated abundance in covered region from MCDS optimised model.

| key | adj | nadj | lnl_R | lnl_MCDS | optimizer | p_R | p_MCDS | Nhat_R | Nhat_MCDS |
|---|---|---:|---:|---:|---|---:|---:|---:|---:|
| unif | cos | 0 | -5.806245e+02 | -580.6245 | mrds (nlminb) | 1.00 | 1.00 | 118.00 | 118.00 |
| unif | cos | 1 | -5.314629e+02 | -531.4629 | mrds (nlminb) | 0.31 | 0.31 | 381.80 | 381.80 |
| unif | cos | 2 | -5.309127e+02 | -530.9127 | mrds (nlminb) | 0.38 | 0.38 | 310.14 | 310.10 |
| unif | cos | 3 | -5.295474e+02 | -529.5405 | MCDS.exe | 0.36 | 0.36 | 332.07 | 331.91 |
| hn | cos | 0 | -5.339206e+02 | -533.9206 | mrds (nlminb) | 0.28 | 0.28 | 427.98 | 427.97 |
| hn | cos | 1 | -5.304114e+02 | -530.4001 | MCDS.exe | 0.33 | 0.33 | 353.86 | 353.57 |
| hn | cos | 2 | -5.285742e+02 | -528.5358 | MCDS.exe | 0.39 | 0.40 | 299.20 | 296.36 |
| hn | herm | 0 | -5.339206e+02 | -533.9206 | mrds (nlminb) | 0.28 | 0.28 | 427.98 | 427.97 |
| hn | herm | 1 | -1.000000e+24 | -532.7566 | MCDS.exe | 0.00 | 0.30 | 56967.30 | 393.40 |
| hn | herm | 2 | -5.301192e+02 | -531.6170 | mrds (nlminb) | 0.34 | 0.32 | 343.63 | 372.80 |
| hr | poly | 0 | -5.269604e+02 | -526.9604 | mrds (nlminb) | 0.40 | 0.40 | 295.58 | 295.58 |
| hr | poly | 1 | -5.269605e+02 | -526.9634 | mrds (nlminb) | 0.40 | 0.40 | 295.58 | 295.63 |
| hr | poly | 2 | -5.276001e+02 | -526.9494 | MCDS.exe | 0.39 | 0.40 | 298.95 | 295.19 |

## dathr1

Some estimates of abundance differ significantly!

```
load(file = "data/dathr1.RData")

model.compare <- test.models(dat,
                             truncation = 30,
                             transect = "point")

save(model.compare, file = "results/dathr1.ROBJ")
```

Table 14: Comparison of R and MCDS model fits for dathr1 data. key - key function, adj - type of adjustment term, nadj - number of adjustments, lnl_R - likelihood value for R optimiser, lnl_MCDS - likelihood value for MCDS optimiser, optimizer - the selected optimiser, p_R the estimated average probability of detection for the R optimised model, p_MCDS the estimated average probability of detection for the MCDS optimised model, Nhat_R - estimated abundance in covered region from R optimised model, Nhat_MCDS - estimated abundance in covered region from MCDS optimised model.

| key | adj | nadj | lnl_R | lnl_MCDS | optimizer | p_R | p_MCDS | Nhat_R | Nhat_MCDS |
|---|---|---:|---:|---:|---|---:|---:|---:|---:|
| unif | cos | 0 | -216.7738 | -216.7738 | mrds (nlminb) | 1.00 | 1.00 | 60.00 | 60.00 |
| unif | cos | 1 | -198.2567 | -198.2567 | mrds (nlminb) | 0.35 | 0.35 | 170.38 | 170.38 |
| unif | cos | 2 | -197.7078 | -197.7078 | mrds (nlminb) | 0.28 | 0.28 | 212.21 | 212.19 |
| unif | cos | 3 | -197.6642 | -197.6642 | mrds (nlminb) | 0.30 | 0.30 | 198.64 | 198.65 |
| hn | cos | 0 | -198.1089 | -198.1089 | mrds (nlminb) | 0.31 | 0.31 | 190.77 | 190.76 |
| hn | cos | 1 | -197.9999 | -197.9999 | mrds (nlminb) | 0.28 | 0.28 | 215.86 | 215.80 |
| hn | cos | 2 | -197.9895 | -197.9895 | mrds (nlminb) | 0.27 | 0.27 | 225.83 | 225.75 |
| hn | herm | 0 | -198.1089 | -198.1089 | mrds (nlminb) | 0.31 | 0.31 | 190.77 | 190.76 |
| hn | herm | 1 | -198.1012 | -198.1012 | mrds (nlminb) | 0.31 | 0.31 | 191.06 | 191.06 |
| hn | herm | 2 | -197.6630 | -197.6522 | MCDS.exe | 0.29 | 0.29 | 208.07 | 206.06 |
| hr | poly | 0 | -198.5277 | -198.5277 | mrds (nlminb) | 0.41 | 0.41 | 146.99 | 146.98 |
| hr | poly | 1 | -197.8696 | -198.5283 | mrds (nlminb) | 0.26 | 0.41 | 234.37 | 147.03 |
| hr | poly | 2 | -198.2563 | -195.0557 | MCDS.exe | 0.42 | 0.19 | 142.31 | 323.83 |

### dathr2

Best AIC is a slightly concerning model which gives a very different Nhat estimate.

```
load(file = "data/dathr2.RData")
fit <- ds(dat,
          truncation = 30,
          transect = "point",
          key = "hr",
          adjustment = "poly",
          nadj = 2)
```

```
## Fitting hazard-rate key function with simple polynomial(4,6) adjustments
```

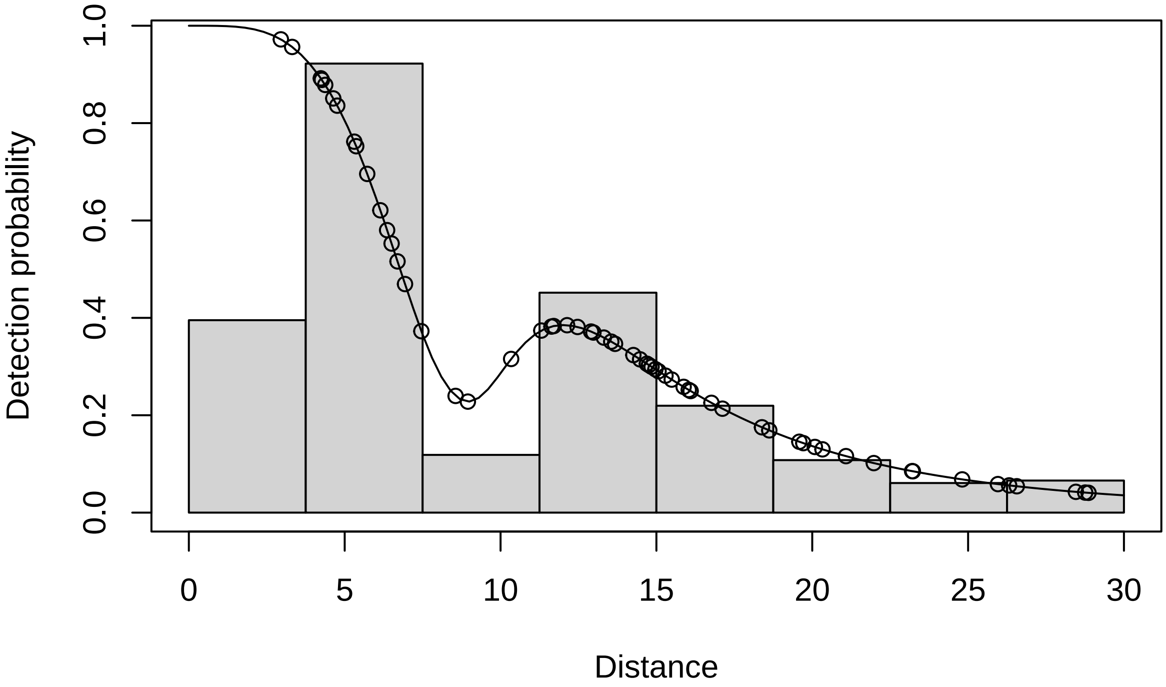
```
## Warning in check.mono(result, n.pts = control$mono.points): Detection function
## is not strictly monotonic!

## Warning in check.mono(result, n.pts = control$mono.points): Detection function
## is not strictly monotonic!
```

```
## AIC= 398.111
```

```
## Warning in mrds::check.mono(model, n.pts = 20): Detection function is not
## strictly monotonic!
```

```
## No survey area information supplied, only estimating detection function.
```

```
plot(fit)
```



```
load(file = "data/dathr2.RData")

model.compare <- test.models(dat,
                             truncation = 30,
                             transect = "point")

save(model.compare, file = "results/dathr2.ROBJ")
```

Table 15: Comparison of R and MCDS model fits for dathr2 data. key - key function, adj - type of adjustment term, nadj - number of adjustments, lnl_R - likelihood value for R optimiser, lnl_MCDS - likelihood value for MCDS optimiser, optimizer - the selected optimiser, p_R the estimated average probability of detection for the R optimised model, p_MCDS the estimated average probability of detection for the MCDS optimised model, Nhat_R - estimated abundance in covered region from R optimised model, Nhat_MCDS - estimated abundance in covered region from MCDS optimised model.

| key | adj | nadj | lnl_R | lnl_MCDS | optimizer | p_R | p_MCDS | Nhat_R | Nhat_MCDS |
|---|---|---:|---:|---:|---|---:|---:|---:|---:|
| unif | cos | 0 | -216.7738 | -216.7738 | mrds (nlminb) | 1.00 | 1.00 | 60.00 | 60.00 |
| unif | cos | 1 | -198.2567 | -198.2567 | mrds (nlminb) | 0.35 | 0.35 | 170.38 | 170.38 |
| unif | cos | 2 | -197.7078 | -197.7078 | mrds (nlminb) | 0.28 | 0.28 | 212.21 | 212.19 |
| unif | cos | 3 | -197.6642 | -197.6642 | MCDS.exe | 0.30 | 0.30 | 198.68 | 198.65 |
| hn | cos | 0 | -198.1089 | -198.1089 | mrds (nlminb) | 0.31 | 0.31 | 190.77 | 190.76 |
| hn | cos | 1 | -197.9999 | -197.9999 | mrds (nlminb) | 0.28 | 0.28 | 215.86 | 215.80 |
| hn | cos | 2 | -197.9895 | -197.9895 | mrds (nlminb) | 0.27 | 0.27 | 225.83 | 225.75 |
| hn | herm | 0 | -198.1089 | -198.1089 | mrds (nlminb) | 0.31 | 0.31 | 190.77 | 190.76 |
| hn | herm | 1 | -198.1012 | -198.1012 | mrds (nlminb) | 0.31 | 0.31 | 191.06 | 191.06 |
| hn | herm | 2 | -197.6630 | -197.6522 | MCDS.exe | 0.29 | 0.29 | 208.07 | 206.06 |
| hr | poly | 0 | -198.5277 | -198.5277 | mrds (nlminb) | 0.41 | 0.41 | 146.99 | 146.98 |
| hr | poly | 1 | -197.8696 | -198.5283 | mrds (nlminb) | 0.26 | 0.41 | 234.37 | 147.03 |
| hr | poly | 2 | -198.2563 | -195.0557 | MCDS.exe | 0.42 | 0.19 | 142.31 | 323.83 |

## dathr3

Some errors / warnings:

```
load(file = "data/dathr3.RData")

model.compare <- test.models(dat,
                             truncation = 30,
                             transect = "point")

save(model.compare, file = "results/dathr3.ROBJ")
```

Table 16: Comparison of R and MCDS model fits for dathr3 data. key - key function, adj - type of adjustment term, nadj - number of adjustments, lnl_R - likelihood value for R optimiser, lnl_MCDS - likelihood value for MCDS optimiser, optimizer - the selected optimiser, p_R the estimated average probability of detection for the R optimised model, p_MCDS the estimated average probability of detection for the MCDS optimised model, Nhat_R - estimated abundance in covered region from R optimised model, Nhat_MCDS - estimated abundance in covered region from MCDS optimised model.

| key | adj | nadj | lnl_R | lnl_MCDS | optimizer | p_R | p_MCDS | Nhat_R | Nhat_MCDS |
|---|---|---|---|---|---|---|---|---|---|
| unif | cos | 0 | -217.4289 | -217.4289 | mrds (nlminb) | 1.00 | 1.00 | 60.00 | 60.00 |
| unif | cos | 1 | -198.8233 | -198.8233 | mrds (nlminb) | 0.35 | 0.35 | 169.81 | 169.80 |
| unif | cos | 2 | -197.8924 | -197.8919 | MCDS.exe | 0.27 | 0.27 | 220.49 | 221.81 |
| unif | cos | 3 | -197.7923 | -197.7923 | mrds (nlminb) | 0.24 | 0.24 | 246.02 | 245.98 |
| hn | cos | 0 | -198.4751 | -198.4751 | mrds (nlminb) | 0.31 | 0.31 | 192.29 | 192.29 |
| hn | cos | 1 | -197.8558 | -197.8558 | mrds (nlminb) | 0.23 | 0.23 | 258.19 | 258.15 |
| hn | cos | 2 | -197.8472 | -197.8472 | mrds (nlminb) | 0.24 | 0.24 | 249.59 | 249.52 |
| hn | herm | 0 | -198.4751 | -198.4751 | mrds (nlminb) | 0.31 | 0.31 | 192.29 | 192.29 |
| hn | herm | 1 | -198.4644 | -198.4644 | mrds (nlminb) | 0.31 | 0.31 | 192.59 | 192.58 |
| hn | herm | 2 | -197.7853 | NA | mrds (nlminb) | 0.25 | NA | 244.31 | NA |
| hr | poly | 0 | -197.6157 | -197.6157 | mrds (nlminb) | 0.26 | 0.26 | 232.46 | 232.43 |
| hr | poly | 1 | -197.5302 | -197.5302 | mrds (nlminb) | 0.25 | 0.25 | 235.85 | 235.81 |
| hr | poly | 2 | -197.5311 | -197.5301 | MCDS.exe | 0.25 | 0.25 | 235.89 | 235.78 |

## dathr4

```
load(file = "data/dathr4.RData")

model.compare <- test.models(dat,
                             truncation = 30,
                             transect = "point")

save(model.compare, file = "results/dathr4.ROBJ")
```

Table 17: Comparison of R and MCDS model fits for dathr4 data. key - key function, adj - type of adjustment term, nadj - number of adjustments, lnl_R - likelihood value for R optimiser, lnl_MCDS - likelihood value for MCDS optimiser, optimizer - the selected optimiser, p_R the estimated average probability of detection for the R optimised model, p_MCDS the estimated average probability of detection for the MCDS optimised model, Nhat_R - estimated abundance in covered region from R optimised model, Nhat_MCDS - estimated abundance in covered region from MCDS optimised model.

| key | adj | nadj | lnl_R | lnl_MCDS | optimizer | p_R | p_MCDS | Nhat_R | Nhat_MCDS |
|---|---|---:|---:|---:|---|---:|---:|---:|---:|
| unif | cos | 0 | -216.9210 | -216.9210 | mrds (nlminb) | 1.00 | 1.00 | 60.00 | 60.00 |
| unif | cos | 1 | -195.3522 | -195.3522 | mrds (nlminb) | 0.32 | 0.32 | 185.55 | 185.55 |
| unif | cos | 2 | -195.3505 | -195.3505 | MCDS.exe | 0.32 | 0.32 | 187.80 | 187.80 |
| unif | cos | 3 | -195.1100 | -195.1100 | mrds (nlminb) | 0.27 | 0.27 | 221.78 | 221.63 |
| hn | cos | 0 | -195.4085 | -195.4085 | mrds (nlminb) | 0.29 | 0.29 | 205.79 | 205.79 |
| hn | cos | 1 | -195.4086 | -195.4083 | MCDS.exe | 0.29 | 0.29 | 208.55 | 206.82 |
| hn | cos | 2 | -195.2546 | -195.2546 | mrds (nlminb) | 0.25 | 0.25 | 242.96 | 242.89 |
| hn | herm | 0 | -195.4085 | -195.4085 | mrds (nlminb) | 0.29 | 0.29 | 205.79 | 205.79 |
| hn | herm | 1 | -195.3781 | -195.3252 | MCDS.exe | 0.30 | 0.31 | 196.85 | 194.22 |
| hn | herm | 2 | -195.3267 | -195.3251 | MCDS.exe | 0.31 | 0.31 | 193.86 | 194.25 |
| hr | poly | 0 | -196.2594 | -196.2594 | mrds (nlminb) | 0.41 | 0.41 | 146.31 | 146.28 |
| hr | poly | 1 | -195.3085 | -195.3085 | MCDS.exe | 0.29 | 0.29 | 209.31 | 209.39 |
| hr | poly | 2 | -195.2953 | -195.0819 | MCDS.exe | 0.29 | 0.29 | 209.42 | 207.56 |

### rocio_dat

```
load(file = "data/rocio_dat.RData")

model.compare <- test.models(dat,
                             truncation = 30,
                             transect = "point")

save(model.compare, file = "results/rocio_dat.ROBJ")
```

Table 18: Comparison of R and MCDS model fits for rocio_dat data. key - key function, adj - type of adjustment term, nadj - number of adjustments, lnl_R - likelihood value for R optimiser, lnl_MCDS - likelihood value for MCDS optimiser, optimizer - the selected optimiser, p_R the estimated average probability of detection for the R optimised model, p_MCDS the estimated average probability of detection for the MCDS optimised model, Nhat_R - estimated abundance in covered region from R optimised model, Nhat_MCDS - estimated abundance in covered region from MCDS optimised model.

| key | adj | nadj | lnl_R | lnl_MCDS | optimizer | p_R | p_MCDS | Nhat_R | Nhat_MCDS |
|---|---|---|---|---|---|---|---|---|---|
| unif | cos | 0 | -1800.225 | -1800.225 | mrds (nlminb) | 1.00 | 1.00 | 500.00 | 500.00 |
| unif | cos | 1 | -1692.738 | -1692.738 | mrds (nlminb) | 0.40 | 0.40 | 1250.09 | 1250.06 |
| unif | cos | 2 | -1677.557 | -1677.350 | MCDS.exe | 0.29 | 0.28 | 1754.32 | 1775.85 |
| unif | cos | 3 | -1676.162 | -1675.853 | MCDS.exe | 0.26 | 0.24 | 1940.48 | 2069.18 |
| hn | cos | 0 | -1695.395 | -1695.395 | mrds (nlminb) | 0.38 | 0.38 | 1318.76 | 1318.69 |
| hn | cos | 1 | -1679.401 | -1679.401 | MCDS.exe | 0.23 | 0.23 | 2196.20 | 2196.70 |
| hn | cos | 2 | -1678.248 | -1678.248 | MCDS.exe | 0.25 | 0.25 | 1964.17 | 1963.41 |
| hn | herm | 0 | -1695.395 | -1695.395 | mrds (nlminb) | 0.38 | 0.38 | 1318.76 | 1318.69 |
| hn | herm | 1 | -1695.216 | -1695.216 | mrds (nlminb) | 0.38 | 0.38 | 1321.14 | 1321.11 |
| hn | herm | 2 | -1676.157 | -1676.157 | mrds (nlminb) | 0.25 | 0.25 | 2014.21 | 2013.56 |
| hr | poly | 0 | -1676.297 | -1676.297 | mrds (nlminb) | 0.24 | 0.24 | 2091.89 | 2091.17 |
| hr | poly | 1 | -1676.302 | -1676.386 | mrds (nlminb) | 0.24 | 0.24 | 2116.31 | 2096.87 |
| hr | poly | 2 | -1675.256 | -1675.234 | MCDS.exe | 0.25 | 0.25 | 1973.53 | 1984.58 |

### rocio_dat2

```
load(file = "data/rocio_dat_2.RData")

model.compare <- test.models(dat,
                             truncation = 30,
                             transect = "point")

save(model.compare, file = "results/rocio_dat2.ROBJ")
```

Table 19: Comparison of R and MCDS model fits for rocio_dat2 data. key - key function, adj - type of adjustment term, nadj - number of adjustments, lnl_R - likelihood value for R optimiser, lnl_MCDS - likelihood value for MCDS optimiser, optimizer - the selected optimiser, p_R the estimated average probability of detection for the R optimised model, p_MCDS the estimated average probability of detection for the MCDS optimised model, Nhat_R - estimated abundance in covered region from R optimised model, Nhat_MCDS - estimated abundance in covered region from MCDS optimised model.

| key | adj | nadj | lnl_R | lnl_MCDS | optimizer | p_R | p_MCDS | Nhat_R | Nhat_MCDS |
|---|---|---:|---:|---:|---|---:|---:|---:|---:|
| unif | cos | 0 | -153.3827 | -153.3827 | mrds (nlminb) | 1.00 | 1.00 | 42.00 | 42.00 |
| unif | cos | 1 | -126.2630 | -126.2630 | MCDS.exe | 0.30 | 0.30 | 141.24 | 141.24 |
| unif | cos | 2 | -126.2630 | -120.3592 | MCDS.exe | 0.30 | 0.29 | 141.24 | 142.45 |
| unif | cos | 3 | -124.7425 | -118.4524 | MCDS.exe | 0.32 | 0.32 | 129.62 | 131.65 |
| hn | cos | 0 | -127.7456 | -127.7456 | mrds (nlminb) | 0.21 | 0.21 | 201.75 | 201.74 |
| hn | cos | 1 | -125.6836 | -125.6764 | MCDS.exe | 0.26 | 0.26 | 162.02 | 161.83 |
| hn | cos | 2 | -122.3967 | -122.0822 | MCDS.exe | 0.30 | 0.23 | 138.45 | 180.95 |
| hn | herm | 0 | -127.7456 | -127.7456 | mrds (nlminb) | 0.21 | 0.21 | 201.75 | 201.74 |
| hn | herm | 1 | -125.4281 | -121.2811 | MCDS.exe | 0.26 | 0.27 | 159.26 | 157.90 |
| hn | herm | 2 | -125.3682 | -121.1492 | MCDS.exe | 0.26 | 0.25 | 158.70 | 166.01 |
| hr | poly | 0 | -118.4312 | -119.2224 | mrds (nlminb) | 0.42 | 0.40 | 101.04 | 105.12 |
| hr | poly | 1 | -118.3055 | -118.9848 | mrds (nlminb) | 0.40 | 0.34 | 106.18 | 122.04 |
| hr | poly | 2 | -118.2833 | -118.5401 | mrds (nlminb) | 0.39 | 0.36 | 108.42 | 117.62 |

### amakihi

There is a very big difference in estimated abundance for the first model here!

```
data("amakihi")

model.compare <- test.cov.models(amakihi,
                             truncation = 82.5,
                             transect = "point",
                             models = list(~as.factor(OBs)+HAS+MAS,
                                           ~as.factor(OBs)+MAS,
                                           ~as.factor(OBs)+HAS))

save(model.compare, file = "results/amakihi.ROBJ")
```

Table 20: Comparison of R and MCDS model fits for amakihi data. key - key function, adj - type of adjustment term, nadj - number of adjustments, lnl_R - likelihood value for R optimiser, lnl_MCDS - likelihood value for MCDS optimiser, optimizer - the selected optimiser, p_R the estimated average probability of detection for the R optimised model, p_MCDS the estimated average probability of detection for the MCDS optimised model, Nhat_R - estimated abundance in covered region from R optimised model, Nhat_MCDS - estimated abundance in covered region from MCDS optimised model.

| models | lnl_R | lnl_MCDS | optimizer | p_R | p_MCDS | Nhat_R | Nhat_MCDS |
|---|---|---|---|---|---|---|---|
| ~as.factor(OBs) + HAS + MAS | -5396.835 | -5396.836 | mrds (nlminb) | 0.34 | 0.34 | 3629.41 | 3629.99 |
| ~as.factor(OBs) + MAS | -5397.937 | -5397.937 | mrds (nlminb) | 0.34 | 0.34 | 3624.30 | 3624.94 |
| ~as.factor(OBs) + HAS | -5397.039 | -5397.039 | mrds (nlminb) | 0.34 | 0.34 | 3628.48 | 3629.01 |

## akepa data

```r
load(file = "data/akepa.RData")

model.compare <- test.cov.models(dat,
                                 truncation = 58,
                                 transect = "line",
                                 models = list(~as.factor(Obs)))

save(model.compare, file = "results/akepa.ROBJ")
```

Table 21: Comparison of R and MCDS model fits for akepa data. key - key function, adj - type of adjustment term, nadj - number of adjustments, lnl_R - likelihood value for R optimiser, lnl_MCDS - likelihood value for MCDS optimiser, optimizer - the selected optimiser, p_R the estimated average probability of detection for the R optimised model, p_MCDS the estimated average probability of detection for the MCDS optimised model, Nhat_R - estimated abundance in covered region from R optimised model, Nhat_MCDS - estimated abundance in covered region from MCDS optimised model.

| models | lnl_R | lnl_MCDS | optimizer | p_R | p_MCDS | Nhat_R | Nhat_MCDS |
|---|---:|---:|---|---:|---:|---:|---:|
| ~as.factor(Obs) | -373.0925 | -373.0925 | mrds (nlminb) | 0.72 | 0.72 | 128.84 | 128.86 |

## ETP Dolphins

Some errors / warnings:

```
data("ETP_Dolphin")

model.compare <- test.cov.models(ETP_Dolphin,
                             truncation = max(ETP_Dolphin$distance, na.rm = TRUE),
                             transect = "line",
                             models = list(~size, ~size+Beauf.class, ~LnCluster))

save(model.compare, file = "results/ETP_Dolphin.ROBJ")
```

Table 22: Comparison of R and MCDS model fits for ETP dolphin data. key - key function, adj - type of adjustment term, nadj - number of adjustments, lnl_R - likelihood value for R optimiser, lnl_MCDS - likelihood value for MCDS optimiser, optimizer - the selected optimiser, p_R the estimated average probability of detection for the R optimised model, p_MCDS the estimated average probability of detection for the MCDS optimised model, Nhat_R - estimated abundance in covered region from R optimised model, Nhat_MCDS - estimated abundance in covered region from MCDS optimised model.

| models | lnl_R | lnl_MCDS | optimizer | p_R | p_MCDS | Nhat_R | Nhat_MCDS |
|---|---:|---:|---|---:|---:|---:|---:|
| ~size | -1682.444 | -1682.445 | mrds (nlminb) | 0.71 | 0.71 | 1544.89 | 1545.41 |
| ~size + Beauf.class | NA | -1682.372 | MCDS.exe | NA | 0.70 | NA | 1546.83 |
| ~LnCluster | -1679.498 | -1679.502 | mrds (nlminb) | 0.69 | 0.69 | 1582.67 | 1585.12 |

## Minke data

```r
data("minke")

model.compare <- test.cov.models(minke,
                                 truncation = max(minke$distance, na.rm = TRUE),
                                 transect = "line",
                                 models = list(~as.factor(Region.Label)))

save(model.compare, file = "results/minke.ROBJ")
```

Table 23: Comparison of R and MCDS model fits for minke data. key - key function, adj - type of adjustment term, nadj - number of adjustments, lnl_R - likelihood value for R optimiser, lnl_MCDS - likelihood value for MCDS optimiser, optimizer - the selected optimiser, p_R the estimated average probability of detection for the R optimised model, p_MCDS the estimated average probability of detection for the MCDS optimised model, Nhat_R - estimated abundance in covered region from R optimised model, Nhat_MCDS - estimated abundance in covered region from MCDS optimised model.

| models | lnl_R | lnl_MCDS | optimizer | p_R | p_MCDS | Nhat_R | Nhat_MCDS |
|---|---:|---:|---|---:|---:|---:|---:|
| ~as.factor(Region.Label) | -26.50247 | -26.50247 | mrds (nlminb) | 0.42 | 0.42 | 212.06 | 212.05 |

## Cluster Exercise

```r
data("ClusterExercise")

model.compare <- test.cov.models(ClusterExercise,
                                 truncation = max(ClusterExercise$distance, na.rm = TRUE),
                                 cutpoints =c(0,0.214285714285714,0.428571428571429,
                                            0.642857142857143,0.857142857142857,
                                            1.07142857142857,1.28571428571429,1.5),
                                 transect = "line",
                                 models = list(~size, ~Cluster.strat))

save(model.compare, file = "results/ClusterExercise.ROBJ")
```

Table 24: Comparison of R and MCDS model fits for ClusterExercise data. key - key function, adj - type of adjustment term, nadj - number of adjustments, lnl_R - likelihood value for R optimiser, lnl_MCDS - likelihood value for MCDS optimiser, optimizer - the selected optimiser, p_R the estimated average probability of detection for the R optimised model, p_MCDS the estimated average probability of detection for the MCDS optimised model, Nhat_R - estimated abundance in covered region from R optimised model, Nhat_MCDS - estimated abundance in covered region from MCDS optimised model.

| models | lnl_R | lnl_MCDS | optimizer | p_R | p_MCDS | Nhat_R | Nhat_MCDS |
|---|---:|---:|---|---:|---:|---:|---:|
| ~size | -157.4264 | -158.1138 | mrds (nlminb) | 0.40 | 0.43 | 218.35 | 202.58 |
| ~Cluster.strat | -158.2488 | -158.9500 | mrds (nlminb) | 0.41 | 0.44 | 216.43 | 199.34 |