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:

- Issue 83 in mrds relating to factor ordering differences between mrds and MCDS (https://github.com/DistanceDevelopment/mrds/issues/83)
- 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?
- Check the passing of parameter starting values to MCDS - also potential issues here regarding factor ordering!
- Check the passing of parameter bound to MCDS - again potential for factor ordering issues. Note this can only be done via mrds NOT via Distance.

Capercaillie Data

Things that might want further investigation:

- When the R optimiser is selected both the lnl_R and lnl_MCDS values appear to be the same in all cases. (After moving on to other datasets this is not found to be the case.)

```
data("capercaillie")

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	NA	NA	NA	NA	NA	NA	NA
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	-477.0722	-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	-477.2162	MCDS.exe	0.67	0.67	166.04	166.14
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	159.46	159.46
hr	poly	2	-476.8707	-476.7331	MCDS.exe	0.71	0.68	157.87	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?

```
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	MCDS.exe	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	145.04	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	145.93	145.92
hr	poly	2	2.130225	4.051256	mrds (nlminb)	0.18	0.29	224.87	138.47

Ducknest Data

Things that might want further investigation:

- Unhelpful error "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"
- What should happen when you have a uniform with no adjustments??? Shouldn't P always be 1?
- p_MCDS is 1 for a few of these models and when it is, it is estimating Nhat much lower than the R optimiser.

```
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	599.63	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	NA	NA	0.86	NA	619.53	NA
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	600.58	600.89
hr	poly	2	-462.4983	-462.1233	MCDS.exe	0.90	0.89	592.86	600.37

DuikerCameraTraps

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

```
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	17293.60	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	NA	mrds (nlminb)	0.34	NA	17224.44	NA
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	14854.70	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	-324.0536	-315.8040	MCDS.exe	0.44	0.37	236.60	280.68
unif	cos	3	-315.5100	-315.3818	MCDS.exe	0.34	0.35	306.92	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	311.17	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	250.32	NA
hr	poly	2	-317.1747	-316.4437	MCDS.exe	0.42	0.39	251.53	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	-467.8913	-457.0976	MCDS.exe	0.32	0.19	446.73	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	-458.1112	MCDS.exe	0.19	0.19	753.01	750.65
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	557.16	557.16
hr	poly	2	-457.5940	-456.5765	MCDS.exe	0.24	0.22	610.22	643.09

Savannah Sparrow 1980

Everything looks to run fine.

```
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	-1152.923	-1103.041	MCDS.exe	0.11	0.16	2466.07	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	1734.66	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	MCDS.exe	0.19	0.19	1479.64	1479.61
hr	poly	2	-1109.428	-1102.601	MCDS.exe	0.19	0.15	1481.09	1843.54

Savannah Sparrow 1981

Everything looks to run fine.

```
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	-808.6186	-1146.4401	mrds (nlminb)	0.32	0.18	582.59	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	-787.7283	-787.5409	MCDS.exe	0.19	0.19	960.24	981.53

Sika Deer

Everything looks to run fine.

```
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	2893.49	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	2887.09	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	NA	-10098.32	MCDS.exe	NA	0.66	NA	2926.67

Wren 5 minute count

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

```
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	-598.5015	-3895.3448	mrds (nlminb)	0.32	0.11	415.71	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	-600.1204	-600.0568	MCDS.exe	0.32	0.32	418.34	413.04
hr	poly	0	-597.2705	-597.2705	mrds (nlminb)	0.39	0.39	345.72	345.71
hr	poly	1	-597.2701	-597.2698	MCDS.exe	0.39	0.39	346.01	346.18
hr	poly	2	NA	-594.3689	MCDS.exe	NA	0.37	NA	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 occured 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	-3437.359	-3424.317	MCDS.exe	0.17	0.16	4518.45	4835.56
unif	cos	3	NA	-35113.874	mrds (nlminb)	NA	0.82	NA	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	4074.67	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	mrds (nlminb)	0.22	0.22	3587.04	3586.67
hr	poly	2	-3414.050	-3409.010	MCDS.exe	0.20	0.20	3820.11	3908.23

Wren line transect

Some errors:

```
# Fitting half-normal key function with Hermite(4,6) adjustments
# AIC= 1417.081
# 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
# Fitting half-normal key function with Hermite(4,6) adjustments
# AIC= 1417.081
# 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("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	-706.9012	-706.8959	MCDS.exe	0.71	0.71	218.96	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	-706.0681	NA	NA	0.73	NA	212.99	NA
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	193.25	208.62

Wren snapshot

Some errors / warnings:

```
# 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
# ...
# Fitting half-normal key function with Hermite(4,6) adjustments
# AIC= 1069.234
# 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("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	332.08	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	53499.62	393.40
hn	herm	2	-5.301191e+02	NA	mrds (nlminb)	0.34	NA	343.11	NA
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	295.63	295.63
hr	poly	2	NA	-526.9494	MCDS.exe	NA	0.40	NA	295.19

dathr1

```
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	198.68	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	-197.6629	-197.6522	MCDS.exe	0.29	0.29	208.12	206.06
hr	poly	0	-198.5277	-198.5277	mrds (nlminb)	0.41	0.41	146.99	146.98
hr	poly	1	-198.5277	-198.5283	mrds (nlminb)	0.41	0.41	146.99	147.03
hr	poly	2	-198.2563	-195.0557	MCDS.exe	0.42	0.19	142.31	323.83

dathr2

```
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	mrds (nlminb)	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	-197.6629	-197.6522	MCDS.exe	0.29	0.29	208.12	206.06
hr	poly	0	-198.5277	-198.5277	mrds (nlminb)	0.41	0.41	146.99	146.98
hr	poly	1	-198.5277	-198.5283	mrds (nlminb)	0.41	0.41	146.99	147.03
hr	poly	2	-198.2563	-195.0557	MCDS.exe	0.42	0.19	142.31	323.83

dathr3

Some errors / warnings:

```
# Fitting half-normal key function with Hermite(4,6) adjustments
# Error in -lt$value : invalid argument to unary operator
# In addition: Warning message:
# In system(paste0(path.to.MCDS.dot.exe, " 0, ", test.file$command.file.name),  :
#   running command 'C:/Users/lhm/AppData/Local/R/win-library/4.2/mrds/MCDS.exe 0, C:\Users\lhm\AppData
# Error in if (lt$message == "FALSE CONVERGENCE") { :
#   argument is of length zero
#
#
# All models failed to fit!
#
# Error in ds(dist.data, truncation = truncation, transect = transect, formula = ~1,  :
#   No models could be fitted.
# Fitting half-normal key function with Hermite(4,6) adjustments
# Error in -lt$value : invalid argument to unary operator
# In addition: Warning message:
# In system(paste0(path.to.MCDS.dot.exe, " 0, ", test.file$command.file.name),  :
#   running command 'C:/Users/lhm/AppData/Local/R/win-library/4.2/mrds/MCDS.exe 0, C:\Users\lhm\AppData
```

```
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	MCDS.exe	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	MCDS.exe	0.25	0.25	235.66	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	MCDS.exe	0.27	0.27	221.64	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	209.39	209.39
hr	poly	2	-195.0819	-195.0819	mrds (nlminb)	0.29	0.29	207.64	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	-1675.855	-1675.853	MCDS.exe	0.24	0.24	2058.96	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	2116.20	2096.87
hr	poly	2	-1675.255	-1675.234	MCDS.exe	0.25	0.25	1973.10	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	-125.9806	-120.3592	MCDS.exe	0.24	0.29	175.48	142.45
unif	cos	3	NA	-118.4524	MCDS.exe	NA	0.32	NA	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	-118.3056	-118.9848	mrds (nlminb)	0.40	0.34	106.18	122.04
hr	poly	2	-118.3551	-118.5401	MCDS.exe	0.40	0.36	104.56	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)

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	-5479.755	mrds (nlminb)	0.34	0.25	3629.41	4999.25
~as.factor(OBs) + MAS	-5397.937	-5472.345	mrds (nlminb)	0.34	0.25	3624.30	4912.49
~as.factor(OBs) + HAS	-5397.039	-5477.323	mrds (nlminb)	0.34	0.25	3628.48	4972.19

akepa data

```
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	-373.646	mrds (nlminb)	0.72	0.78	128.84	118.85

ETP Dolphins

Some errors / warnings:

```
# Fitting half-normal key function
# Error in -lt$value : invalid argument to unary operator
#
#
# All models failed to fit!
#
# Error in ds(dist.data, truncation = truncation, transect = transect, formula = models[[i]],  :
#   No models could be fitted.
```

```
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

```
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	-47.38918	mrds (nlminb)	0.42	0.4	212.06	226.1

Cluster Exercise

```
data("ClusterExercise")

model.compare <- test.cov.models(ClusterExercise,
                                 truncation = max(ClusterExercise$distance, na.rm = TRUE),
                                 cutpoints = c(0,0.214285714285714,0.428571428571429,0.642857142857143,0.85
                                 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