

MCDS.exe Testing

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This report details a number of analyses which have been run using both the default R optimiser within mrds and also the MCDS.exe optimiser. The MCDS.exe optimiser requires manual installation by the user, see below. This document is designed to allow users to assess the differences in results between the two optimisers.

The code below can be used to install the MCDS.exe optimizer.

```
# Install the MCDS.exe optimiser
download.file("http://distancesampling.org/R/MCDS.exe",
             paste0(system.file(package="mrds"),"/MCDS.exe"), mode = "wb")

# Help on the optimiser can be obtained using
?MCDS.exe
```

```
## These results were generated at: 12:55 27/07/2023
```

Capercaillie Data

```
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	-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

```
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	2.569997	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	2.963831	4.051256	mrds (nlminb)	0.28	0.29	143.43	138.47

Ducknest Data

```
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, lnI_R - likelihood value for R optimiser, lnI_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	lnI_R	lnI_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	NA	-462.6443	MCDS.exe	NA	0.89	NA	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

```
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, ln_l_R - likelihood value for R optimiser, ln_l_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	ln_l_R	ln_l_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	17293.80	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

LTEExercise Data

```
data("LTEExercise")

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

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

Table 5: Comparison of R and MCDS model fits for LTEExercise data. key - key function, adj - type of adjustment term, nadj - number of adjustments, ln_l_R - likelihood value for R optimiser, ln_l_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	ln_l_R	ln_l_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	306.92	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	311.19	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

```
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, lnI_R - likelihood value for R optimiser, lnI_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	lnI_R	lnI_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	NA	-457.0976	MCDS.exe	NA	0.19	NA	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

```
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.R0BJ")
```

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, ln_l_R - likelihood value for R optimiser, ln_l_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	ln_l_R	ln_l_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	1589.96	1632.38
unif	cos	3	-1103.043	-1103.041	MCDS.exe	0.16	0.16	1701.39	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

```
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, lnI_R - likelihood value for R optimiser, lnI_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	lnI_R	lnI_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	-787.6427	-787.5409	MCDS.exe	0.19	0.19	966.92	981.53

Sika Deer

```
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, ln_l_R - likelihood value for R optimiser, ln_l_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	ln_l_R	ln_l_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	2893.40	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

```
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	NA	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	-597.7567	-594.3689	MCDS.exe	0.36	0.37	375.37	361.61

Wren cue counting

```
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, lnI_R - likelihood value for R optimiser, lnI_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	lnI_R	lnI_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	-3430.145	-35113.874	mrds (nlminb)	0.14	0.82	5524.86	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

```
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, lnI_R - likelihood value for R optimiser, lnI_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	lnI_R	lnI_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	NA	-705.2152	MCDS.exe	NA	0.76	NA	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

```
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, lnI_R - likelihood value for R optimiser, lnI_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	lnI_R	lnI_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

```
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	-197.6630	-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

```
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

```
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, lnI_R - likelihood value for R optimiser, lnI_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	lnI_R	lnI_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	-197.8271	-197.7923	MCDS.exe	0.26	0.24	229.26	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	221.67	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, ln_l_R - likelihood value for R optimiser, ln_l_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	ln_l_R	ln_l_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	1754.29	1775.85
unif	cos	3	-1676.221	-1675.853	MCDS.exe	0.26	0.24	1924.88	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, lnI_R - likelihood value for R optimiser, lnI_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	lnI_R	lnI_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

```
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, lnI_R - likelihood value for R optimiser, lnI_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	lnI_R	lnI_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

```
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

```
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, lnI_R - likelihood value for R optimiser, lnI_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	lnI_R	lnI_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, lnI_R - likelihood value for R optimiser, lnI_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	lnI_R	lnI_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

```
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, lnI_R - likelihood value for R optimiser, lnI_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	lnI_R	lnI_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