

Bischof, R., Dupont, P., Milleret, C., Chipperfield, J. and Royle, J. A. 2020. Consequences of ignoring group association in spatial capture-recapture analysis. – *Wildlife Biology* 2020: wlb.00649

## Appendix 1

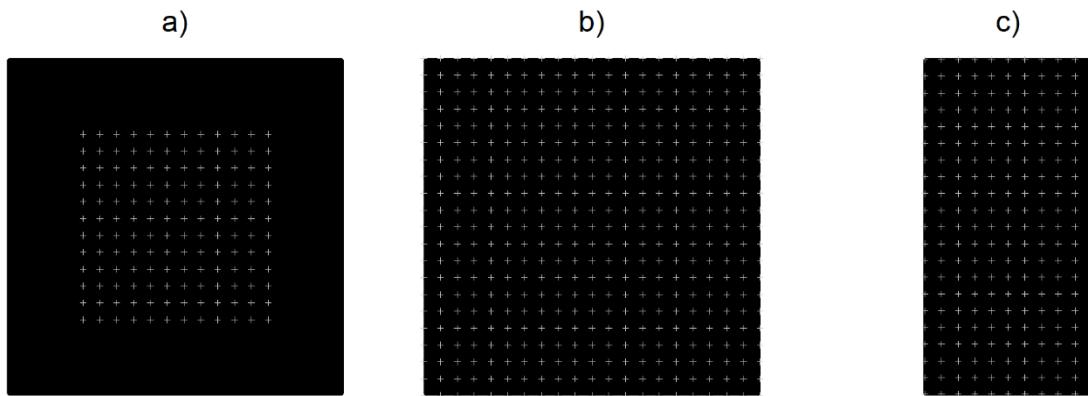


Figure A1. Three different habitat (black region) and detector grid (light crosses) configurations used for spatial capture-recapture simulations: a)  $12 \times 12$  detector grid with 4.5 distance units (du) habitat buffer (total habitat  $20 \times 20$  du), b)  $21 \times 21$  detector grid without buffer (total habitat  $20 \times 20$  du), and c)  $11 \times 21$  detector grid without buffer (total habitat  $10 \times 20$  du). Simulated population density was identical in all three configurations.

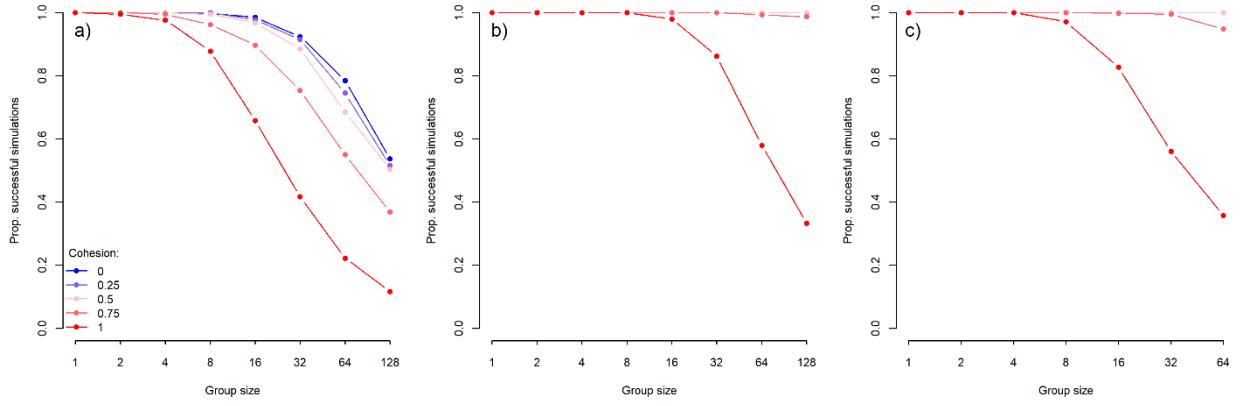


Figure A2. Proportion of simulations to which SCR models were successfully fitted for different levels of aggregation (group size) and cohesion (colors). Results are shown for the three different state-space configurations: a)  $12 \times 12$  detector grid with 4.5 du habitat buffer (total habitat  $20 \times 20$  du), b)  $21 \times 21$  detector grid without buffer (total habitat  $20 \times 20$  du), and c)  $11 \times 21$  detector grid without buffer (total habitat  $10 \times 20$  du). Simulated population density was identical in all three configurations.

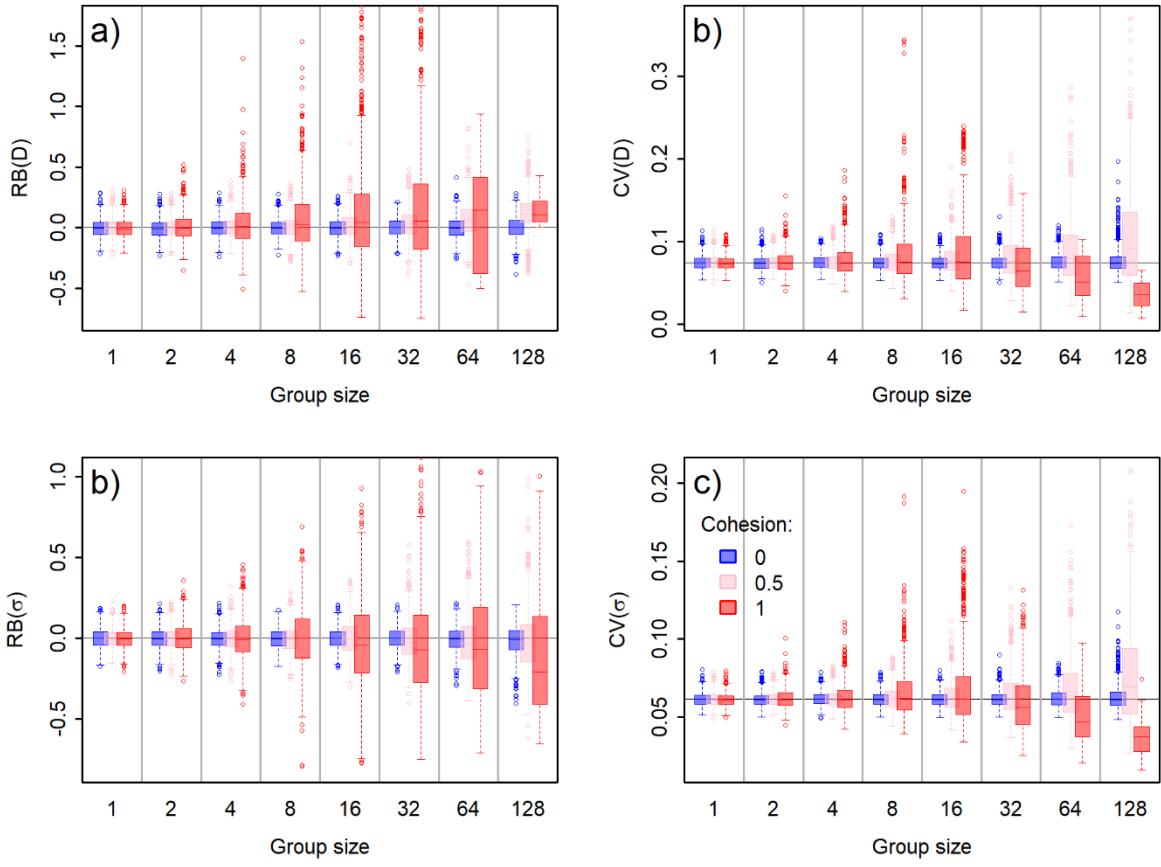


Figure A3. Bias and precision for the fully sampled (no buffer)  $20 \times 20$  du habitat configuration. Boxplots showing the effect of different levels of group association (aggregation: x axis; cohesion: colors) on key parameters estimated by SCR models fitted to simulated data. Shown are relative bias (RB, left column) and coefficient of variation (CV, right column) for density ( $D$ , top row) and the scale parameter of the utilization function ( $\sigma$ , bottom row). The chosen aspect ratio excludes some extreme outliers from the graphs.

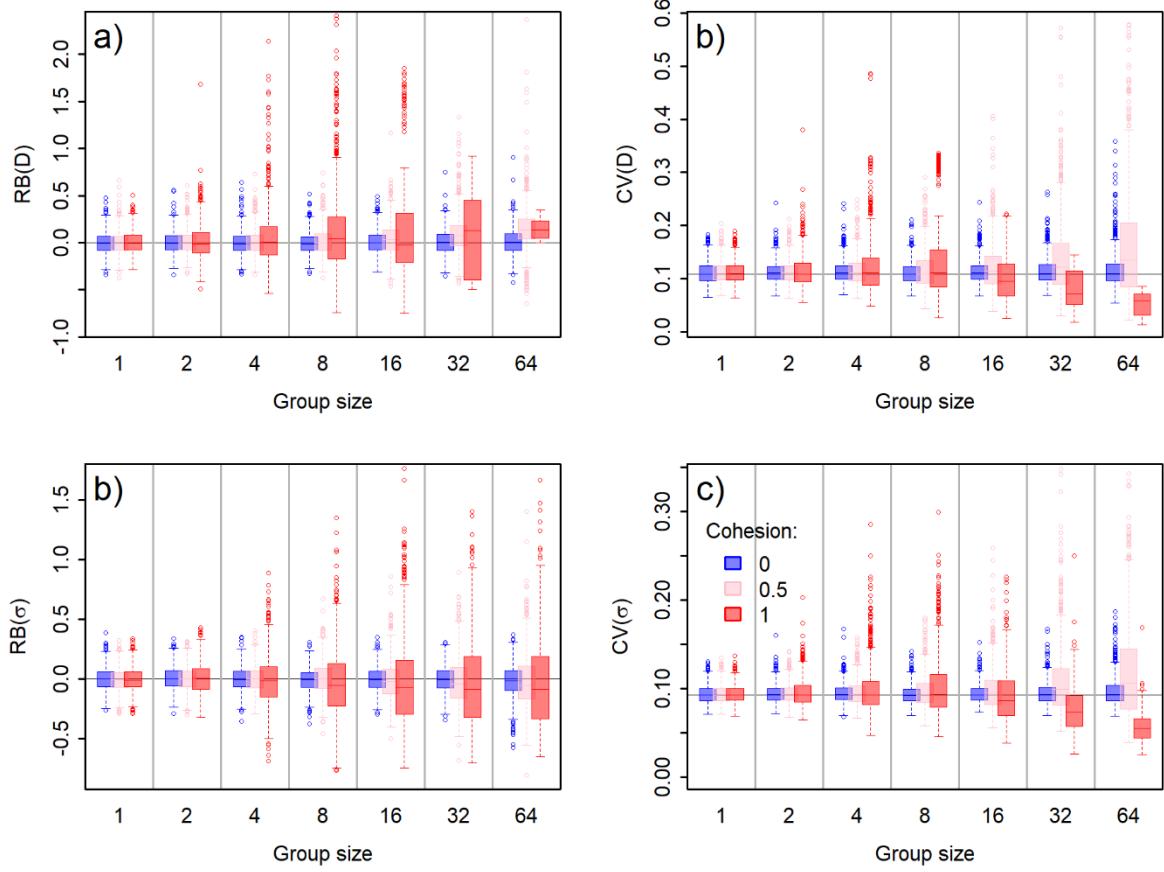


Figure A4. Bias and imprecision for the fully sampled (no buffer)  $10 \times 20$  du habitat configuration. Boxplots showing the effect of different levels of group association (aggregation: x-axis; cohesion: colors) on key parameters estimated by SCR models fitted to simulated data. Shown are relative bias (RB, left column) and coefficient of variation (CV, right column) for density ( $D$ , top row) and the scale parameter of the utilization function ( $\sigma$ , bottom row). The chosen aspect ratio excludes some extreme outliers from the graphs.

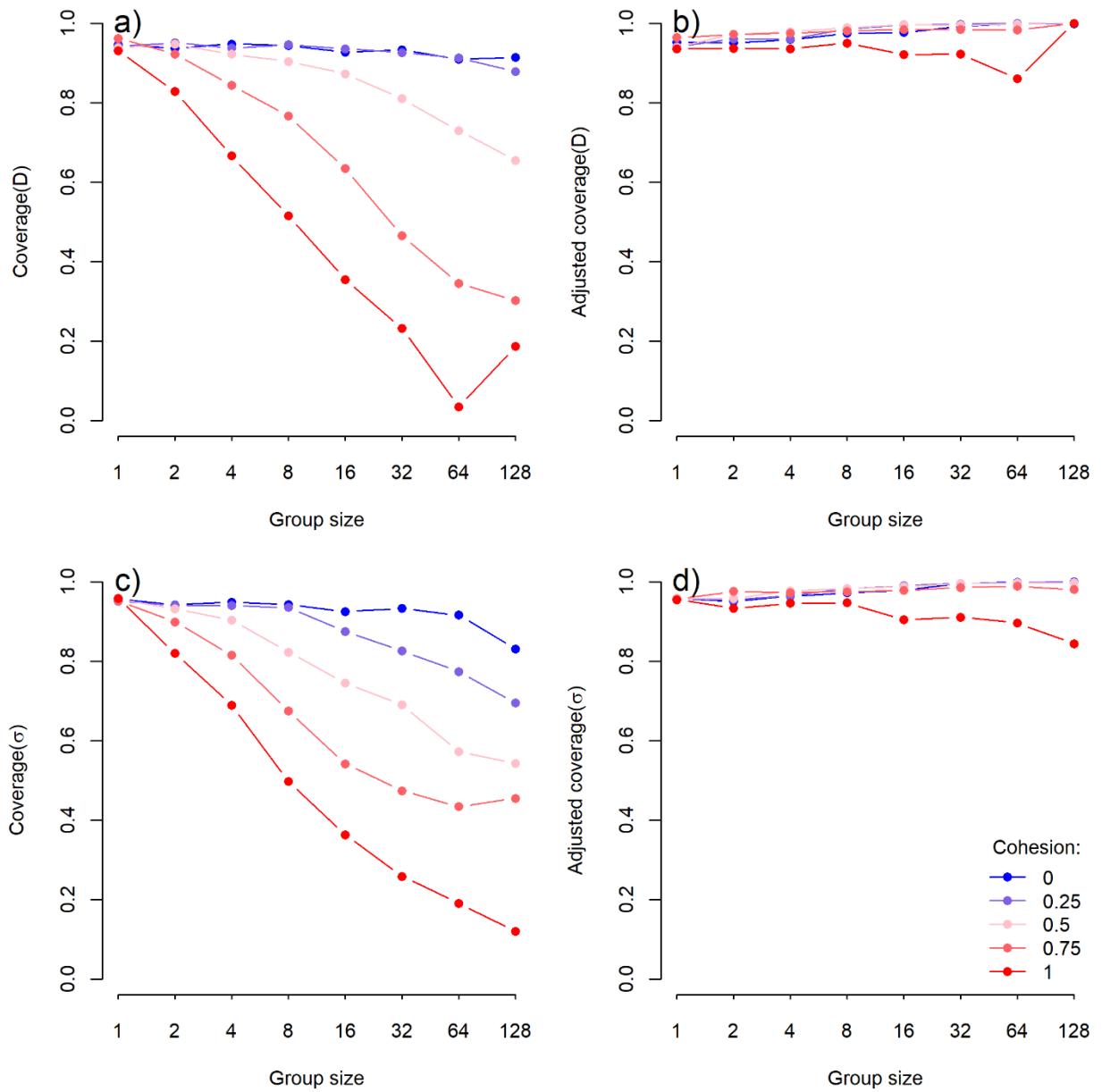


Figure A5. Coverage results for the fully sampled (no buffer)  $20 \times 20$  du habitat configuration.

Panels a) and c) show the decrease in coverage probability of density ( $D$ ) and the scale parameter of the detection function ( $\sigma$ ) for data simulated with different levels of aggregation (group size; x-axes) and cohesion (probability of shared detection pattern, colors). Coverage is the proportion of simulations where the 95% confidence interval around the prediction contains the true parameter value. Panels b) and d) show coverage returning to near its nominal value once variance estimates have been corrected for overdispersion.

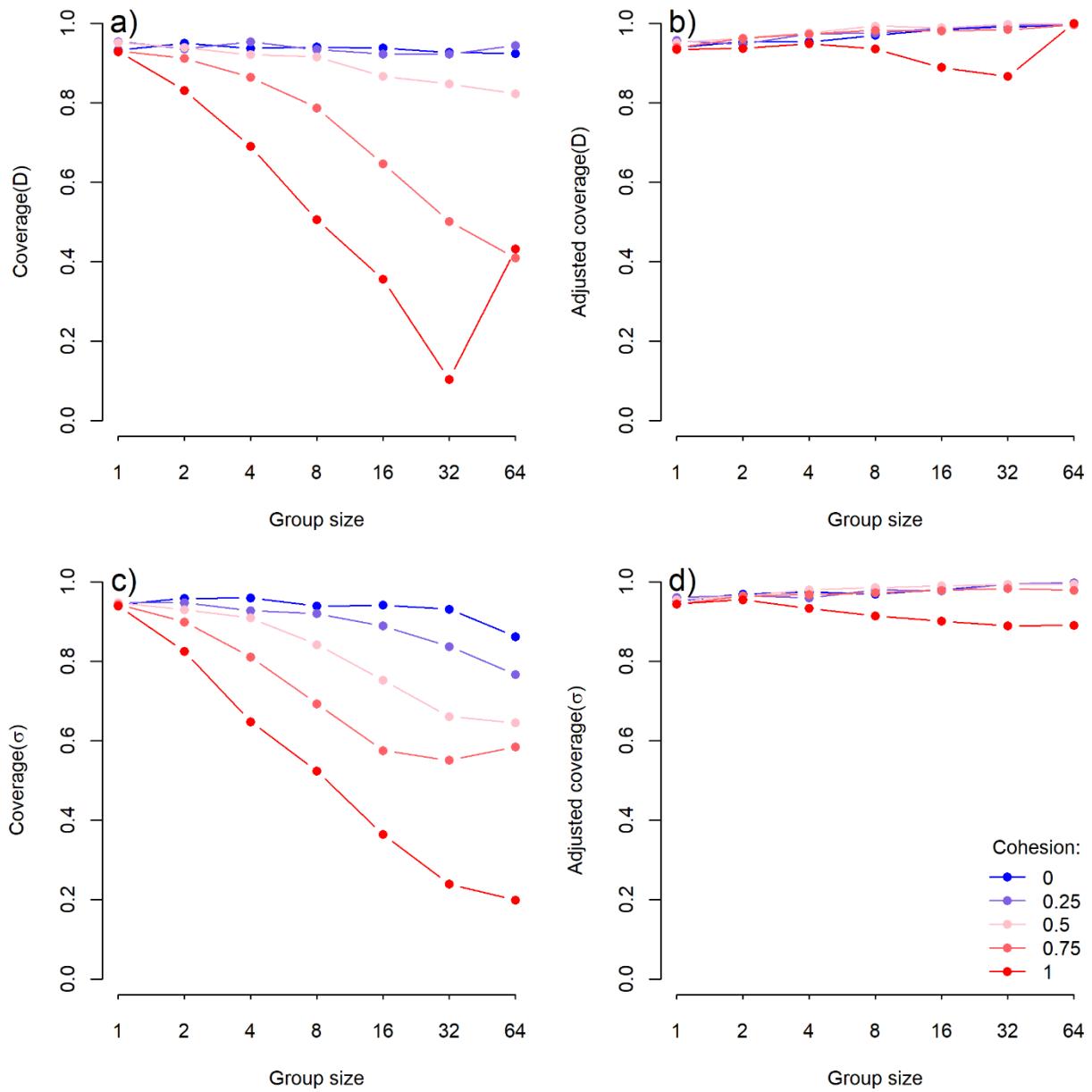


Figure A6. Coverage results for the fully sampled (no buffer)  $10 \times 20$  du habitat configuration.

Panels a) and c) show the decrease in coverage probability of density ( $D$ ) and the scale parameter of the detection function ( $\sigma$ ) for data simulated with different levels of aggregation (group size; x-axes) and cohesion (probability of shared detection pattern, colors). Coverage is the proportion of simulations where the 95% credible interval around the prediction contains the true parameter value. Panels b) and d) show coverage returning to near its nominal value once variance estimates have been corrected for overdispersion.

Table A1. Number of simulation sets to which spatial capture-recapture models were successfully fitted, number of detections per simulation (median and 95% quantiles), and number of individuals detected (median and 95% quantiles) for all aggregation and cohesion scenarios of the  $20 \times 20$  du habitat configuration, including a 4.5 du unsampled buffer area.

<b>Aggregation (group size)</b>	<b>Cohesion</b>	<b>Number of successful simulations (out of 1000)</b>	<b>Number of detections</b>	<b>Number of individuals detected (out of 128)</b>
<b>1</b>	<b>0</b>	1000	65 (46-84)	42 (31-52)
<b>2</b>	<b>0</b>	1000	65 (44-88)	42 (29.98-55)
<b>4</b>	<b>0</b>	1000	65 (39-94)	42 (27-58)
<b>8</b>	<b>0</b>	997	64 (32-102)	42 (23-61)
<b>16</b>	<b>0</b>	985	66 (26-116.4)	42 (19-70.4)
<b>32</b>	<b>0</b>	927	67 (16-141)	44 (14-82.85)
<b>64</b>	<b>0</b>	788	82 (10.68-175.32)	50 (9-98)
<b>128</b>	<b>0</b>	540	119 (10.48-195)	78 (9-104)
<b>1</b>	<b>0.25</b>	1000	65 (49-85)	42 (32-52.02)
<b>2</b>	<b>0.25</b>	1000	65 (43-89)	42 (29-54)
<b>4</b>	<b>0.25</b>	1000	65 (38-96)	42 (26-58)
<b>8</b>	<b>0.25</b>	1000	65 (29.98-102.02)	42 (22-61)
<b>16</b>	<b>0.25</b>	977	64 (20-114)	41 (16-67.6)
<b>32</b>	<b>0.25</b>	916	67 (16-146.25)	44 (13-84)
<b>64</b>	<b>0.25</b>	752	79.5 (12.78-177.68)	50 (10.78-100)
<b>128</b>	<b>0.25</b>	520	115.5 (8-227.07)	79 (7-112)
<b>1</b>	<b>0.5</b>	1000	65 (48-86)	42 (32-53)
<b>2</b>	<b>0.5</b>	1000	65 (40-91)	42 (29-54)
<b>4</b>	<b>0.5</b>	999	65 (37-98)	42 (26-58)
<b>8</b>	<b>0.5</b>	995	62 (30-110)	41 (22-64)
<b>16</b>	<b>0.5</b>	967	64 (19.15-128)	42 (15-74)
<b>32</b>	<b>0.5</b>	888	66 (14.18-154.65)	44 (12-83)
<b>64</b>	<b>0.5</b>	686	80 (9-220.75)	52 (7-111.88)
<b>128</b>	<b>0.5</b>	508	116.5 (10-293.27)	87 (9-123)

<b>1</b>	<b>0.75</b>	1000	65 (47-85)	42 (32-53)
<b>2</b>	<b>0.75</b>	1000	64 (42-91)	41 (29-56)
<b>4</b>	<b>0.75</b>	995	64 (35-101)	41 (25-59)
<b>8</b>	<b>0.75</b>	962	63 (24-117)	41 (18-66)
<b>16</b>	<b>0.75</b>	899	65 (18-140.65)	43 (15-80.55)
<b>32</b>	<b>0.75</b>	759	70 (9-186)	46 (7-92.1)
<b>64</b>	<b>0.75</b>	554	80 (8-258.52)	60 (7-122)
<b>128</b>	<b>0.75</b>	373	136 (8-348.5)	106 (7-127.7)
<b>1</b>	<b>1</b>	1000	64 (45-85.02)	42 (31-53)
<b>2</b>	<b>1</b>	995	64 (40-94)	42 (28-56)
<b>4</b>	<b>1</b>	976	64 (28-108)	40 (20-64)
<b>8</b>	<b>1</b>	878	64 (32-128)	40 (16-72)
<b>16</b>	<b>1</b>	658	80 (32-160)	48 (16-80)
<b>32</b>	<b>1</b>	417	96 (64-224)	64 (32-96)
<b>64</b>	<b>1</b>	222	192 (128-320)	64 (64-128)
<b>128</b>	<b>1</b>	116	256 (256-640)	128 (128-128)

Table A2. Relative bias (RB, median and 95% quantiles), coefficient of variation (CV, median and 95% quantiles), and coverage of the 95% confidence interval around estimates of density ( $D$ ) and the scale parameter ( $\sigma$ ) or all scenarios of the  $20 \times 20$  du habitat configuration, including a 4.5 du unsampled buffer area.

Aggregation (group size)	Cohesion	$D$			$\sigma$		
		RB	CV	Coverage	RB	CV	Coverage
1	0	0 (-0.31-0.43)	0.18 (0.15-0.25)	0.95	-0.01 (-0.23-0.22)	0.12 (0.09-0.17)	0.95
2	0	0 (-0.33-0.53)	0.18 (0.15-0.28)	0.92	0 (-0.23-0.22)	0.12 (0.1-0.18)	0.96
4	0	0.01 (-0.37-0.5)	0.18 (0.14-0.28)	0.91	0 (-0.24-0.24)	0.12 (0.09-0.19)	0.95
8	0	0.01 (-0.44-0.56)	0.19 (0.14-0.31)	0.82	0 (-0.27-0.27)	0.12 (0.09-0.21)	0.95
16	0	0.02 (-0.55-0.78)	0.18 (0.13-0.37)	0.72	-0.01 (-0.3-0.28)	0.12 (0.08-0.24)	0.94
32	0	0.07 (-0.64-0.98)	0.18 (0.12-0.62)	0.61	-0.02 (-0.4-0.25)	0.12 (0.08-0.37)	0.94
64	0	0.23 (-0.74-1.37)	0.16 (0.11-0.63)	0.56	-0.01 (-0.47-0.27)	0.11 (0.07-0.39)	0.9
128	0	0.86 (-0.65-1.62)	0.13 (0.1-0.6)	0.25	-0.02 (-0.46-0.2)	0.1 (0.06-0.39)	0.9
1	0.25	0.01 (-0.31-0.51)	0.18 (0.15-0.25)	0.94	-0.01 (-0.25-0.28)	0.12 (0.1-0.16)	0.94
2	0.25	0.01 (-0.33-0.5)	0.18 (0.15-0.27)	0.93	-0.01 (-0.24-0.26)	0.12 (0.09-0.18)	0.94
4	0.25	0 (-0.4-0.51)	0.18 (0.14-0.29)	0.88	0 (-0.25-0.26)	0.12 (0.09-0.19)	0.95
8	0.25	0.02 (-0.47-0.6)	0.18 (0.14-0.35)	0.83	-0.02 (-0.26-0.29)	0.12 (0.09-0.22)	0.92
16	0.25	0.02 (-0.61-0.76)	0.19 (0.13-0.48)	0.7	-0.02 (-0.35-0.29)	0.13 (0.08-0.32)	0.9
32	0.25	0.1 (-0.65-1.06)	0.19 (0.11-0.56)	0.61	-0.02 (-0.37-0.31)	0.12 (0.07-0.37)	0.88
64	0.25	0.29 (-0.62-1.45)	0.17 (0.1-0.56)	0.55	-0.03 (-0.5-0.37)	0.12 (0.06-0.4)	0.81
128	0.25	0.94 (-0.76-1.94)	0.15 (0.09-0.61)	0.26	-0.04 (-0.53-0.39)	0.1 (0.05-0.4)	0.78
1	0.5	0.01 (-0.3-0.44)	0.18 (0.15-0.25)	0.96	-0.01 (-0.23-0.25)	0.12 (0.1-0.16)	0.95
2	0.5	0.02 (-0.33-0.55)	0.18 (0.14-0.29)	0.93	-0.02 (-0.27-0.3)	0.12 (0.09-0.18)	0.91
4	0.5	0.03 (-0.4-0.53)	0.18 (0.14-0.3)	0.87	-0.01 (-0.27-0.32)	0.12 (0.09-0.19)	0.91
8	0.5	0.03 (-0.48-0.78)	0.19 (0.13-0.38)	0.79	-0.02 (-0.32-0.41)	0.13 (0.08-0.24)	0.85
16	0.5	0.1 (-0.61-1.14)	0.19 (0.12-0.54)	0.67	-0.04 (-0.39-0.47)	0.13 (0.07-0.34)	0.79
32	0.5	0.16 (-0.61-1.41)	0.19 (0.1-0.58)	0.6	-0.06 (-0.48-0.52)	0.13 (0.06-0.38)	0.75
64	0.5	0.41 (-0.75-1.97)	0.18 (0.09-0.86)	0.47	-0.06 (-0.54-0.52)	0.12 (0.05-0.55)	0.7

<b>128</b>	<b>0.5</b>	1.2 (-0.63-2.88)	0.16 (0.08-0.61)	0.17	-0.06 (-0.51-0.45)	0.11 (0.04-0.39)	0.66
<b>1</b>	<b>0.75</b>	0.01 (-0.31-0.52)	0.18 (0.15-0.26)	0.94	0 (-0.25-0.24)	0.12 (0.1-0.17)	0.94
<b>2</b>	<b>0.75</b>	0.02 (-0.36-0.61)	0.18 (0.14-0.28)	0.9	-0.02 (-0.28-0.29)	0.12 (0.09-0.18)	0.91
<b>4</b>	<b>0.75</b>	0.04 (-0.45-0.84)	0.19 (0.13-0.36)	0.81	-0.03 (-0.34-0.37)	0.12 (0.08-0.23)	0.83
<b>8</b>	<b>0.75</b>	0.08 (-0.58-1.1)	0.19 (0.12-0.47)	0.67	-0.05 (-0.47-0.52)	0.13 (0.08-0.28)	0.72
<b>16</b>	<b>0.75</b>	0.13 (-0.66-1.66)	0.19 (0.11-0.65)	0.58	-0.07 (-0.5-0.64)	0.13 (0.07-0.41)	0.65
<b>32</b>	<b>0.75</b>	0.32 (-0.65-2.88)	0.2 (0.1-0.8)	0.48	-0.07 (-0.55-0.77)	0.13 (0.05-0.55)	0.66
<b>64</b>	<b>0.75</b>	0.62 (-0.79-3.73)	0.21 (0.08-0.95)	0.32	-0.11 (-0.69-0.69)	0.13 (0.04-0.58)	0.58
<b>128</b>	<b>0.75</b>	1.62 (-0.65-5.85)	0.17 (0.07-0.7)	0.15	-0.1 (-0.53-2.35)	0.11 (0.03-0.48)	0.52
<b>1</b>	<b>1</b>	0.01 (-0.29-0.46)	0.18 (0.15-0.26)	0.96	-0.01 (-0.26-0.26)	0.12 (0.1-0.17)	0.94
<b>2</b>	<b>1</b>	0.01 (-0.4-0.79)	0.18 (0.14-0.32)	0.85	-0.01 (-0.37-0.38)	0.12 (0.09-0.2)	0.82
<b>4</b>	<b>1</b>	0.03 (-0.58-1.23)	0.19 (0.13-0.36)	0.7	-0.05 (-0.59-0.57)	0.12 (0.08-0.26)	0.62
<b>8</b>	<b>1</b>	0.03 (-0.67-1.84)	0.18 (0.11-0.35)	0.54	-0.07 (-0.74-0.88)	0.12 (0.07-0.26)	0.51
<b>16</b>	<b>1</b>	0 (-0.78-2.01)	0.16 (0.1-0.25)	0.44	-0.13 (-0.72-1.1)	0.1 (0.05-0.2)	0.35
<b>32</b>	<b>1</b>	0.18 (-0.66-2.38)	0.14 (0.08-0.19)	0.24	-0.05 (-0.71-3.4)	0.08 (0.04-0.28)	0.26
<b>64</b>	<b>1</b>	0.37 (-0.38-2.74)	0.1 (0.07-0.13)	0.32	-0.11 (-0.69-3.46)	0.06 (0.03-0.2)	0.19
<b>128</b>	<b>1</b>	1.21 (0.27-2.06)	0.07 (0.05-0.09)	0	-0.11 (-0.66-5.45)	0.04 (0.02-0.17)	0.16

Table A3. The number of simulation sets to which spatial capture-recapture models were successfully fitted the median (95% quantiles) number of detections per simulation, and the median (95% quantiles) number of individuals detected for all scenarios of the fully sampled (no buffer)  $20 \times 20$  du habitat configuration.

<b>Aggregation (group size)</b>	<b>Cohesion</b>	<b>Number of successful simulations (out of 1000)</b>	<b>Number of detections</b>	<b>Number of individuals detected (out of 128)</b>
<b>1</b>	<b>0</b>	1000	167.5 (144-192)	94 (85-103)
<b>2</b>	<b>0</b>	1000	168 (141-194)	94 (84-104)
<b>4</b>	<b>0</b>	1000	167 (140-192)	94 (83-104)
<b>8</b>	<b>0</b>	1000	168 (141-196)	94 (84-104)
<b>16</b>	<b>0</b>	1000	168 (140-197.02)	94 (83-105)
<b>32</b>	<b>0</b>	1000	169 (134.98-199)	95 (82-105)
<b>64</b>	<b>0</b>	1000	169 (126.98-199)	95 (79-105)
<b>128</b>	<b>0</b>	1000	171.5 (112-203)	95 (75-106)
<b>1</b>	<b>0.25</b>	1000	167 (143.97-194)	94 (84-104)
<b>2</b>	<b>0.25</b>	1000	168 (140-197)	94 (84-103.02)
<b>4</b>	<b>0.25</b>	1000	168 (140-195.02)	94 (83.97-104)
<b>8</b>	<b>0.25</b>	1000	168 (139-200)	94 (83-104.02)
<b>16</b>	<b>0.25</b>	1000	166.5 (132-204.02)	94 (82-106)
<b>32</b>	<b>0.25</b>	1000	166 (120-215.02)	94 (78-107)
<b>64</b>	<b>0.25</b>	1000	167 (109-231.02)	95 (73-112)
<b>128</b>	<b>0.25</b>	1000	164 (91.95-263.05)	95 (65-116)
<b>1</b>	<b>0.5</b>	1000	167 (145-193.02)	94 (85-104)
<b>2</b>	<b>0.5</b>	1000	168 (140-196)	95 (83-104.02)
<b>4</b>	<b>0.5</b>	1000	167 (135-203.02)	94.5 (82-106)
<b>8</b>	<b>0.5</b>	1000	168 (125.97-213)	94 (79-108.02)
<b>16</b>	<b>0.5</b>	1000	165 (116.97-228)	94 (76-111)
<b>32</b>	<b>0.5</b>	1000	166 (98-256)	95 (68.97-116)
<b>64</b>	<b>0.5</b>	1000	163 (80.9-286.02)	96 (59.98-120)
<b>128</b>	<b>0.5</b>	1000	157.5 (63-347.02)	100 (49-125)

<b>1</b>	<b>0.75</b>	1000	168 (144-194)	95 (85-103)
<b>2</b>	<b>0.75</b>	1000	167 (137.97-201.02)	94 (82-105)
<b>4</b>	<b>0.75</b>	1000	167 (127.95-210)	94 (78-110)
<b>8</b>	<b>0.75</b>	1000	165 (116-222.02)	94 (74-111)
<b>16</b>	<b>0.75</b>	1000	163 (101.97-247.05)	94 (68-117)
<b>32</b>	<b>0.75</b>	1000	165 (76.97-287.02)	96 (54-124)
<b>64</b>	<b>0.75</b>	998	151 (39-353.37)	105 (33.92-127)
<b>128</b>	<b>0.75</b>	998	142 (30-435)	108 (27-128)
<b>1</b>	<b>1</b>	1000	168 (144-195)	94 (83-104)
<b>2</b>	<b>1</b>	1000	168 (136-204)	94 (80-108)
<b>4</b>	<b>1</b>	1000	168 (120-220)	96 (76-112)
<b>8</b>	<b>1</b>	1000	168 (104-240)	96 (64-120)
<b>16</b>	<b>1</b>	982	160 (96-272)	96 (48-128)
<b>32</b>	<b>1</b>	869	192 (96-320)	96 (32-128)
<b>64</b>	<b>1</b>	595	192 (128-384)	128 (64-128)
<b>128</b>	<b>1</b>	357	256 (256-640)	128 (128-128)

Table A4. Relative bias (RB, median and 95% quantiles), coefficient of variation (CV, median and 95% quantiles), and coverage of the 95% confidence interval around estimates of density ( $D$ ) and the scale parameter ( $\sigma$ ) for all scenarios of the fully sampled (no buffer)  $20 \times 20$  du habitat configuration.

Aggregation (group size)	Cohesion	$D$			$\sigma$		
		RB	CV	Coverage	RB	CV	Coverage
1	0	-0.01 (-0.13-0.15)	0.07 (0.06-0.09)	0.95	0 (-0.11-0.13)	0.06 (0.05-0.07)	0.96
2	0	-0.01 (-0.15-0.16)	0.07 (0.06-0.09)	0.94	0 (-0.13-0.12)	0.06 (0.05-0.07)	0.94
4	0	0 (-0.15-0.15)	0.07 (0.06-0.09)	0.95	0 (-0.12-0.12)	0.06 (0.05-0.07)	0.95
8	0	0 (-0.14-0.16)	0.07 (0.06-0.09)	0.94	-0.01 (-0.12-0.13)	0.06 (0.05-0.07)	0.94
16	0	0 (-0.15-0.16)	0.07 (0.06-0.09)	0.93	0 (-0.14-0.13)	0.06 (0.05-0.07)	0.92
32	0	0 (-0.16-0.16)	0.07 (0.06-0.1)	0.93	0 (-0.13-0.12)	0.06 (0.05-0.07)	0.93
64	0	0 (-0.17-0.17)	0.07 (0.06-0.1)	0.91	0 (-0.15-0.13)	0.06 (0.05-0.08)	0.92
128	0	0 (-0.18-0.17)	0.07 (0.06-0.11)	0.91	-0.01 (-0.23-0.14)	0.06 (0.05-0.08)	0.83
1	0.25	0 (-0.15-0.15)	0.07 (0.06-0.09)	0.94	0 (-0.12-0.12)	0.06 (0.05-0.07)	0.95
2	0.25	0 (-0.13-0.15)	0.07 (0.06-0.1)	0.95	-0.01 (-0.13-0.13)	0.06 (0.05-0.07)	0.94
4	0.25	-0.01 (-0.14-0.15)	0.07 (0.06-0.1)	0.94	-0.01 (-0.12-0.13)	0.06 (0.05-0.07)	0.94
8	0.25	0 (-0.14-0.15)	0.07 (0.06-0.09)	0.95	0 (-0.12-0.13)	0.06 (0.05-0.07)	0.94
16	0.25	0 (-0.15-0.16)	0.07 (0.06-0.1)	0.94	-0.01 (-0.15-0.15)	0.06 (0.05-0.08)	0.88
32	0.25	0.01 (-0.16-0.17)	0.08 (0.05-0.11)	0.93	-0.01 (-0.17-0.17)	0.06 (0.05-0.08)	0.83
64	0.25	0.02 (-0.17-0.2)	0.08 (0.05-0.12)	0.91	-0.02 (-0.2-0.22)	0.06 (0.05-0.09)	0.77
128	0.25	0.03 (-0.2-0.24)	0.08 (0.04-0.15)	0.88	-0.02 (-0.25-0.27)	0.06 (0.04-0.1)	0.7
1	0.5	0 (-0.15-0.17)	0.07 (0.06-0.09)	0.94	0 (-0.12-0.12)	0.06 (0.05-0.07)	0.96
2	0.5	0 (-0.13-0.17)	0.07 (0.06-0.1)	0.95	-0.01 (-0.13-0.14)	0.06 (0.05-0.07)	0.93
4	0.5	0 (-0.15-0.18)	0.07 (0.06-0.1)	0.92	0 (-0.14-0.14)	0.06 (0.05-0.07)	0.9
8	0.5	0 (-0.16-0.2)	0.07 (0.05-0.11)	0.9	-0.01 (-0.17-0.16)	0.06 (0.05-0.08)	0.82
16	0.5	0.01 (-0.19-0.22)	0.08 (0.05-0.12)	0.87	0 (-0.19-0.22)	0.06 (0.05-0.08)	0.74
32	0.5	0.03 (-0.2-0.31)	0.08 (0.04-0.15)	0.81	-0.03 (-0.23-0.27)	0.06 (0.04-0.1)	0.69
64	0.5	0.06 (-0.21-0.37)	0.08 (0.03-0.19)	0.73	-0.03 (-0.29-0.37)	0.06 (0.04-0.12)	0.57

<b>128</b>	<b>0.5</b>	0.11 (-0.21-0.44)	0.09 (0.03-0.24)	0.66	-0.04 (-0.34-0.4)	0.07 (0.03-0.14)	0.54
<b>1</b>	<b>0.75</b>	-0.01 (-0.13-0.15)	0.07 (0.06-0.09)	0.96	0 (-0.12-0.12)	0.06 (0.05-0.07)	0.95
<b>2</b>	<b>0.75</b>	-0.01 (-0.15-0.18)	0.07 (0.06-0.1)	0.92	0 (-0.13-0.14)	0.06 (0.05-0.07)	0.9
<b>4</b>	<b>0.75</b>	0 (-0.19-0.22)	0.07 (0.05-0.11)	0.84	-0.01 (-0.17-0.18)	0.06 (0.05-0.08)	0.82
<b>8</b>	<b>0.75</b>	0 (-0.23-0.28)	0.07 (0.05-0.12)	0.77	-0.01 (-0.24-0.23)	0.06 (0.05-0.09)	0.68
<b>16</b>	<b>0.75</b>	0.03 (-0.27-0.47)	0.08 (0.04-0.15)	0.63	-0.02 (-0.28-0.34)	0.06 (0.04-0.1)	0.54
<b>32</b>	<b>0.75</b>	0.08 (-0.34-0.84)	0.08 (0.03-0.24)	0.46	-0.03 (-0.37-0.49)	0.06 (0.04-0.14)	0.47
<b>64</b>	<b>0.75</b>	0.19 (-0.33-1.22)	0.08 (0.02-0.43)	0.35	-0.06 (-0.45-0.55)	0.07 (0.03-0.24)	0.43
<b>128</b>	<b>0.75</b>	0.25 (-0.39-1.56)	0.14 (0.02-0.71)	0.3	-0.09 (-0.51-0.68)	0.09 (0.03-0.33)	0.45
<b>1</b>	<b>1</b>	-0.01 (-0.15-0.15)	0.07 (0.06-0.09)	0.93	0 (-0.11-0.12)	0.06 (0.05-0.07)	0.96
<b>2</b>	<b>1</b>	0 (-0.2-0.25)	0.07 (0.05-0.11)	0.83	0 (-0.17-0.2)	0.06 (0.05-0.08)	0.82
<b>4</b>	<b>1</b>	0.01 (-0.25-0.42)	0.07 (0.05-0.12)	0.67	-0.01 (-0.24-0.27)	0.06 (0.05-0.08)	0.69
<b>8</b>	<b>1</b>	0.03 (-0.32-0.69)	0.07 (0.04-0.17)	0.52	0 (-0.34-0.38)	0.06 (0.04-0.11)	0.5
<b>16</b>	<b>1</b>	0.05 (-0.48-1.43)	0.08 (0.03-0.22)	0.36	-0.04 (-0.62-0.58)	0.06 (0.04-0.13)	0.36
<b>32</b>	<b>1</b>	0.05 (-0.69-1.58)	0.06 (0.03-0.15)	0.23	-0.07 (-0.71-0.72)	0.06 (0.04-0.1)	0.26
<b>64</b>	<b>1</b>	0.14 (-0.49-0.82)	0.05 (0.02-0.1)	0.03	-0.07 (-0.7-0.85)	0.05 (0.03-0.08)	0.19
<b>128</b>	<b>1</b>	0.11 (0-0.33)	0.04 (0.01-0.06)	0.19	-0.21 (-0.65-1.1)	0.04 (0.02-0.05)	0.12

Table A5. The number of simulation sets to which spatial capture-recapture models were successfully fitted the number of detections per simulation (median and 95% quantiles), and the number of individuals detected (median and 95% quantiles) for all scenarios of the fully sampled (no buffer)  $10 \times 20$  du habitat configuration.

<b>Aggregation (group size)</b>	<b>Cohesion</b>	<b>Number of successful simulations (out of 1000)</b>	<b>Number of detections</b>	<b>Number of individuals detected (out of 128)</b>
1	0	1000	81 (64-99)	46 (38.98-53)
2	0	1000	80.5 (64-99)	46 (40-53)
4	0	1000	80 (63-98)	46 (38.98-53)
8	0	1000	81 (62-101)	46 (38-53)
16	0	1000	81 (61-102)	47 (39-53)
32	0	1000	81 (59-102)	47 (38-54)
64	0	1000	82 (50-106)	47 (35-54)
1	0.25	1000	80 (64-98)	46 (39-53)
2	0.25	1000	80 (63-100)	46 (39-53)
4	0.25	1000	80 (61-101)	46 (38-53)
8	0.25	1000	81 (60-104)	46 (37.98-54)
16	0.25	1000	80 (57-107)	46 (36.98-55)
32	0.25	1000	80 (51-116.02)	47 (34-57)
64	0.25	1000	79 (45.95-126.07)	47 (32-58)
1	0.5	1000	81 (63-99)	46 (39-53)
2	0.5	1000	80 (62-101)	46 (38-54)
4	0.5	1000	81 (58-103)	46 (37-54)
8	0.5	1000	80 (54-112.02)	46 (36-56)
16	0.5	1000	79 (48-121.02)	47 (33-58)
32	0.5	1000	78 (37-139)	47 (27.98-61)
64	0.5	1000	75 (28-170.02)	49 (22-63)
1	0.75	1000	81 (63-97)	46 (39-53)
2	0.75	1000	80 (59-104.02)	46 (38-54.02)

<b>4</b>	<b>0.75</b>	1000	80 (55-114)	47 (36-56.02)
<b>8</b>	<b>0.75</b>	1000	79 (46-118)	47 (31-59)
<b>16</b>	<b>0.75</b>	999	77 (30-137.05)	47 (24-62)
<b>32</b>	<b>0.75</b>	996	76 (18-167)	50 (15.88-64)
<b>64</b>	<b>0.75</b>	955	70 (14-211.15)	54 (12-64)
<b>1</b>	<b>1</b>	1000	81 (64-98.02)	46 (39-53)
<b>2</b>	<b>1</b>	1000	80 (58-106)	46 (36-56)
<b>4</b>	<b>1</b>	1000	80 (48-116)	48 (32-60)
<b>8</b>	<b>1</b>	972	80 (40-136)	48 (24-64)
<b>16</b>	<b>1</b>	831	80 (48-160)	48 (16-64)
<b>32</b>	<b>1</b>	570	96 (64-192)	64 (32-64)
<b>64</b>	<b>1</b>	373	128 (128-320)	64 (64-64)

Table A6. Relative bias (RB, median and 95% quantiles), coefficient of variation (CV, median and 95% quantiles), and coverage of the 95% confidence interval around estimates of density ( $D$ ) and the scale parameter ( $\sigma$ ) for all scenarios of the fully sampled (no buffer)  $10 \times 20$  du habitat configuration.

Aggregation (group size)	Cohesion	$D$			$\sigma$		
		RB	CV	Coverage	RB	CV	Coverage
1	0	-0.01 (-0.21-0.24)	0.11 (0.08-0.15)	0.93	0 (-0.19-0.18)	0.09 (0.08-0.12)	0.94
2	0	0 (-0.2-0.24)	0.11 (0.08-0.15)	0.95	0 (-0.16-0.18)	0.09 (0.08-0.12)	0.96
4	0	-0.01 (-0.21-0.23)	0.11 (0.08-0.16)	0.94	-0.01 (-0.17-0.2)	0.09 (0.08-0.12)	0.96
8	0	-0.01 (-0.21-0.24)	0.11 (0.08-0.15)	0.94	-0.01 (-0.21-0.17)	0.09 (0.08-0.12)	0.94
16	0	0 (-0.2-0.25)	0.11 (0.08-0.16)	0.94	-0.01 (-0.19-0.19)	0.09 (0.08-0.12)	0.94
32	0	0.01 (-0.22-0.27)	0.11 (0.08-0.17)	0.93	-0.01 (-0.21-0.19)	0.09 (0.08-0.12)	0.93
64	0	0.01 (-0.25-0.26)	0.11 (0.08-0.19)	0.92	-0.02 (-0.29-0.21)	0.09 (0.08-0.13)	0.86
1	0.25	-0.01 (-0.2-0.22)	0.11 (0.08-0.15)	0.95	0 (-0.19-0.18)	0.09 (0.08-0.12)	0.95
2	0.25	-0.01 (-0.21-0.25)	0.11 (0.08-0.16)	0.94	-0.01 (-0.17-0.19)	0.09 (0.08-0.12)	0.95
4	0.25	-0.01 (-0.2-0.23)	0.11 (0.08-0.16)	0.95	-0.01 (-0.19-0.22)	0.09 (0.08-0.12)	0.93
8	0.25	-0.01 (-0.22-0.24)	0.11 (0.08-0.17)	0.93	-0.01 (-0.2-0.2)	0.09 (0.08-0.12)	0.92
16	0.25	0 (-0.23-0.29)	0.11 (0.08-0.18)	0.92	-0.02 (-0.23-0.26)	0.09 (0.07-0.13)	0.89
32	0.25	0.03 (-0.24-0.3)	0.11 (0.07-0.2)	0.92	-0.02 (-0.25-0.29)	0.09 (0.07-0.14)	0.84
64	0.25	0.04 (-0.23-0.33)	0.12 (0.06-0.23)	0.94	-0.02 (-0.32-0.29)	0.1 (0.07-0.15)	0.77
1	0.5	-0.01 (-0.19-0.25)	0.11 (0.08-0.16)	0.95	-0.01 (-0.18-0.18)	0.09 (0.08-0.12)	0.95
2	0.5	0 (-0.2-0.27)	0.11 (0.08-0.16)	0.94	0 (-0.2-0.19)	0.09 (0.08-0.12)	0.93
4	0.5	0 (-0.23-0.31)	0.11 (0.08-0.17)	0.92	0 (-0.2-0.24)	0.09 (0.07-0.12)	0.91
8	0.5	0 (-0.22-0.32)	0.11 (0.07-0.2)	0.92	0 (-0.24-0.28)	0.09 (0.07-0.14)	0.84
16	0.5	0.04 (-0.25-0.38)	0.11 (0.06-0.23)	0.87	-0.02 (-0.29-0.32)	0.1 (0.07-0.15)	0.75
32	0.5	0.07 (-0.28-0.55)	0.12 (0.05-0.31)	0.85	-0.05 (-0.35-0.43)	0.1 (0.06-0.21)	0.66
64	0.5	0.14 (-0.33-0.64)	0.14 (0.04-0.45)	0.82	-0.05 (-0.38-0.5)	0.11 (0.05-0.25)	0.64
1	0.75	-0.01 (-0.21-0.23)	0.11 (0.08-0.16)	0.93	0 (-0.2-0.19)	0.09 (0.08-0.12)	0.94
2	0.75	0 (-0.23-0.29)	0.11 (0.07-0.18)	0.91	-0.01 (-0.22-0.22)	0.09 (0.07-0.13)	0.9

<b>4</b>	<b>0.75</b>	0.01 (-0.26-0.38)	0.11 (0.07-0.19)	0.86	-0.02 (-0.26-0.28)	0.09 (0.07-0.14)	0.81
<b>8</b>	<b>0.75</b>	0.03 (-0.29-0.58)	0.11 (0.06-0.25)	0.79	-0.03 (-0.34-0.4)	0.09 (0.07-0.16)	0.69
<b>16</b>	<b>0.75</b>	0.09 (-0.39-1.03)	0.12 (0.05-0.42)	0.65	-0.06 (-0.41-0.52)	0.1 (0.06-0.26)	0.58
<b>32</b>	<b>0.75</b>	0.18 (-0.38-1.58)	0.12 (0.04-0.72)	0.5	-0.05 (-0.49-0.73)	0.1 (0.05-0.38)	0.55
<b>64</b>	<b>0.75</b>	0.28 (-0.57-2.04)	0.2 (0.02-1.21)	0.41	-0.09 (-0.58-0.82)	0.13 (0.04-0.56)	0.58
<b>1</b>	<b>1</b>	-0.01 (-0.22-0.26)	0.11 (0.08-0.15)	0.93	-0.01 (-0.19-0.19)	0.09 (0.08-0.12)	0.94
<b>2</b>	<b>1</b>	-0.01 (-0.27-0.38)	0.11 (0.07-0.18)	0.83	0 (-0.25-0.28)	0.09 (0.07-0.13)	0.82
<b>4</b>	<b>1</b>	0.01 (-0.36-0.75)	0.11 (0.06-0.25)	0.69	-0.02 (-0.41-0.43)	0.09 (0.07-0.17)	0.65
<b>8</b>	<b>1</b>	0.04 (-0.47-1.53)	0.11 (0.05-0.32)	0.51	-0.06 (-0.59-0.59)	0.09 (0.06-0.2)	0.52
<b>16</b>	<b>1</b>	-0.02 (-0.71-1.44)	0.09 (0.03-0.21)	0.36	-0.07 (-0.71-0.9)	0.09 (0.05-0.16)	0.36
<b>32</b>	<b>1</b>	0.13 (-0.49-0.8)	0.07 (0.03-0.14)	0.1	-0.09 (-0.71-0.85)	0.07 (0.04-0.12)	0.24
<b>64</b>	<b>1</b>	0.14 (0-0.33)	0.06 (0.01-0.08)	0.43	-0.09 (-0.65-1.01)	0.06 (0.03-0.09)	0.2

# Simulating SCR with group aggregation and cohesion

This vignette shows an example of spatial capture-recapture (SCR) data simulation with group association (aggregation and cohesion) and subsequent model fitting.

```
library(secr)

## This is secr 3.2.0. For overview type ?secr

library(raster)

## Loading required package: sp

##
## Attaching package: 'raster'

## The following objects are masked from 'package:secr':
##   flip, rotate, shift, trim

library(sp)

# simulation parameters
parms <- list(grid.size.x = 12,
             grid.size.y = 12,
             cell.size = 10,
             habitat.buffer = 45,
             group.size = 8,
             N.ind = 128,
             p0 = 0.1,
             sigma = 15,
             cohesion = 0.25
)
)
```

Simulated null capture histories (animals never detected) are dropped automatically by `sim.capthist`. To allow alignment between capture histories of all group members, all-zero capture histories are added back in with this function:

```
expandCH <- function(CH) {# Function from M. Efford (pers. comm., 5/13/2019).
  pop <- attr(CH, 'pop')
  fullCH <- array(0, dim = c(nrow(pop), dim(CH)[2:3]))
  rownames(fullCH) <- rownames(pop)
  fullCH[rownames(CH), ] <- CH
  traps(fullCH) <- traps(CH)
  class(fullCH) <- 'capthist'
  fullCH
}
```

Function to run one replicate.

```
runone <- function (parms, plot.check = TRUE, do.fit = TRUE) {
  # Function modified/expanded from version shared by M. Efford (pers. comm., 5/13/2019)

  out <- list()
  detectpar <- list(g0 = parms$p0, sigma = parms$sigma)

  # detector grid
```

```

tr <- make.grid(nx = parms$grid.size.x, ny = parms$grid.size.y,
                 spacing = parms$cell.size, detector = 'proximity')

# available habitat
msk <- make.mask(traps = tr, buffer = parms$habitat.buffer)

# expected n etc.
p <- sum(pdot(X = msk, traps = tr,
                detectfn = 'HN', detectpar = detectpar, nooccasions = 1) *
            attr(msk, 'area')) / maskarea(msk)
out$expectation <- c(p = p, exp.n = p * parms$N.ind,
                     sd.n = parms$N.ind * (p * (1-p) / parms$N.ind)^0.5)

# clone at level of capthist for maximal cohesion (identical detection pattern)
pop <- sim.popn(Nbuffer = parms$N.ind / parms$group.size, core = tr,
                  buffer = parms$habitat.buffer,
                  Ndist = "fixed")
ch <- sim.capthist(tr, popn = pop, detectfn = 'HN', renumber = FALSE,
                    detectpar = detectpar, nooccasions = 1, savepopn = TRUE)
chi <- secr::clone(expandCH(ch), 'constant', parms$group.size)

# clone only popn for minimal cohesion (identical AC location)
clonedpop <- secr::clone(pop, 'constant', parms$group.size)
chg <- sim.capthist(tr, popn = clonedpop, detectfn = 'HN', renumber = FALSE,
                     detectpar = detectpar, nooccasions = 1, savepopn = TRUE)
chg <- expandCH(chg)

# mix individual and group detection patterns
ch <- chi
p <- runif(prod(dim(ch))) < parms$cohesion # Bernoulli by animal and detector
ch[] <- p * chi + (1-p) * chg # mixture of group and individual detection patterns
ch2 <- subset(ch) # drops null histories

# PLOTTING
if(plot.check){
  # detectors
  tr.sp <- data.frame(tr)
  coordinates(tr.sp) <- tr.sp

  # habitat
  mask.sp <- data.frame(msk)
  coordinates(mask.sp) <- mask.sp
  e <- extent(mask.sp)
  e.sp <- as(e, 'SpatialPolygons')

  # ACs without jitter
  AC.orig.sp <- data.frame(clonedpop)
  coordinates(AC.orig.sp) <- AC.orig.sp

  # ACs with jitter
  AC.sp <- data.frame(clonedpop)
}

```

```

AC.sp$ID <- dimnames(clonedpop)[[1]]
jitter.f <- parms$cell.size/10*sqrt(parms$group.size)
coordinates(AC.sp) <- apply(AC.sp[,1:2],c(1,2),function(x)
  runif(1,x-jitter.f,x+jitter.f))

# PLOT HABITAT EXTENT
plot(e.sp,pch = 19,col = NA,border = "black")

# PLOT DETECTIONS
ids.detected <- dimnames(ch2)[[1]]
AC.colors <- sample(colors(),length(AC.sp),replace = TRUE)
names(AC.colors) <- AC.sp$ID
for(i in ids.detected){
  x <- ch2[i,1]
  locs <- data.frame(tr[which(x == 1),])
  coordinates(locs) <- locs
  xx <- coordinates(locs)
  yy <- coordinates(AC.sp[AC.sp$ID == i,])
  segments(yy[,1],yy[,2],xx[,1],xx[,2],col = AC.colors[i],lwd = 0.8)
}

# PLOT ACs
plot(AC.sp,pch = 21,bg = AC.colors,add = TRUE,col = "black",lwd = 0.2,cex = 0.7)
plot(tr.sp,col = grey(0.8),cex = 0.7,add = TRUE)
}

# MODEL FITTING
if(do.fit){
  out$fit <- out$error <- NULL
  try(out$fit <- summary(secr.fit(ch2, mask = msk, trace = F,
                                    details = list(distribution = "binomial")))
      ,silent = TRUE)
}

# CALCULATE chat
chat<-NA

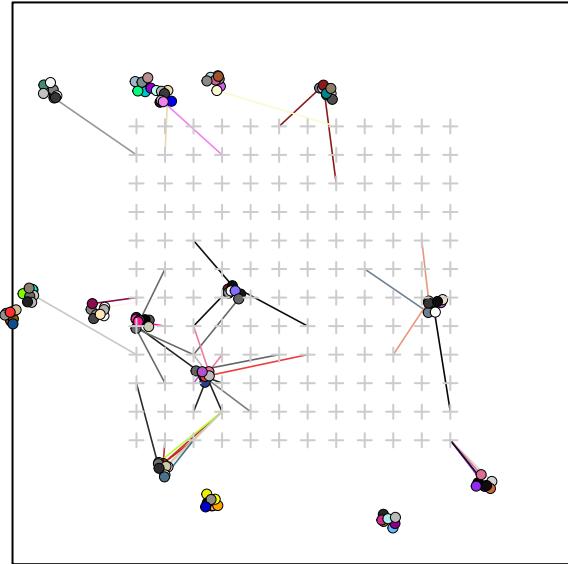
D <- parms$N.ind$mask$Area   #density
fn <- function (r) r * detectpar$g0 * exp(-r^2/2/(detectpar$sigma/100)^2)
expected.nk <- 2 * pi *D * integrate(fn, 0, 5*detectpar$sigma/100)$value
nk <- apply(apply(ch2,c(1,3),sum)>0,2,sum)  #realized number of detections
X2 <- sum((nk - expected.nk)^2 / expected.nk)
si <- mean((nk - expected.nk) / expected.nk)
nu <- dim(ch2)[3] - 1
chat <- X2/nu / (1 + si)  #Fletcher 2012
out$dispersion <- c(mean.nk = mean(nk), var.nk = sd(nk)^2, chat = chat)

return(out)
}

```

Run one simulation and display the results.

```
secr.out <- runone(parms = parms, plot.check = TRUE)
```



```
secr.out$fit
```

```
## $versiontime
## [1] "3.2.0, run 15:41:31 17 Feb 2020"
##
## $traps
##   Detector Number Spacing
##   proximity      144        10
##
## $capthist
##   Occasions Detections     Animals Detectors      Moves
##           1          46         34       144        12
##
## $mask
##   Cells Spacing Area
##   4096    3.125     4
##
## $modeldetails
##   CL fixed distribution hcov
##   FALSE  none    binomial
##
```

```

## $AICtable
##           model   detectfn npar    logLik      AIC     AICc
## D~1 g0~1 sigma~1 halfnormal     3 -149.5421 305.084 305.884
##
## $coef
##       beta   SE.beta      lcl      ucl
## D     3.386540 0.2502807 2.895999 3.877081
## g0   -2.658507 0.4040816 -3.450492 -1.866521
## sigma 2.809957 0.1665540 2.483517 3.136396
##
## $predicted
##       link   estimate SE.estimate      lcl      ucl
## D     log 29.56348460 7.51656702 18.10157346 48.2830746
## g0   logit 0.06546664 0.02472202 0.03075419 0.1339448
## sigma log 16.60919610 2.78562335 11.98333291 23.0207570
secr.out$dispersion

##   mean.nk   var.nk     chat
## 0.3194444 0.5266123 1.7042393

```

## References

- Anderson, D. R., Burnham, K. P. and White, G. C. 1994. AIC model selection in overdispersed capture–recapture data. *Ecology* **75**, 1780–1793.
- Fletcher, D. J. 2012. Estimating overdispersion when fitting a generalized linear model to sparse data. *Biometrika* **99**, 230–237.