Oikos

OIK-06286

Cayuela, H., Cruickshank, S. S., Brandt, H., Ozgul, A. and Schmidt, B. R. 2019. Habitat-driven life history variation in an amphibian metapopulation . – Oikos doi: 10.1111/oik.06286

Appendix 1

Study sites

The kml file can be loaded into the Swiss government map server at <http://map.geo.admin.ch>. Available languages are German, French, Italian and English. Users must select Advanced Tools > Import and then select the kml file ('Coordinates.kml'). Stable sites are marked as red points on the map, and variable sites as black points. It is possible to view aerial imagery, topographical and other information by exploring the layers available on the website.

Pond_numbers.csv provided XY coordinates for each site in the study, and lists the number of ponds present at each site. There are a number of sites (e.g. HOP) in which most or all individuals were captures in very temporary waterbodies (e.g. puddles) around the site, rather than the ponds themselves.

Table A1. Number of individuals captured at each capture sessions over the 5-years period in the stable and variable sites.

	2011			2012		2013				2014				2015			
Site	S1	S2	S3	S4	S5	S6	S7	S8	S9	S10	S11	S12	S13	S14	S15	S16	S17
Stable	237	284	372	240	222	17	158	218	227	162	531	572	657	493	612	558	450
Variable	8	2	2	15	16	11	83	33	32	65	41	66	34	147	9	62	106

Model implementation in E-SURGE

We provide an example of implementation of survival model in E-SURGE.

First, the matrices of state transitions and events described in the article are introduced in the module GEPAT (matrix editor). Then, we define the model in the module GEMACO. Below, we present the codes used to build a survival model where all the parameters (survival, breeding, and recapture probabilities) are constant:

- For Initial State: IS - Step 1 - (1): to

- For Transition: Survival - Step 1 - (2): from(1:4).t(1 2 4 6 7 8 10 11 12 14 15 16)+[from(1:4).t(3 5 9 13)]
- For Transition: Breeding - Step 2 - (2): from(1:4).t(1 2 4 6 7 8 10 11 12 14 15 16)+from(1:4).t(3 5 9 13)
- For Event: Events - Step 1 - (3): firste+nexte

For survival transitions, we consider that two type of transitions, i.e., intra-annual survival probability and interannual survival probability. The intra-annual survival probability [t(1 2 4 6 7 8 10 11 12 14 15 16)] is fixed at 1 in the IVFV module. For breeding transitions, we consider early breeding probability [t(3 5 9 13)] and late breeding probability [t(1 2 4 6 7 8 10 11 12 14 15 16)].

More information about multievent model implementation in the program E-SURGE can be found in the following tutorial: <www.cefe.cnrs.fr/images/stories/DPTEEvolution/biostatistiques/LOGICIELS/E-SURGE-MANUAL.pdf>.

Table A2. Survival analyses: model selection procedure. We show the 10 best-supported models based on their QAICc rank (the complete selection procedure is provided in Supplementary material Appendix 2). The models include four parameters: φ = survival, Υ_{early} = early skipping breeding probability, Υ_{late} = late skipping breeding probability, p = recapture probability. k = number of model parameters, Deviance = residual deviance, ΔQAICc = difference of QAICc points between the model and the best-supported model.

Model	k	Deviance	ΔQAICc	w
φ(Site), Υ_{early}(Site), Υ_{late}(Site), p(Het+Year+Site)	14	16772.94	0.00	0.57
φ(Site), Υ_{early}(Site), Υ_{late}(Site), p(Het+Year)	13	16775.58	0.63	0.42
φ(.), Υ_{early}(Site), Υ_{late}(Site), p(Het+Year+Site)	13	16783.35	8.40	0.01
φ(Site), Υ_{early}(.), Υ_{late}(.), p(Het+Year+Site)	13	16786.71	11.76	0.00
φ(.), Υ_{early}(Site), Υ_{late}(Site), p(Het+Year)	12	16790.66	13.70	0.00
φ(Site), Υ_{early}(.), Υ_{late}(.), p(Het+Year)	12	16791.41	14.45	0.00
φ(.), Υ_{early}(.), Υ_{late}(.), p(Het+Year)	11	16797.80	18.83	0.00
φ(.), Υ_{early}(.), Υ_{late}(.), p(Het+Year+Site)	12	16797.70	20.74	0.00
φ(Site), Υ_{early}(Site), Υ_{late}(Site), p(Year+Site)	12	17041.53	264.57	0.00
φ(.), Υ_{early}(Site), Υ_{late}(Site), p(Year+Site)	11	17060.77	281.80	0.00
φ(Site), Υ_{early}(Site), Υ_{late}(Site), p(Year)	11	17098.45	319.48	0.00
φ(Site), Υ_{early}(.), Υ_{late}(.), p(Year+Site)	11	17100.00	321.04	0.00

φ(.), Υ_{early}(Site), Υ_{late}(Site), p(Year)	10	17116.59	335.61	0.00
φ(.), Υ_{early}(.), Υ_{late}(.), p(Year+Site)	10	17117.32	336.35	0.00
φ(Site), Υ_{early}(Site), Υ_{late}(Site), p(Het+Site)	10	17118.98	338.01	0.00
φ(Site), Υ_{early}(.), Υ_{late}(.), p(Year)	9	17121.57	338.59	0.00
φ(.), Υ_{early}(.), Υ_{late}(.), p(Year)	8	17127.19	342.21	0.00
φ(Site), Υ_{early}(.), Υ_{late}(.), p(Het+Site)	9	17148.90	365.92	0.00
φ(.), Υ_{early}(Site), Υ_{late}(Site), p(Het+Site)	9	17150.49	367.51	0.00
φ(Site), Υ_{early}(Site), Υ_{late}(Site), p(Het)	9	17153.43	370.45	0.00
φ(.), Υ_{early}(Site), Υ_{late}(Site), p(Het)	8	17158.06	373.08	0.00
φ(Site), Υ_{early}(.), Υ_{late}(.), p(Het)	7	17171.05	384.06	0.00
φ(.), Υ_{early}(.), Υ_{late}(.), p(Het+Site)	8	17183.53	398.55	0.00
φ(.), Υ_{early}(.), Υ_{late}(.), p(Het)	6	17188.89	399.90	0.00
φ(Site), Υ_{early}(Site), Υ_{late}(Site), p(Site)	7	17441.48	654.49	0.00
φ(.), Υ_{early}(Site). Υ_{late}(Site), p(Site)	6	17466.48	677.49	0.00
φ(Site), Υ_{early}(.), Υ_{late}(.), p(Site)	6	17466.74	677.75	0.00
φ(Site), Υ_{early}(Site), Υ_{late}(Site), p(.)	6	17467.99	679.00	0.00
φ(Site), Υ_{early}(.), Υ_{late}(.), p(.)	5	17492.62	701.62	0.00
φ(.), Υ_{early}(.), Υ_{late}(.), p(.)	5	17494.33	703.34	0.00
φ(.), Υ_{early}(.), Υ_{late}(.), p(Site)	6	17493.62	704.62	0.00
φ(.), Υ_{early}(Site), Υ_{late}(Site), p(.)	6	17495.92	706.93	0.00

Table A3. Recruitment analyses: model selection procedure. We show the 10 best-supported models based on their QAICc rank (the complete selection procedure is provided in Supplementary material 2). The models include four parameters: ψ = recruitment, Υ_{early} = early skipping breeding probability, Υ_{late} = late skipping breeding probability, p = recapture probability. k = number of model parameters, Deviance = residual deviance, ΔQAICc = difference of QAICc points between the model and the best-supported model.

Model	k	Deviance	ΔQAICc	w
ψ(Site), Υ_{early}(Site), Υ_{late}(Site), p(Het+Year+Site)	14	18098.58	0.00	0.89
ψ(.), Υ_{early}(Site), Υ_{late}(Site), p(Het+Year+Site)	13	18104.85	4.25	0.11
ψ(.), Υ_{early}(Site), Υ_{late}(Site), p(Het+Year)	12	18113.02	10.42	0.00
ψ(Site), Υ_{early}(Site), Υ_{late}(Site), p(Het+Year)	13	18112.79	12.20	0.00
ψ(.), Υ_{early}(.), Υ_{late}(.), p(Het+Year+Site)	12	18139.94	37.34	0.00

ψ(Site), γ_{early}(.), γ_{late}(.), p(Het+Year+Site)	13	18138.16	37.57	0.00
ψ(Site), γ_{early}(.), γ_{late}(.), p(Het+Year)	12	18157.17	54.57	0.00
ψ(.), γ_{early}(.), γ_{late}(.), p(Het+Year)	11	18161.29	56.68	0.00
ψ(Site), γ_{early}(Site), γ_{late}(Site), p(Year+Site)	12	18258.68	156.08	0.00
ψ(.), γ_{early}(Site), γ_{late}(Site), p(Year+Site)	11	18265.83	161.23	0.00
ψ(.), γ_{early}(Site), γ_{late}(Site), p(Year)	10	18298.20	191.58	0.00
ψ(Site), γ_{early}(Site), γ_{late}(Site), p(Year)	11	18298.09	193.48	0.00
ψ(.), γ_{early}(.), γ_{late}(.), p(Year+Site)	10	18325.61	218.99	0.00
ψ(Site), γ_{early}(.), γ_{late}(.), p(Year+Site)	11	18325.38	220.77	0.00
ψ(Site), γ_{early}(.), γ_{late}(.), p(Year)	9	18340.46	231.84	0.00
ψ(.), γ_{early}(.), γ_{late}(.), p(Year)	8	18346.66	236.04	0.00
ψ(.), γ_{early}(Site), γ_{late}(Site), p(Het)	8	18983.98	873.35	0.00
ψ(Site), γ_{early}(Site), γ_{late}(Site), p(Het)	9	18983.66	875.04	0.00
ψ(.), γ_{early}(Site), γ_{late}(Site), p(Het+Site)	9	18983.71	875.09	0.00
ψ(.), γ_{early}(.), γ_{late}(.), p(Het+Site)	8	18986.33	875.71	0.00
ψ(.), γ_{early}(.), γ_{late}(.), p(Het)	8	18986.33	875.71	0.00
ψ(Site), γ_{early}(Site), γ_{late}(Site), p(Het+Site)	10	18983.54	876.93	0.00
ψ(Site), γ_{early}(.), γ_{late}(.), p(Het+Site)	9	18986.32	877.70	0.00
ψ(Site), γ_{early}(.), γ_{late}(.), p(Het)	9	18986.32	877.70	0.00
ψ(.), γ_{early}(Site), γ_{late}(Site), p(.)	6	19128.23	1013.60	0.00
ψ(.), γ_{early}(Site), γ_{late}(Site), p(Site)	6	19128.23	1013.60	0.00
ψ(.), γ_{early}(.), γ_{late}(.), p(Site)	5	19130.59	1013.96	0.00
ψ(Site), γ_{early}(Site), γ_{late}(Site), p(Site)	7	19127.87	1015.25	0.00
ψ(Site), γ_{early}(Site), γ_{late}(Site), p(.)	7	19127.87	1015.25	0.00
ψ(Site), γ_{early}(.), γ_{late}(.), p(Site)	6	19130.43	1015.80	0.00
ψ(Site), γ_{early}(.), γ_{late}(.), p(.)	5	19144.18	1027.54	0.00
ψ(.), γ_{early}(.), γ_{late}(.), p(.)	4	19151.04	1032.40	0.00

Table A4. Goodness-of-fit tests (GOF) performed in U-CARE program.

Test	df	Quadratic χ^2	p-level
Global test	152	597.99	<0.0001
Overall test 3SR	15	142.85	<0.0001
Overall test 3SM	55	78.74	0.02
Overall test 2CT	14	218.49	<0.0001
Overall test 2CI	68	157.92	<0.0001

Table A5. Jeyam's test for recapture heterogeneity. For more information about this test see Jeyam et al. (2018).

Occasion	Gamma	var(B&B)	test-stat(B&B)	pval (B&B)	n
3	-0.24	0.03	-1.41	0.921	75
4	0.07	0.012	0.644	0.26	158
5	0.12	0.009	1.264	0.103	224
6	0.23	0.005	3.198	0.001	297
7	0.25	0.004	3.8	<0.001	333
8	0.29	0.004	4.724	<0.001	333
9	0.23	0.003	4.133	<0.001	382
10	0.28	0.003	5.267	<0.001	402
11	0.2	0.003	3.786	<0.001	362
12	0.23	0.003	4.089	<0.001	304
13	0.18	0.004	2.811	0.002	235
14	0.13	0.007	1.647	0.05	192
Global	0.22	0.002	5.081	<0.001	651

Jeyam, A. et al. 2018. A test of positive association for detecting heterogeneity in capture for capture–recapture data. – J. Agric. Biol. Environ. Stat. 23: 1–19.

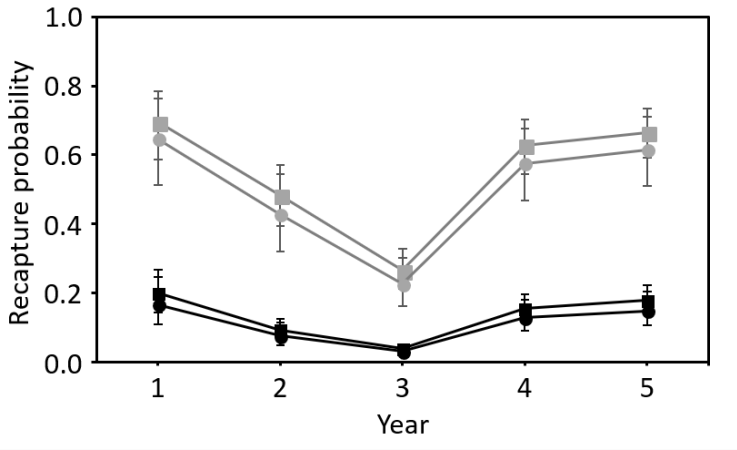

Figure A1. Model-averaged recapture probabilities extracted from survival models. The recapture probabilities estimated for the heterogeneity mixture 1 are shown in black, for heterogeneity mixture 2 in grey. The recapture probabilities in predictable sites are shown as squares, in unpredictable sites as circles.