

Mark-recapture

Growth

We used the R package `fishmethods` (Nelson, 2018), which uses the methods of Hampton (1991) to estimate von Bertalanffy growth curves. Using our mark-recapture data, including both genetic and tagged recaptures, we broke each recapture history into recapture pairs (so a fish caught 4 times has 3 pairs of captures).

Notes from reading (Hampton, 1991):

- Many of our recapture pairs are from the same fish (say it was captured 4 times, that's 3 recapture pairs) so the individually-variable L_∞ (estimated by the Kirkwood and Somers model and the Sainsbury model) and K (estimated by the Sainsbury model) are going to be off because recaptures of the same fish will have the same L_∞ and K , which isn't captured by the model.
- We definitely have release length measurement error but unlike the tuna data he uses, we also have recapture length measurement error. Maybe there's a way to make that random variable they add to be the release length measurement error handle both at the same time?

Fitting notes from running `fishmethods`

When I run `growhamp` with all the models fit as default and leaving the starting parameters as Michelle had them, there are 22 warnings that come up about NaNs produced, which I think would occur if growth was infinite (like no time between recaptures). There aren't any zero-days in the data set, though, so I'm exploring a bit more to make sure I'm fitting things sensically (without spending tons of time on this and having to write my own stuff).

- Fit all models with the same starting values as Michelle used but only one pair of recapture values per fish (chosen randomly for fish caught >2 times) - still get some error messages (In `log(2 * pi * parms[3])` : NaNs produced)

- Fit all models with same starting values as Michelle used but only pairs caught more than one month apart
- Fit all models with same starting values as Michelle used but only pairs caught more than one month apart and only one pair of recapture values per fish
- Comparing those three above, definitely get some differences in estimates, both in Linf and K estimates and in error - Kirkwood and Somers model with model error seems particularly off/different than the rest. Also still get some error messages about NaNs.

```
> grow_base$results
```

	Model	Linf	K	s2Linf	s2K	s2error	boundary	-Log Likelihood	AIC	method
1	Faber	10.63846	0.8667696	NA	NA	0.539579526	0	844.9446	1695.889	Nelder-Mead
2	Kirkwood and Somers	9.34346	29.1463900	1.7150454	NA	NA	0	1244.5842	2495.168	Nelder-Mead
3	Kirkwood and Somers with ME	23.09452	0.1104505	146.9153464	NA	0.149534352	0	1084.9119	2177.824	Nelder-Mead
4	Kirkwood and Somers with ME & RLE	23.09452	0.1104505	146.9153464	NA	0.149534352	0	1084.9119	2177.824	Nelder-Mead
5	Sainsbury	10.12533	21.7886552	0.7174711	1925.15064	NA	0	1010.5916	2029.183	Nelder-Mead
6	Sainsbury with ME	15.22239	0.6799133	94.8754459	79.66388	0.003545803	0	1390.8068	2791.614	Nelder-Mead
7	Sainsbury with ME & RLE	15.22239	0.6799133	94.8754459	79.66388	0.003545803	0	1390.8068	2791.614	Nelder-Mead

Figure 1: The base model, without making changes to data inputs or starting values.

```
> grow_1pair$results
```

	Model	Linf	K	s2Linf	s2K	s2error	boundary	-Log Likelihood	AIC	method
1	Faber	10.612935	0.9056469	NA	NA	0.57620517	0	573.9711	1153.942	Nelder-Mead
2	Kirkwood and Somers	9.251121	5.5774347	1.9066243	NA	NA	0	750.1112	1506.222	Nelder-Mead
3	Kirkwood and Somers with ME	24.048165	0.1135008	150.7639014	NA	0.12783048	0	737.5069	1483.014	Nelder-Mead
4	Kirkwood and Somers with ME & RLE	24.048165	0.1135008	150.7639014	NA	0.12783048	0	737.5069	1483.014	Nelder-Mead
5	Sainsbury	9.899764	7.2404918	0.9249544	93.79703	NA	0	660.7630	1329.526	Nelder-Mead
6	Sainsbury with ME	19.806942	0.8260985	-54.0380738	72.61079	-0.01555624	0	849.4910	1708.982	Nelder-Mead
7	Sainsbury with ME & RLE	19.806942	0.8260985	-54.0380738	72.61079	-0.01555624	0	849.4910	1708.982	Nelder-Mead

```
> grow_1month$results
```

	Model	Linf	K	s2Linf	s2K	s2error	boundary	-Log Likelihood	AIC	method
1	Faber	10.63941	0.8673571	NA	NA	0.6285317	0	733.4301	1472.860	Nelder-Mead
2	Kirkwood and Somers	10.30386	1.0588206	2.076469	NA	NA	0	809.7573	1625.515	Nelder-Mead
3	Kirkwood and Somers with ME	23.30473	0.1095641	150.406830	NA	0.1382206	0	1015.2120	2038.424	Nelder-Mead
4	Kirkwood and Somers with ME & RLE	23.30473	0.1095641	150.406830	NA	0.1382206	0	1015.2120	2038.424	Nelder-Mead
5	Sainsbury	10.33760	1.3964490	1.077584	0.8766613	NA	0	780.9984	1569.997	Nelder-Mead
6	Sainsbury with ME	16.67551	1.6879458	-12.473849	266.5485934	-0.2806502	0	1071.0219	2152.044	Nelder-Mead
7	Sainsbury with ME & RLE	16.67551	1.6879458	-12.473849	266.5485934	-0.2806502	0	1071.0219	2152.044	Nelder-Mead

```
> grow_1pair1month$results
```

	Model	Linf	K	s2Linf	s2K	s2error	boundary	-Log Likelihood	AIC	method
1	Faber	10.61616	0.9055843	NA	NA	0.67609913	0	503.9317	1013.863	Nelder-Mead
2	Kirkwood and Somers	10.29667	1.1038684	2.0171857	NA	NA	0	556.7488	1119.498	Nelder-Mead
3	Kirkwood and Somers with ME	24.40461	0.1119453	149.8617960	NA	0.18824091	0	702.0420	1412.084	Nelder-Mead
4	Kirkwood and Somers with ME & RLE	24.40461	0.1119453	149.8617960	NA	0.18824091	0	702.0420	1412.084	Nelder-Mead
5	Sainsbury	10.33120	1.2389200	1.1924390	0.513014	NA	0	536.9923	1081.985	Nelder-Mead
6	Sainsbury with ME	10.13040	4.6897947	0.6307548	30.597918	0.04884122	0	562.7657	1135.531	Nelder-Mead
7	Sainsbury with ME & RLE	10.13040	4.6897947	0.6307548	30.597918	0.04884122	0	562.7657	1135.531	Nelder-Mead

Figure 2: Run results with different data inputs, comparing model fit.

```

> grow_1pair1month_startvals$results

```

	Model	Linf	K	s2Linf	s2K	s2error	boundary	-Log Likelihood	AIC	method
1	Faber	10.61544	0.9058238	NA	NA	0.6758966	0	503.9317	1013.863	Nelder-Mead
2	Kirkwood and Somers	10.29685	1.1038331	2.01653354	NA	NA	0	556.7488	1119.498	Nelder-Mead
3	Kirkwood and Somers with ME	10.61616	0.9120830	1.10584594	NA	0.2573303	0	500.0579	1008.116	Nelder-Mead
4	Kirkwood and Somers with ME & RLE	10.61616	0.9120830	1.10584594	NA	0.2573303	0	500.0579	1008.116	Nelder-Mead
5	Sainsbury	10.34768	1.3438829	1.08997940	0.64538457	NA	0	535.9138	1079.828	Nelder-Mead
6	Sainsbury with ME	14.67344	0.2597715	-0.05757859	0.03652736	0.2163503	0	601.0766	1212.153	Nelder-Mead
7	Sainsbury with ME & RLE	14.67344	0.2597715	-0.05757859	0.03652736	0.2163503	0	601.0766	1212.153	Nelder-Mead

Figure 3: Changing the start values for model error and Linf error.

Survival - mark-recapture

Data inputs and model set-up

We have two ways of tagging a fish - genetic identification from fin-clips and scans of PIT tags. Generally, fish are only clipped if they do not have a tag (which includes not being of taggable size).

Data sets to consider:

- all recaptures, genetic + tag, including only certain genetic recaptures (so no site-changing fish, even if lab work doesn't signal error potential)
- all recaptures, genetic + tag, including uncertain genetic recaptures too (which can be found by searching "genetic recapture" in the notes section, will give the gen_id that might match)
- just recaptures based on tags, incorporated estimated tag loss (do I really need to do this one?)

Cleaning and preparing data

- Adding distance covariate: To account for uneven sampling across years, since we dive slightly different routes and haven't always covered all sections of each site, we include a time-varying covariate that is the minimum distance we surveyed from the anemone where the fish was first caught and marked. We can calculate this easily for all fish after they are first marked, even if we don't catch them, by finding the closest point on the GPS tracks to the anemone where we first caught them.
- Adding size covariate: To include sizes for fish at all recapture points, we used the growth curve to estimate sizes for fish not captured or fish with missing capture years. We took the size at which they were previously captured and used the growth curve to project their size at the next sampling time point(s).

Tips and notes on MARK

- p.35/62 of Chapter 11 of MARK book (file name: chap11.pdf): Don't standardize individual covariates (that vary with time) - "standardizing them will cause them to no longer relate to one another on the same scale", so things like common slope parameter won't make sense. If you must standardize, do so before putting the values into an encounter histories input file and make sure all the values are included and standardized together so they share a common mean and standard error.
- p.49/62 of Chapter 11 of MARK book (chap11.pdf): model averaging with models with individual covariates: "Mechanically, what you would need to do, if doing it by hand, is take the reconstituted values of φ for each model, for a given value of the covariate, then average them using the AIC weights as weighting factors (for models without the covariate, the β for the covariate is, in fact, 0." - still have the issue of calculating standard errors, though...

Mark-recapture models

List of models to consider:

- survival constant, recapture constant (eall_mean.Phi.dot.p.dot)
- survival constant, recapture time (eall_mean.Phi.dot.p.time)
- survival time, recapture constant (eall_mean.Phi.time.p.dot)
- survival constant, recapture distance (eall_mean.Phi.dot.p.dist)
- survival size, recapture size (eall_mean.Phi.size.p.size)
- survival size, recapture distance (eall_mean.Phi.size.p.dist)
- survival constant, recapture size + distance (eall_mean.Phi.dot.p.size.plus.dist)
- survival size, recapture size + distance (eall_mean.Phi.size.p.size.plus.dist)
- survival capture stage, recapture size + distance (eall_mean.Phi.stage.p.size.plus.dist)
- survival capture stage, recapture constant (eall_mean.Phi.stage.p.dot)
- survival site, recapture constant (eall_mean.Phi.site.p.dot)
- survival site, recapture size + distance (eall_mean.Phi.site.p.size.plus.dist)

Model results and output

Here are the relative AICs of the models considered, first with all twelve models shown, and second without the models that have site or capture stage as factors.

```
> model_comp
```

	model	AIC	dAIC
1	eall_mean.Phi.size.p.size.plus.dist	2936.787	0.0000
2	eall_mean.Phi.size.p.size	3126.137	-189.3498
3	eall_mean.Phi.stage.p.size.plus.dist	3147.756	-210.9686
4	eall_mean.Phi.dot.p.size.plus.dist	3229.024	-292.2371
5	eall_mean.Phi.size.p.dist	3364.830	-428.0426
6	eall_mean.Phi.dot.p.dist	3384.531	-447.7439
7	eall_mean.Phi.time.p.dot	3408.342	-471.5553
8	eall_mean.Phi.site.p.dot	3440.842	-504.0548
9	eall_mean.Phi.site.p.size.plus.dist	3440.842	-504.0548
10	eall_mean.Phi.dot.p.time	3453.609	-516.8220
11	eall_mean.Phi.stage.p.dot	3564.241	-627.4536
12	eall_mean.Phi.dot.p.dot	3570.908	-634.1206

Figure 4: Comparing AICc among models fit with different factors and covariates.

```

> model_comp

```

	model	AIC	dAIC
1	eall_mean.Phi.size.p.size.plus.dist	2936.787	0.0000
2	eall_mean.Phi.size.p.size	3126.137	-189.3498
3	eall_mean.Phi.dot.p.size.plus.dist	3229.024	-292.2371
4	eall_mean.Phi.size.p.dist	3364.830	-428.0426
5	eall_mean.Phi.dot.p.dist	3384.531	-447.7439
6	eall_mean.Phi.time.p.dot	3408.342	-471.5553
7	eall_mean.Phi.dot.p.time	3453.609	-516.8220
8	eall_mean.Phi.dot.p.dot	3570.908	-634.1206

```

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```

Figure 5: Comparing AICc among models fit with different factors and covariates, without site or capture stage considered.

Estimating recruitment

Estimating egg-recruit survival

LEP (or LRP)

To-do

Growth

MARK

- Re-run MARK runs with 0 instead of mean distance in each year for the distances to anems before the first capture of a fish

LEP calc

Other

References

- John Hampton. Estimation of southern bluefin tuna *thunnus maccoyii* growth parameters from tagging data, using von bertalanffy models incorporating individual variation. *Fishery Bulletin*, 89:577–590, 1991.
- Gary A. Nelson. *fishmethods: Fishery Science Methods and Models*, 2018. URL <https://CRAN.R-project.org/package=fishmethods>. R package version 1.11-0.