



Spatial CKMR: an introduction



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O&A
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Spatial CKMR is easy!

... from a lofty-enough viewpoint...

Non-spatial version:

$$\begin{aligned} & \mathbb{P} [\text{Amy is Julian's mum} | \text{stuff about A \& J}] \\ = & \mathbb{E} \left[\frac{\#A's \text{ J-like offspring (when J born)}}{\text{Total \# J-like offs (when J born)}} | \text{covariates of A, J} \right] \end{aligned}$$

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Spatial version:

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Spatial CKMR: discussion points

- * Will “spatial” really matter ?
- * Checking from real data
- * Assignable ie genetically distinct source popns
- * Theory
- * Cryptic subpops don't matter
- * Even if a cline / ill-mixing, then...
- * Discrete spawning sites
- * Continuous case(s)?

Real examples

Thornbacks - BoB

G. glyphis - NT

(Eastern ABTuna)

(Bearded Seals: PConn)

What is “well-mixed”?

If there are different spawning sites within **one population***

... and adults show **fidelity to one site**

... regardless of whether that fidelity is heritable

... then it matters to CKMR.

* IE no genetic assignment is possible



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A sample (of adults and of juves) are **well-mixed** if it is drawn from the different spawning-site-groups in proportion to their true abundance.

< E-ABFT (counter)examples >

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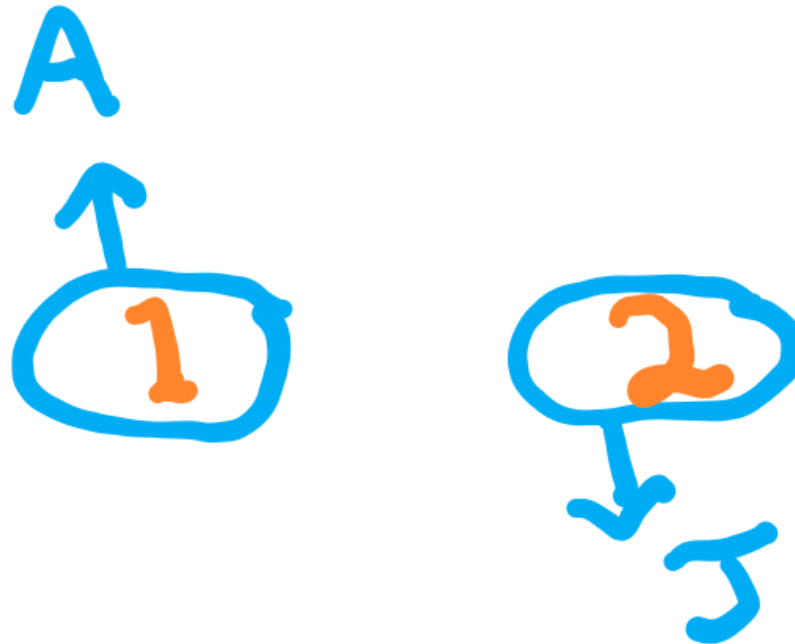
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A sample (of adults and of juves) are **well-mixed** if it is drawn from the different spawning-site-groups in proportion to their true abundance.

If juves **and** adult samples are both well-mixed, then any fidelity is **irrelevant** and all the beautiful results from just now apply!

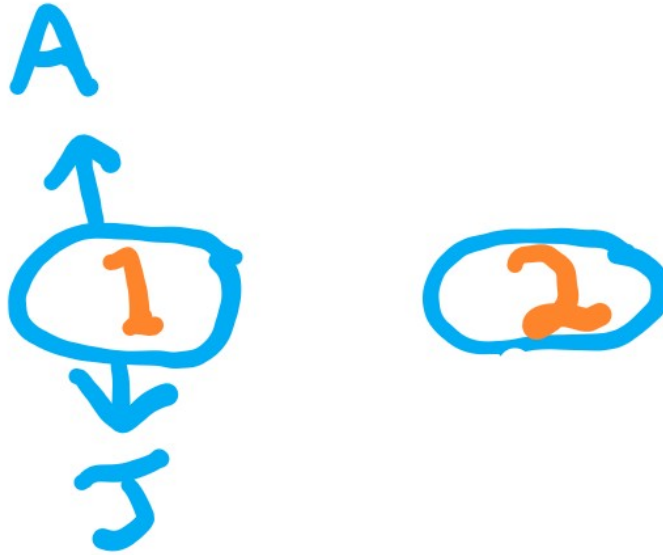
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Hypothetical bad mixing: #1



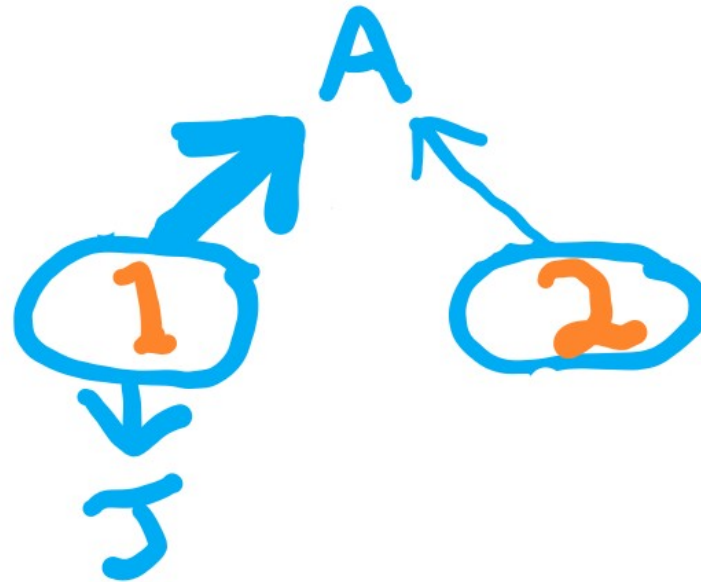
no POPs: “abundance must be HUGE” \times
at least the HSPs will *tell* you it’s wrong!

Hypothetical bad mixing: #2



Estimates only apply to LH stock
total catches to both
no M
no internal signal

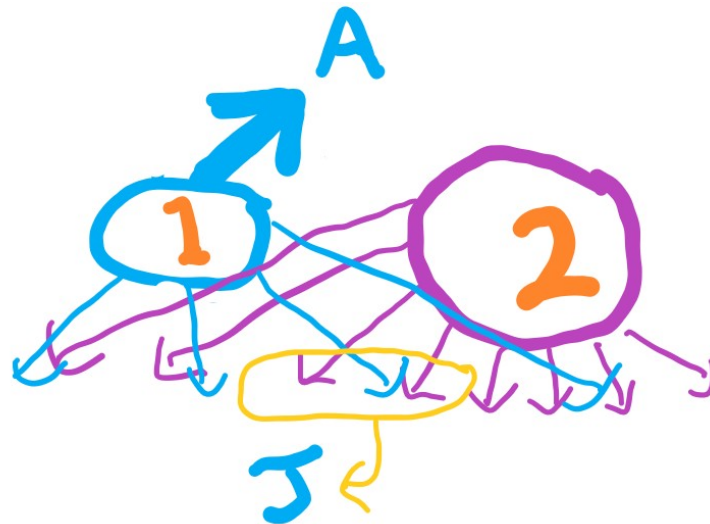
Hypothetical bad mixing: #3



Biased estimate of TRO if you don't realize
or no trustworthy estimate if you do realize *and* you're honest about it

Innumerable more-complicated scenarios can be devised...

Not-so-bad mixing: #4



Both stocks contribute to Juve samps, proportional to (adult) N

Adult samps come only from stock 1

Things pretty much work OK !

What if only juves (or only adults) Well-Mixed?

TRO, Fec@A: **still OK**

If *juves* WM but *adults* not: probably doesn't matter

If *adults* WM but *juves* not:

What if only juves (or only adults) Well-Mixed?

TRO, Fec@A: **still OK**

If *juves* WM but *adults* not: may not matter except for C,M

If *adults* WM but *juves* not:

\bar{A} : not OK. Which means...

Z : not as good and specific to adults from site sampled

M: not as good not at all, unless C can be split

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NB If juves sampled in 2 places, **only one place** need be **well-mixed...**
and the YHS (later-born) can even be **an adult**

Very important details !

What is “well-mixed”?

Usual advice for CKMR when incomplete mixing is plausible:

“Spread sampling spatially,
so you’ll at least detect any,
and if so can possibly model it away”

Doesn’t necessarily apply neatly to EABFT (discrete sites) but don’t put all your eggs in one sampling basket unless you’re sure it’s a *well-mixed* basket. (for at least one of adults / juves)

If neither juves nor adults is well-mixed?

Things get dicey...

Fec@A probably OK

TRO not OK

... unless you can e.g. split by site and cover all main sites

Z not as good and applies only to adults from that juvenile site

May depend on whether sampling can be split by site, vs lumped

Maybe more options than you think (eg adults as Offspring too)

**Mixing may not have to be *perfect*
for CKMR to still give *useful*
albeit *provisional* results.**

**As long as you *eventually* get enough
well-mixed ones, you can check assumptions.**