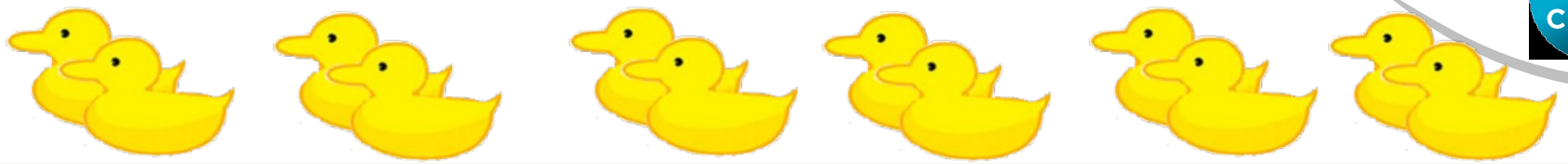
Design for CKMR

Mark Bravington, CSIRO: June 2021

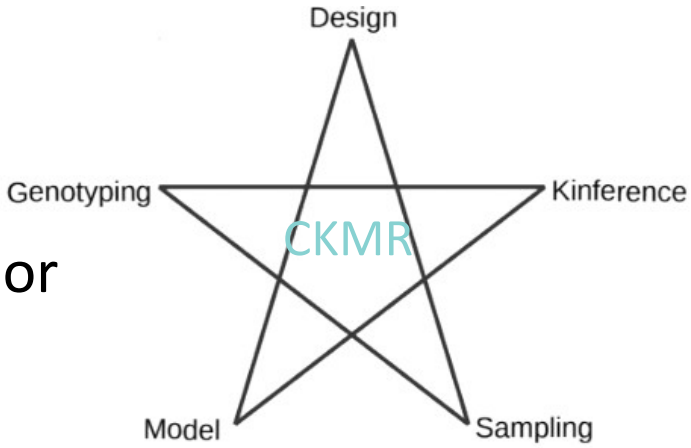


Design in CKMR

If You...

- do not collect *enough* samples, or
- do not collect the right *types* of sample, or
- do not measure their stuff adequately

... **then** CKMR will **fail**



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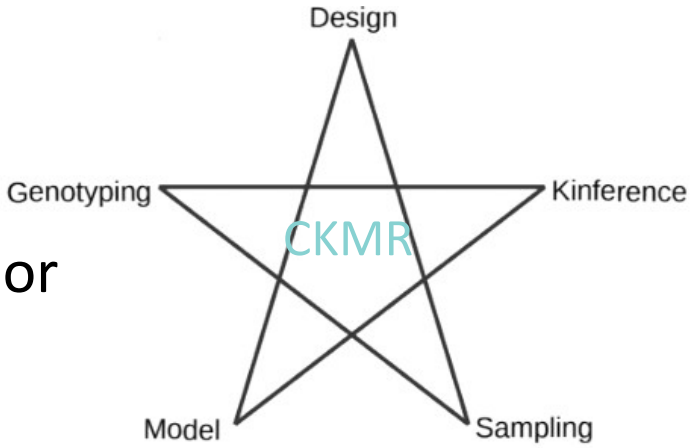

"*enough samples*" really means "enough kin-pairs" ...

Can't control latter, but can plan former and types, and stuff

via... **DESIGN**

Levels of design

0. Qualitative considerations..?
1. Aim for at least XXX kin-pairs
    - by calculating E[total POPs] & E[total HSPs]

    (the laugh test)
2. Variance straight from model code
3. Inverse design
4. Optimal design
5. “Long CKMR”
6. Role of simulation

Design: qualitative sampling needs

What I reckon... for *Fish*

1. POPs **&** HSPs

   ie ads & "juves"

   how old can a "juve" be?

2. Accurate-enuf juve age
3. Ads: age or length both is best

   and sex, of course

4. Full size range of ads
5. Reasonable # juve cohorts
6. Adequate spatial coverage

   to allow for checks; a priori important

What I reckon... for *Mammals*

1. Are you sure?
2. Fish version is best
3. At a pinch, "juve" HSPs only

   or even POPs only-- less likely ?

4. Accurate-enuf juve age
5. Plenty of juve cohorts

   NB eg skip-spawning

6. Adequate spatial coverage

Design: beyond the qualitative

IJAD

KISS

FFS

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It’s Just A Design...

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Design: beyond the qualitative

IJAD — It's Just A Design...

KISS — Keep It Simple, Stupid!

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Design: beyond the qualitative

IJAD	It's Just A Design...
KISS	Keep It Simple, Stupid!
FFS	Fast and Fairly Simple

CKMR design: the rock-bottom line

- For a precise estimate*, must find a fair number of kin-pairs
- $\mathbb{P}\left[K_{ij} \neq \mathrm{UP}\right] \sim \bar{N}_{\mathrm{adult}}^{-1}$
- $\hat{\bar{N}}_{\mathrm{adult}} \propto (\#\mathrm{POPs\ and/or\ HSPs})^{-1}$

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- Group "alike" comparisons (same z, z')

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Wanna get 50–100

- Group "alike" comparisons (same z, z')

Each comp has prob ~O(1/*N*)

m samples, so ~m^2 comps

... so m^2 * “const” / *N* = 50–100

... so *m* = “const (a different one)” * sqrt(*N*)

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$$\mathbb{E}\left[\#\mathrm{POPs}|\theta_0\right] = \sum_{z,z'} c_{zz'} \times (m_z m_{z'}) \times p_{\mathrm{POP}zz'}(\theta_0)$$

usually 1

guess at demographic params

comps of this "type"

this kinship prob

CKMR design: the rock-bottom line

"*If we sample X of these and Y of those--- will we get enuf kin?*"

Software `microscoping::ckmr_laugh_test` for stock-assessed

It's rough--- but it's ready.

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"PASSING THE LAUGH TEST" IS NOT "DOING A DESIGN"

CKMR design: total Exp[Kin] is not enough

Even if you get lots of kin-pairs, does not guarantee good CV

- depends on covars
- and measuring stuff adequately!

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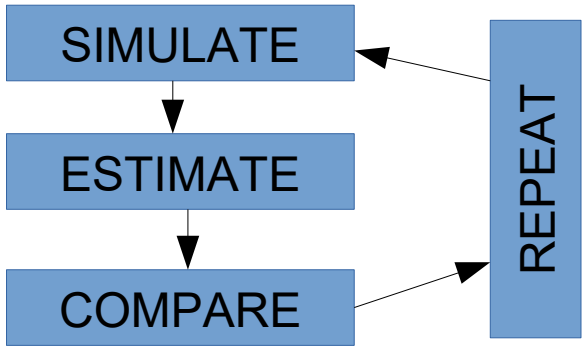
- To *properly* evaluate a design: choose a *goal* $g(\theta)$ e.g. trend in biomass
  - check that sample sizes $\{m_{z \in \mathcal{Z}}\}$ will give low enough $\mathbb{V}\left[g(\hat{\theta})\right]$

"Generic" process for evaluation:



That's a **lot** of work !!

CKMR design: an easier way

- Big populations, sparse sampling: pairwise comps independent
- Each pair comp is Poisson: expected Fisher Info is

$$H\left(z,z'\right)=4\left[\frac{d\sqrt{p_{zz'}}}{d\theta}\right]\left[\frac{d\sqrt{p_{zz'}}}{d\theta}\right]^{\top}$$

$$H=H_0+\sum_{z,z'}m_z m_{z'}H\left(z,z'\right)$$

$$\mathbb{V}\left[g\left(\hat{\theta}\right)\right]\approx\left[\frac{dg}{d\theta}\right]^{\top}H^{-1}\left[\frac{dg}{d\theta}\right]$$

Quadratic dependence on sample size

Numerical derivatives are OK for *p* and *g*

NO simulation; NO estimation; NO repetition !

Other data: priors into H_0 ; pure multinomials (age samples)

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eg from stock assessment

You **don't** need to simulate* nor to actually *fit* your model;
there's a generic "glue framework" that does the maths

CKMR design: NAtl makos

CKMR design: NAtl makos etc

Q: *But that's just under one scenario about "truth". Shouldn't I explore others?*

A: Arguably, that's not really necessary...

CKMR design: Inverse design

What if *no* prior stock assessment ?

eg SAtl makos; Blue-Eye Trevalla

Optimal design

- Everybody knows: "*don't trust optimal designs*"
- Not always appropriate to try

NEVERTHELESS

- it lets you know when to stop trying
- "CKMR design space" is a big place. Optimal designs are *beacons*
  - ie several optimal designs for different goals
- You learn a lot about where the "information" comes from

Optimal design for CKMR

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$$\mathbb{V}\left[g\left(\hat{\theta}\right)\right] \approx \left[\frac{dg}{d\theta}\right]^{\top} H^{-1}\left[\frac{dg}{d\theta}\right]$$

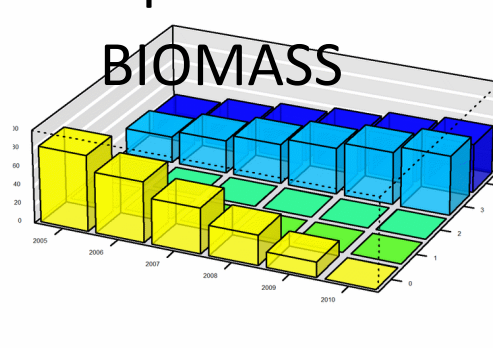
$$V(m) \triangleq \mathbb{V}\left[\hat{g}(\theta)\,|m\right]$$

- *H* is sum of outer products: closed form inverse Sherman-Woodbury
- d*V*/d*m* , d²*V*/d*m*² easily found by Automatic Differentiation
- Cost constraint (or target variance for minimum cost)
- Replace *V*(*m*) by 2nd order approx; solve Quadratic Program; repeat
  - reliable and quick
  - NB *non-convex* QP

Optimal design: example

- "Fish-like": age structure, fecundity depends on age, survival depends on year
- Cross-cohort HSPs with 0-year-olds; POPs (all age classes)
- 10-year trend in abundance, 5 ages (5 fixed effects, 10 random effects)

Opt. for BIOMASS

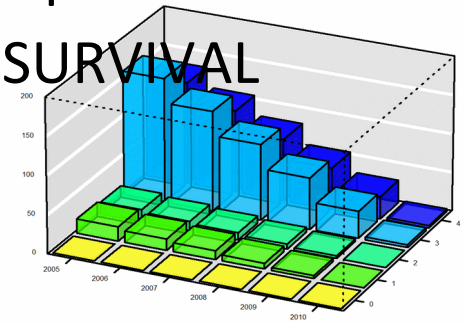


At these two optima :

3X variance (biomass)

2X variance (survival)

Opt. for SURVIVAL



- Optimal design does depend on goal
- Runtime: ~5 seconds

Summary

- CKMR can handle big problems (big population sizes)
  - but you'll need a lot of samples
- *Bare minimum* due diligence: will your design give enough kin-pairs ?
  - need to compute kinship probs based on a guess at parameters
  - maybe `ckmr_laugh_test` will do...
  - or maybe you need to code up your planned lglk. If so, then...
- ... not much extra work to properly evaluate a design
  - just supply a goal function (in R is OK)
- & almost no extra work to consider *optimal* designs

Design in CKMR: niggling concerns laid to rest

Q: I have 1000 samples but 1000*1000/2 comparisons. Are they *really* all independent? Really?

A: Yeah pretty much, prolly.

At least, if yr popn is Big ”sparse sampling”

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Post hoc diagnostic: # triads etc.

Larval sampling? different, tricky; *not* the first resort!

“Long CKMR”

To date, fisheries interest in CKMR has come from The Desperate

- “how on earth can we ground-truth the assessment?”

Then... lots of work to get to that point.

But what happens next?!

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CKMR is easy once you’ve gotten your first “N”
?Use in ongoing MPs?
Needs simulation--- can’t do via nifty variance calcs

Role of simulation in CKMR

MUCH LESS THAN YOU THINK!

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- For MSE, can just simulate "from" the CKMR model:

    `dpois() ---> qpois()`

- OK: everyone is allowed to do *one* sim... if you must...