

Replacing lognormal indices in stock assessments: a first step

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Quick review of indices

- GAP/MACE give us a mean and CV, and we **assume** the distribution is lognormal
- Lognormal indices are ubiquitous
 - Globally in bespoke and generic ones like SS3, WHAM, GADGET, JABBA, MULTIFAN-CTL, CASAL
 - Likely used in all AFSC assessments (T1,3,5)
- Arise from design- or model-based (e.g., VAST) estimators
- Both are sums of positive quantities for smaller areas (strata, spatial cells)

$$I(c, t, l) = \sum_{x=1}^{n_x} (a(s, l) \times d^*(s, c, t))$$

$$\hat{B}_{Tk} = \sum_{i} \hat{B}_{ik}$$

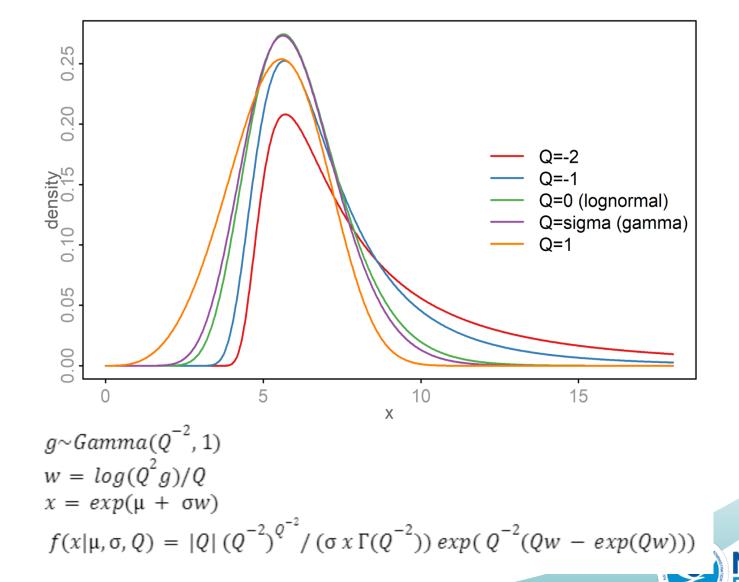
Are lognormal indices justified / does it matter?

- No, lognormal indices have no statistical justification
- Indices are most important data (get the trend right; Francis 2011)
- Our goals are:
 - a. To understand how common non-lognormality is at AFSC
 - b. Find a more appropriate/flexible distribution
 - c. Test implications of replacing the lognormal in assessments
- Enter the generalized gamma distribution (GGD)

Beaulieu (2012); Beaulieu et al. (1995); Dufrense (2004); Romeo et al. (2003), etc.

Basics of the generalized gamma

- Flexible distribution characterized by 3 parameters
 - Mean, variance, skewness (Q)
- Special cases
 - Q=0 lognormal
 - Q=sigma gamma
 - Also Weibull, exponential, halfnormal



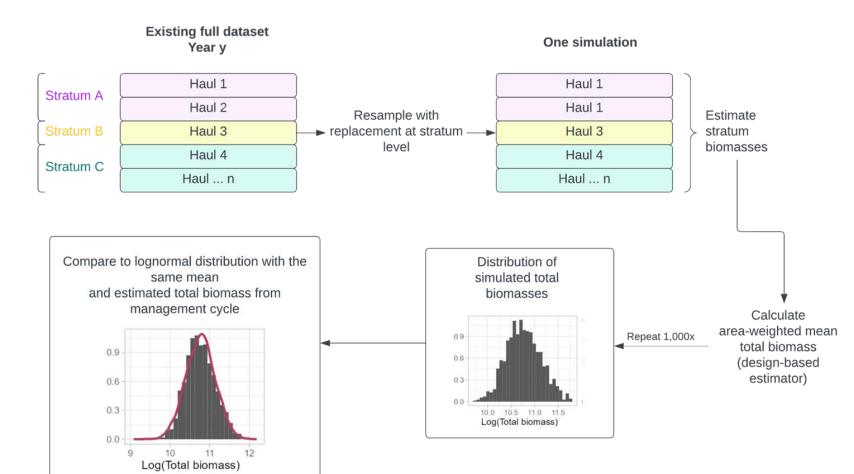
Sums of lognormals are not lognormal

Experiment:

- Simulate draws from 4 normal rvs, X1,...,Xn then let Y=log(e^X1+..+e^Xn)
- Is Y~normal?
- No, it is not, except in very narrow circumstances
- A more flexible generalized gamma distribution (GGD) fits better than a lognormal
- Y is not GGD, but it can better approximate it
- Stats literature very clear that sums of lognormals are not lognormal and in fact have no known analytical form



Design-based bootstrapping procedure



Proposed procedure:

- 1. Simulate samples from the distribution of biomass
- 2. Fit the GGD to those samples to get an estimate for the mean, SD, and Q
- 3. Read those into stock assessment and use GGD pdf in place of lognormal

This is done for each year separately



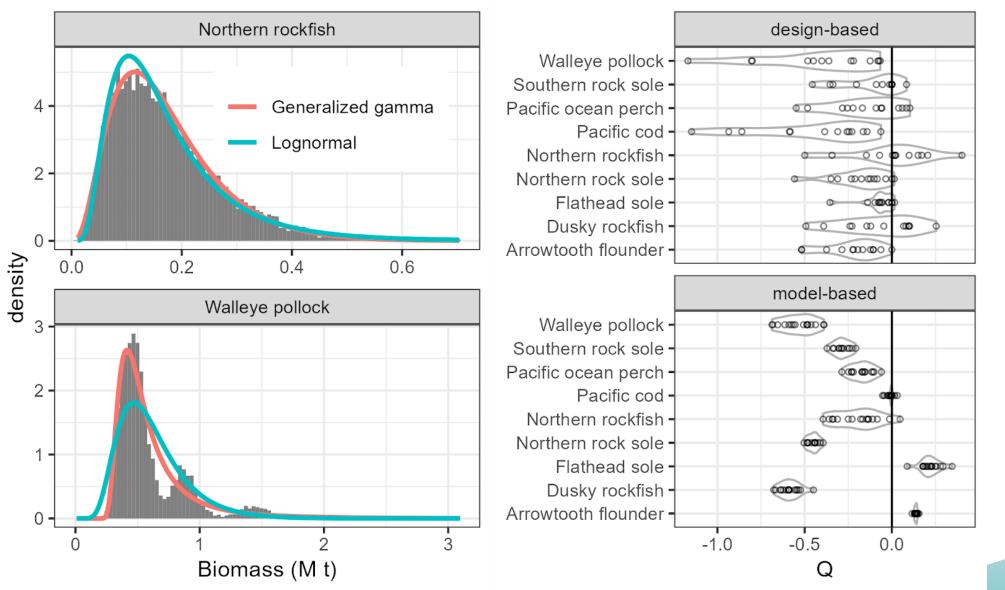
Model-based "bootstrapping" procedure

 VAST estimates biomass B, then uses the delta method to get σ=SE(log(B)), and we then assume N(log(B),σ)

But what is the real distribution of B? Three options to quantify it:

- Data bootstrapping too slow!
- Posterior sampling w/ MCMC too slow!
- Model-based bootstrapping-ish promising!
 - Assume MLE of all parameters is MVN and resample
 - Uses "joint precision matrix" of fixed and random effects
 - Is this valid to do?

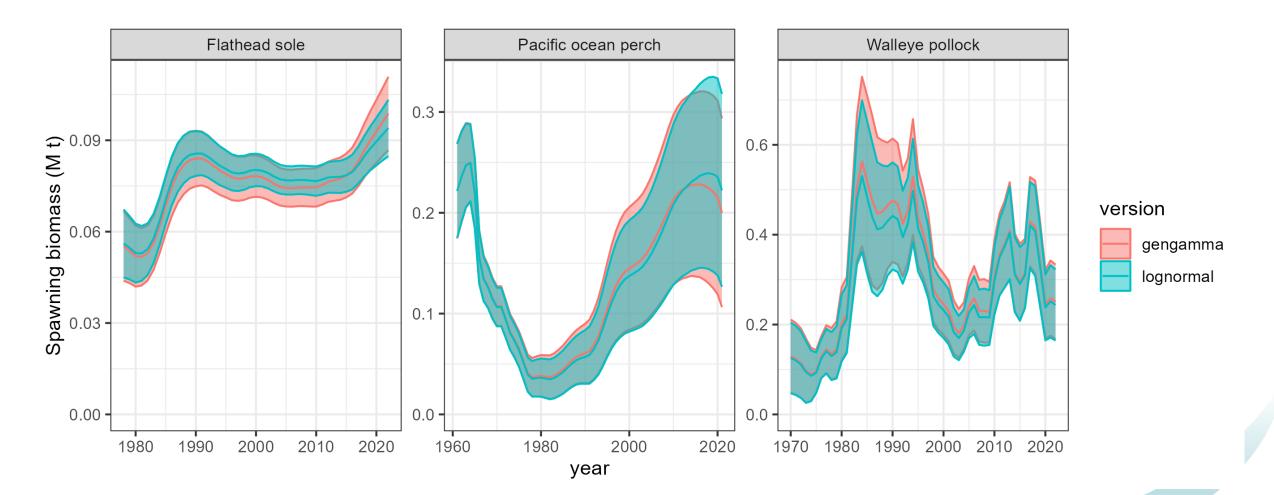
Results of lognormality



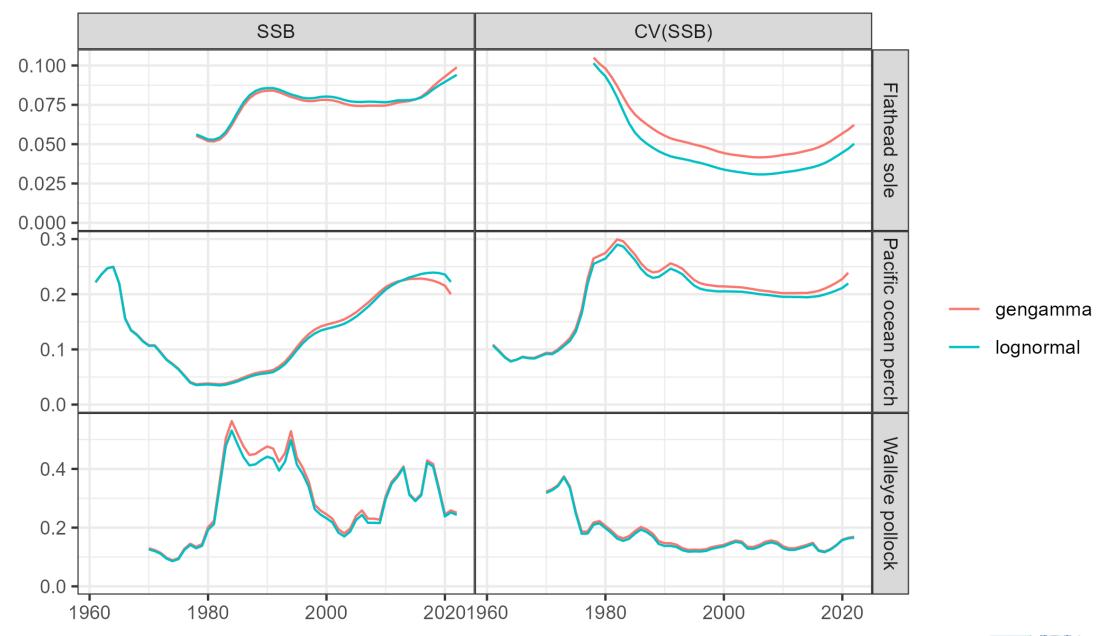
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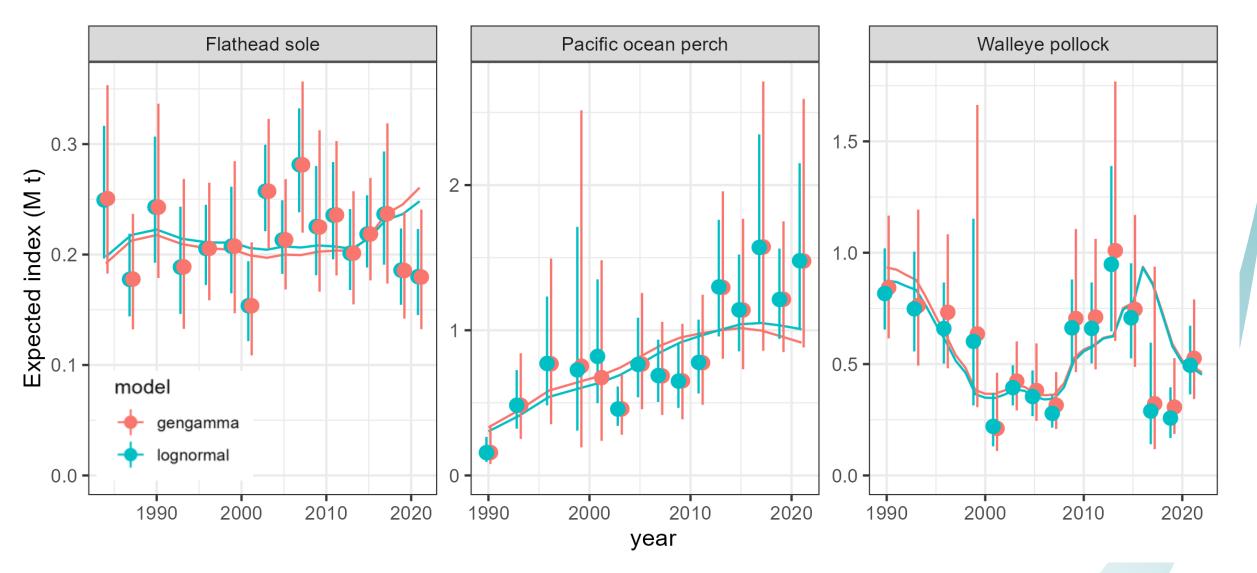
Impact on stock assessments













Implications and recommendations for modelbased estimators

- adding 1 extra parameter (vs. lognormal, gamma, etc.) gains dexterity of fit
- Not too computationally burdensome
- GAP/MACE would have to operationalize and provide GGD estimates to SSMA/MESA
- Need to refine bootstrapping procedure
- What about multimodal bootstrap distributions?



Implications and recommendations for stock assessment

- Q!=0 changes index leverage & thus its statistical weight
- We should get the likelihood right
- The burden is on justifying a lognormal index
- Both bootstrap approaches are straightforward & easy-ish
- GGD seems to work in assessments (bespoke+SS3)
- When will this impacts assessments? Hard to know but if:
 - Q<0 and there are large residuals
 - Conflicting indices, interacts w/ data weighting



Discussion points and future work

- Evidence that Q<0 often in haul-level data and indices
- What causes Q<0?
 - A fundamental property of fish biology? Population characteristics?
 - Survey design/execution? Traits of haul-level data?
 - Something inherent in the design- and model-based estimators?
- Do the bootstrap procedures accurately estimate distribution?
- Does the precautionary principle come into play?
- We need to apply this to more GOA assessments



Request for Plan Team feedback

Should we

- Expand to AI and BS BT surveys?
- Expand to MACE surveys? (Plays particularly well with Sam Urmy's work)
- Abandon?

Thanks for listening! Thanks to collaborators

References

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TMB code

template<class Type>

```
Type dgengamma( Type x, Type mean, Type sigma, Type Q, int give_log=0){
  Type k = pow(Q, -2);
  Type Beta = pow(sigma, -1)*Q;
  Type log_theta = log(mean) - lgamma((k*Beta+1)/Beta)+lgamma(k);
  Type mu = log_theta + log(k)/Beta;
  Type w = (log(x) - mu) / sigma;
  Type abs_q = sqrt(Q*Q); // = abs(Q); not differentiable at 0!!
  Type qi = 1/square(Q);
  Type qw = Q*w;
  Type logres = -log(sigma*x) + log(abs_q)*(1-2*qi) + qi*(qw-exp(qw)) - lgamma(qi);
  if(give_log) return logres; else return exp(logres);
}
```



ADMB code

FUNCTION dvariable dgengamma(const double& x, dvariable mean, const double& sigma, const double& Q)

```
RETURN_ARRAYS_INCREMENT();
double k = pow( Q, -2 );
double Beta = pow( sigma, -1 ) * Q;
dvariable log_theta = log(mean) - lgamma( (k*Beta+1)/Beta ) + lgamma( k );
dvariable mu = log_theta + log(k) / Beta;
dvariable w = (log(x) - mu) / sigma;
double abs_q = sqrt(Q*Q); // = abs(Q); not differentiable!
double qi = 1/square(Q);
dvariable qw = Q*w;
dvariable logres = -log(sigma*x)+log(abs_q)*(1-2*qi) + qi * (qw-exp(qw))-lgamma(qi);
RETURN_ARRAYS_DECREMENT();
return(logres);
```

