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Impact of Time-Varying Biology on Reference Points in SS3

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Previewing SS3.30.24

Overview

- Review relevant equations
- Describe incomplete SS3 logic for reference points
- Describe changed logic
- Demonstrate impact of time-varying biology in old code and new
- Demonstrate equilibrium vs long-projection
- New user controls
- Bev-Holt with alpha, beta
- What happens if SR parms themselves are changed (regime)?
- Next steps

Beverton-Holt Spawner-Recruitment

$$R_{t+a_r} = \frac{\alpha S_t}{1 + \beta S_t}$$

$$R_{t+a_r} = \frac{4\tilde{R}_0 h S_t}{(1-h)\tilde{R}_0 \phi_0 + (5h-1)S_t}$$

Implicit in values of α, β

Φ_0 is the unfished, virgin SSB/R
Miller and Brooks, 2021

R_0 , h interconversion with α , β

unexploited spawning biomass per recruit

$$\tilde{S}_0/\tilde{R}_0 = \phi_0$$

$$h = \frac{\alpha\phi_0}{4 + \alpha\phi_0}$$

$$R_0 = \frac{1}{\beta} \left(\alpha - \frac{1}{\phi_0} \right)$$

Miller and Brooks, 2021

Equilibrium SSB and R calculations

Φ_0 is the unfished, virgin SSB/R

SS3 has always used alpha, beta transitionally in the equilibrium spawn_recr calculations:

$$\alpha = 4.0 * \text{steepness} / (\Phi_0 * (1. - \text{steepness}));$$

$$\beta = (5.0 * \text{steepness} - 1.0) / ((1 - \text{steepness}) * \text{SSB_virgin});$$

$$B_{\text{equil}} = (\alpha * \Phi_F - 1.0) / \beta;$$

$$R_{\text{equil}} = \alpha * B_{\text{equil}} / (1.0 + \beta * B_{\text{equil}});$$

Where Φ_F is SSB/R under some level of F and taking into account time-varying biology

Φ_0 and **SSB_virgin** are not updated over time, even if there is time-varying biology. They are computed using start year biology, then kept constant throughout the time series.

Equivalently, the values of alpha & beta computed in start year could be saved for all other spawn_recr calculations.

SSB/R in Benchmark - current

1. Calculate Φ_B as unfished SSB/R using benchmark biology
2. Use it, not Φ_0 , in the equilibrium spawner-recruitment calculations to find F_{MSY} , $F_{B40\%}$, etc.
3. Use it to report unfished SSB as $R_0 * \Phi_B$

Steps 2 and 3 are accurate only if $\Phi_B = \Phi_0$

What is Time-varying Biology?

- Anything that affects SSB/R
- Occurs with parametric growth and with empirical wt-at-age (EWAA)
- With parametric growth, the equilibrium body weight-at-age is only calculated in start year
- It can take many years for wt-at-age to approach new equilibrium after a change in growth parameters. SS3 benchmark uses the resultant wt-at-age averaged over the specified range of years, it does not calculate equilibrium wt-at-age from parameters averaged over that range of years
 - So, hard to get forecast biology to be same as benchmark biology
- With EWAA, there is no year-to-year continuity of size-at-age, so equilibrium and forecast can be forced to use the same biology.
- However, noisy EWAA data may need to be externally averaged to create a EWAA vector for start year that is good to use for the calculation of Φ_0

What's the issue when there is time-varying biology?

- ✓ Everything is fine if there is constant biology over time
- ✓ Time series is correct even with time-varying biology
- Benchmark is correct if using start year biology, but illogical to not use recent biology
- ≠ Benchmark calculations that use spawn_recr are not consistent with findings of Miller & Brooks
- ≠ Reported unfished SSB is not the new equilibrium
- ≠ Long projection with F_{MSY} will not replicate B_{MSY}
- Not enough reporting/transparency of what calculations were being done
- Not enough user-controls to allow exploration of options and backward compatibility

Impact depends upon degree of change in biology and the level of steepness

What needed to change?

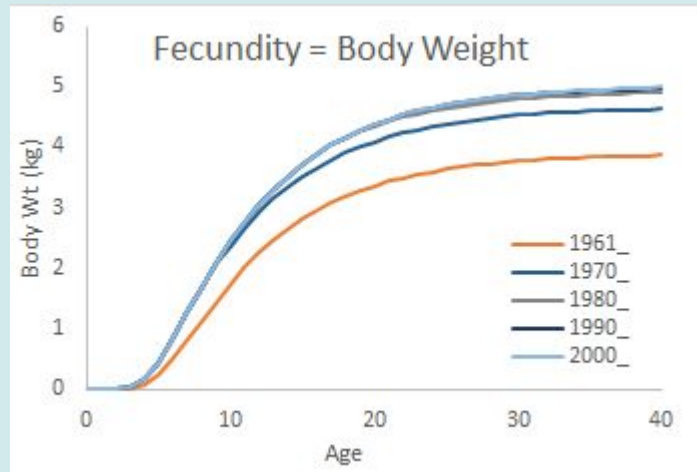
- Major refactoring of entity names to clarify the code
- Retain copy of start year (virgin) SSB/R, e.g. Φ_0 , so can be used in benchmark spawner-recruitment calcs.
 - Benchmark body wt-at-age affects how much catch and SSB you get from those recruits, but shouldn't change the SRR itself.
- Add user control that does backward compatibility
- Add more control for denominator in depletion calculations
- Add more control for inflection point in control rule calculation
- Add options for setting B_{target} in benchmark
- Carry changes into SPR/YPR profile and global_MSY

SSB/R in Benchmark - improved

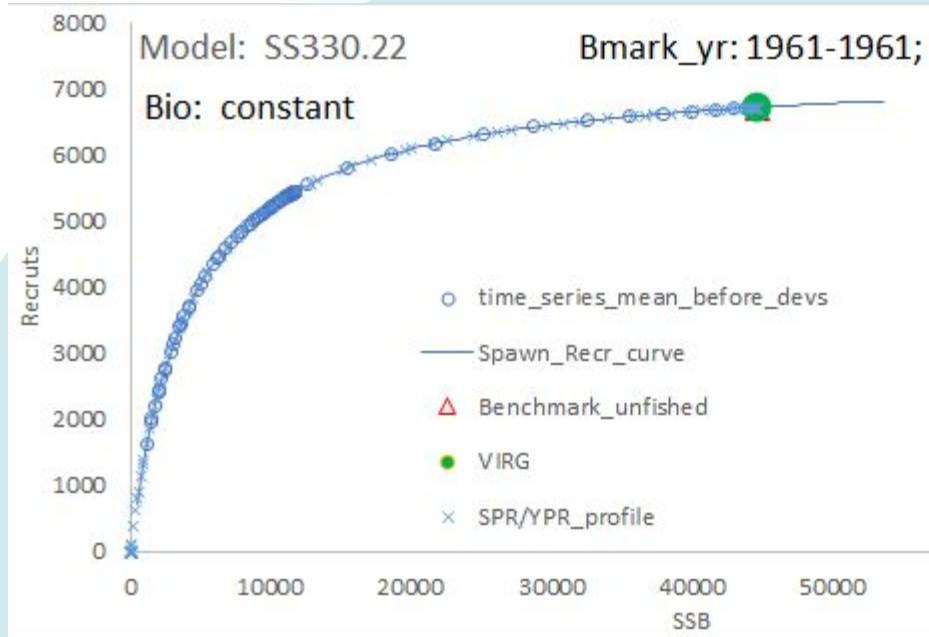
- Retain Φ_0 from the start year calculations
- Use benchmark biology when calculating Φ_F
- Find F_{MSY} , $F_{SPR40\%}$, etc. using equilibrium spawn_recruitment
 - $\alpha = 4.0 * \text{steepness} / (\Phi_0 * (1. - \text{steepness}));$
 - $\beta = (5.0 * \text{steepness} - 1.0) / ((1 - \text{steepness}) * SSB_{\text{virgin}});$
 - $B_{\text{equil}} = (\alpha * \Phi_F - 1.0) / \beta;$
 - $R_{\text{equil}} = \alpha * B_{\text{equil}} / (1.0 + \beta * B_{\text{equil}});$
- Report unfished SSB as equilibrium with $F=0$

Test Model Configuration

- Start with “simple” with parametric growth
- Extend start year back to 1961 to allow the growth change to equilibrate by endyear, 2001
- Increase female L_{inf} in 1962 from 70 cm to 75 cm
 - Base L_{inf} of 70 cm in start year is used for virgin
- Extend forecast to 2081 to provide an alternative way to get MSY values
- R_0 and h kept same for all runs



SS330_22 with Constant Biology



Output pulled from Spawn_Recr table, Spawn_Recr_curve, Mgmt_Quant table, and the SPR/YPR profile

All use the same spawn_recr curve, so should align

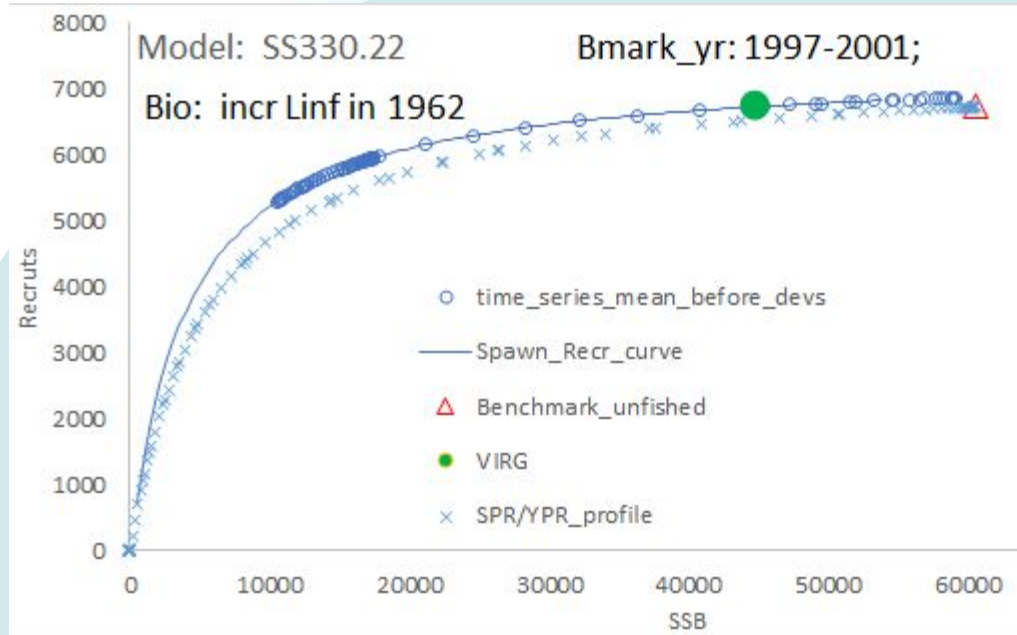
They do if adult biology is constant, and/or the benchmark uses the start year biology

Reference Point Values

| Benchmark_UNF | | Virgin | | | Btarget | SPR_target | MSY | Forecast |
|--|-------|--------|--|----------|---------|------------|-------|----------|
| SSB | 55925 | 55925 | | SSB | 15005 | 15005 | 15005 | 15005 |
| Recruits | 7107 | 7107 | | Recruits | | | | 5445 |
| <div>0.329279 # SPR target</div> <div>0.268305 # Biomass</div> | | | | SPR | 0.329 | 0.329 | 0.329 | 0.329 |
| | | | | F | 0.186 | 0.186 | 0.186 | 0.186 |
| | | | | | | | 0.268 | |
| | | | | Catch | 4590 | 4590 | 4590 | 4590 |

MSY output used to set B_{target} and SPR_{target}
 Forecast uses F_{MSY}

SS330_22 with Time-Varying Biology (TVB)



- Benchmark_unfished moved straight to the right
- So, is off the time series' SRR
- Unintentionally creates a new SRR for the reference points
- Difference depends on steepness and degree of TVB

TVB impact on reference points

| | Benchmark_UNF | Virgin | | | Btarget | SPR_target | MSY | Forecast |
|----------|--|--------|--|------------|---------|------------|-------|----------|
| SSB | 58548 | 43335 | | SSB | 15496 | 15496 | 15496 | 16879 |
| Recruits | 6429 | 6429 | | Recruits | | | | 5686 |
| | 0.325954 # SPR target 0.264677 # Biomass target | | | SPR | 0.326 | 0.326 | 0.326 | 0.326 |
| | | | | F | 0.141 | 0.141 | 0.141 | 0.141 |
| | | | | Bmsy/B_unf | | | 0.265 | |
| | | | | Catch | 4092 | 4092 | 4092 | 4457 |

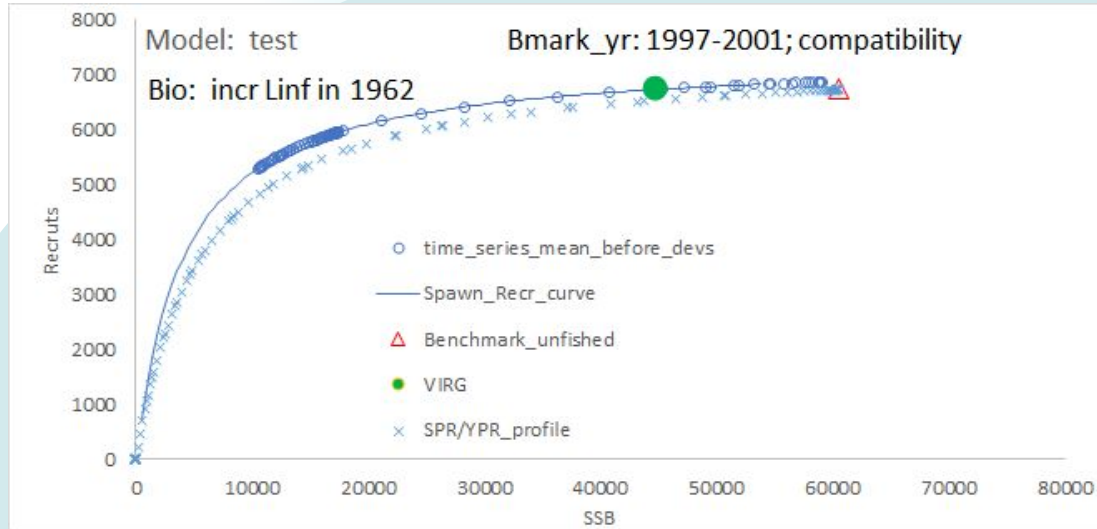
▼ Benchmark recruits have not been updated with the Spawn_Recr curve

▲ Long Forecast differs from equilibrium calculations

Per Recruit calculations

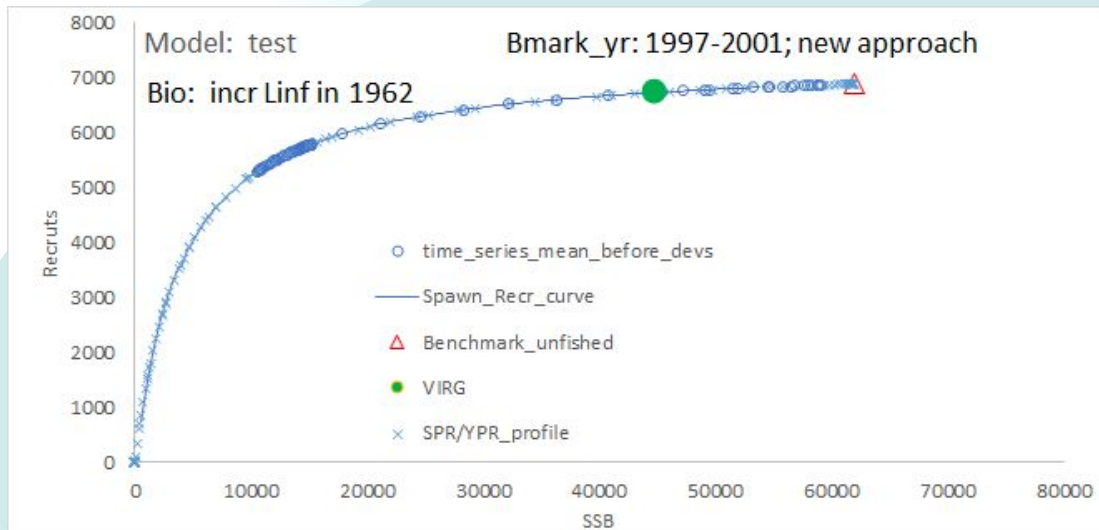
- The search for the F that gives a specific %SPR is unaffected because it is based on per/recruit calculation using benchmark biology
- The search for MSY and a B_{target} are affected because they involve the SRR
- Although the search for a F %SPR is unaffected, the equilibrium catch and SSB that come from that F are affected because they use the SRR

SS330_new with compatibility



New code has compatibility flag to demonstrate repeatability of old output

SS330.new



- With compatibility turned off, new code gives expected result
- All values are along the same SRR
- SRR calculations use virgin SSB/R0, not the benchmark

Consistent Reference Points

| | Benchmark_UNF | Virgin | | | Btarget | SPR_target | MSY | Forecast |
|----------|--|--------|--|------------|---------|------------|-------|----------|
| SSB | 59930 | 43335 | | SSB | 14680 | 14680 | 14680 | 14680 |
| Recruits | 6581 | 6429 | | Recruits | | | 5529 | 5529 |
| | | | | SPR | 0.292 | 0.292 | 0.292 | 0.292 |
| | 0.291523 # SPR target 0.244952 # Biomass target | | | F | 0.162 | 0.162 | 0.162 | 0.162 |
| | | | | Bmsy/B_unf | | | 0.245 | |
| | | | | Catch | 4484 | 4484 | 4484 | 4484 |

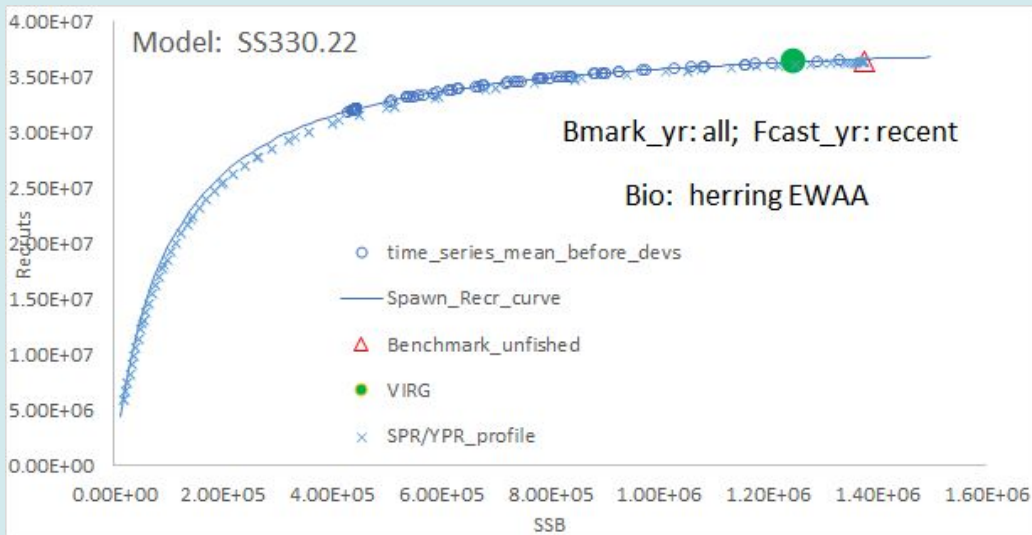
All values are consistent

Comparison

| | Original | | Corrected | |
|------------|----------|----------|-----------|----------|
| | MSY | Forecast | MSY | Forecast |
| SSB | 15496 | 16879 | 14680 | 14680 |
| Recruits | 5220 | 5686 | 5529 | 5529 |
| SPR | 0.3260 | 0.3260 | 0.2915 | 0.2915 |
| F | 0.1409 | 0.1409 | 0.1617 | 0.1617 |
| Bmsy/B_unf | 0.2647 | | 0.2450 | |
| MSY_Catch | 4092 | 4457 | 4484 | 4484 |

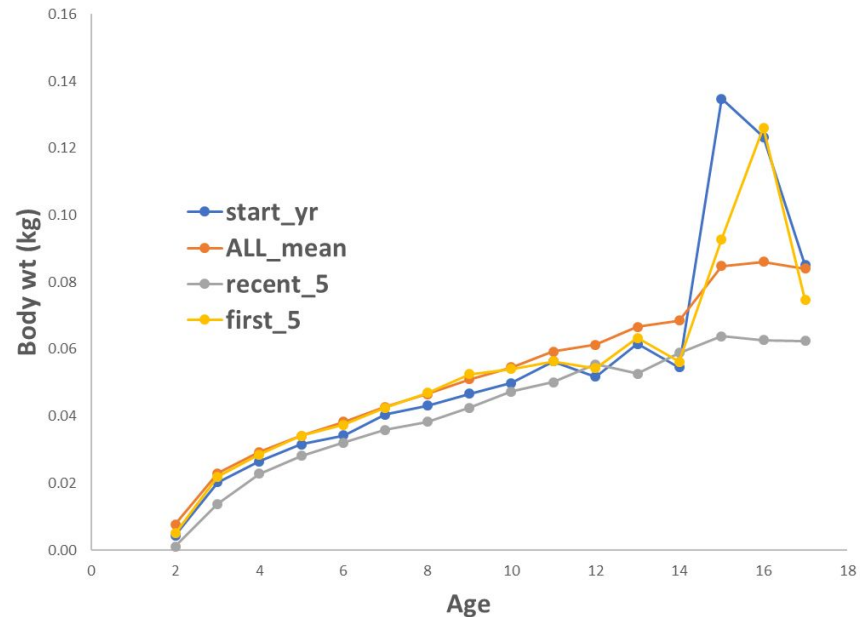
Empirical Weight-at-Age (EWAA) Example

Differences occur with EWAA also because start year biology used for SSB/R0 can differ from biology over benchmark years



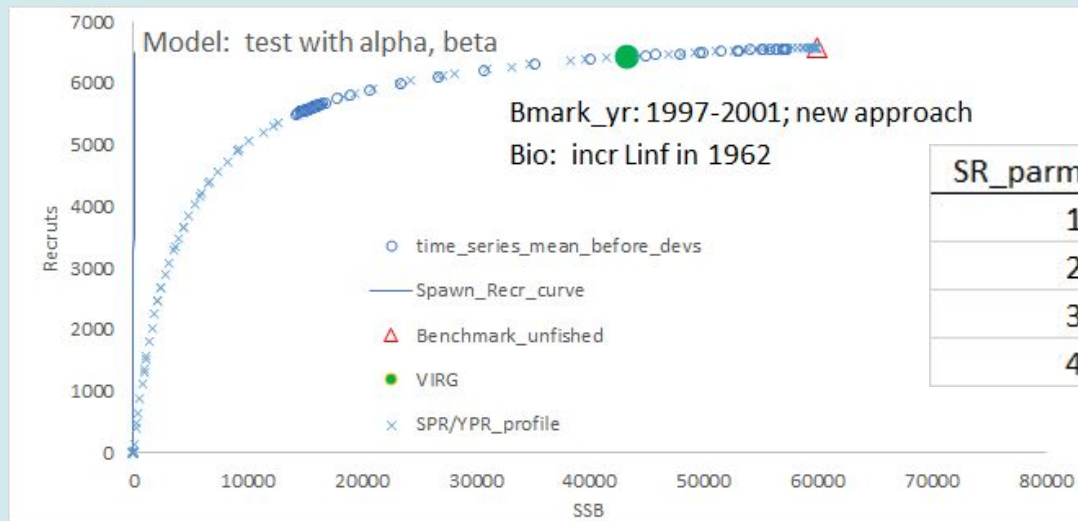
EWAA Consideration

- The single start year biology can be noisy
- SS3 cannot use a later year's biology for the S/R calcs
- You can extend time series back one year and provide an averaged biology for that year.
- Could use all years, or early years for that mean
- Could smooth over ages



Test with alpha, beta parameterization of SRR

- SS3 adds SRR 10 with the $\ln(\alpha)$, $\ln(\beta)$ parameterization
- SS3 **must** have R0 as the first SRR parameter
- R0, h get derived from alpha, beta and placed into the SR_parm list
- You can estimate using alpha, beta as parameters and still put a prior on the derived h



| SR_parm | INIT | | parm_name |
|---------|----------|------|---------------------|
| 1 | 8.76855 | | SR_LN(R0)_derived |
| 2 | 0.749996 | | SR_BH_steep_derived |
| 3 | 0.576742 | | SR_BH_Ln(alpha) |
| 4 | -8.27882 | | SR_BH_Ln(beta) |

What else depends on R_0 ?

- Everything! It's equivalent to K in a biomass dynamics model
- These depend on either virgin B_0 or Benchmark B_0
 - Depletion
 - Inflection point in control rule
 - B_{target} as benchmark output
- Clarify and expand options

Compatibility Switch

New line in starter.ss:

-1 # random number seed

1 # Compatibility flag for legacy (0) vs improved (1) impact of timevary
biology on benchmark SRR calcs >=3.30.24

3.30 # check value for end of file and for version control

NOTE: if line with compatibility flag is missing, SS3 will run as if the flag was set to 0,

except if there is time-varying biology, which will generate an EXIT warning until the flag line is included

Depletion Basis

In starter.ss, add option 6:

2 # Depletion basis: denom is: 0=skip; 1=X*SSBvirgin; 2=X*SSBmsy;
3=X*SSB_styr; 4=X*SSB_endyr; 5=X*dyn_Bzero; **6=X*Bmark_SSB_unf**

Where Bmark_SSB_unf used to be just $R_0 * SSB / R_{Bmark}$

Now it is the unfished equilibrium using the virgin spawn_recr relationship and the SSB / R_{Bmark}

Note that options 2 and 6 use benchmark biology, others use virgin or time series biology

Control Rule Inflection Basis

1 # Control rule method (0: none; 1: ramp does catch=f(SSB), buffer on F; 2: ramp does F=f(SSB), buffer on F; 3: ramp does catch=f(SSB), buffer on catch; 4: ramp does F=f(SSB), buffer on catch)

0.2 # Control rule inflection for constant F (as frac of Bzero, e.g. 0.40); must be > control rule cutoff {-1 approach for Bmsy deprecated here; see below}

.....

1 # Forecast base recruitment: 0= spawn_recr; 1=mult*spawn_recr_fxn; 2=mult*VirginRecr; 3=deprecated; 4=mult*mean_over_yr_range

for option 4, set phase for fore_recr_devs to -1 in control to get constant mean in MCMC, else devs will be applied

1 # multiplier on base recruitment

2 # HCR_anchor: 0 or 2 uses unfished benchmark SSB (old hardwired approach); 1 = virgin SSB; 3 = Bmsy

{This repurposes a previously unused input}

B_{target} Basis

0.35 # Biomass target (e.g. 0.40) as fraction of SSB_virgin if depletion basis = 1, else as fraction of SSB_unfished in benchmark

Previously, SSB_unfished was the only hardwired option.

If you set Do_benchmark = 3 to invoke calculation of B_{limit} also, then options are:

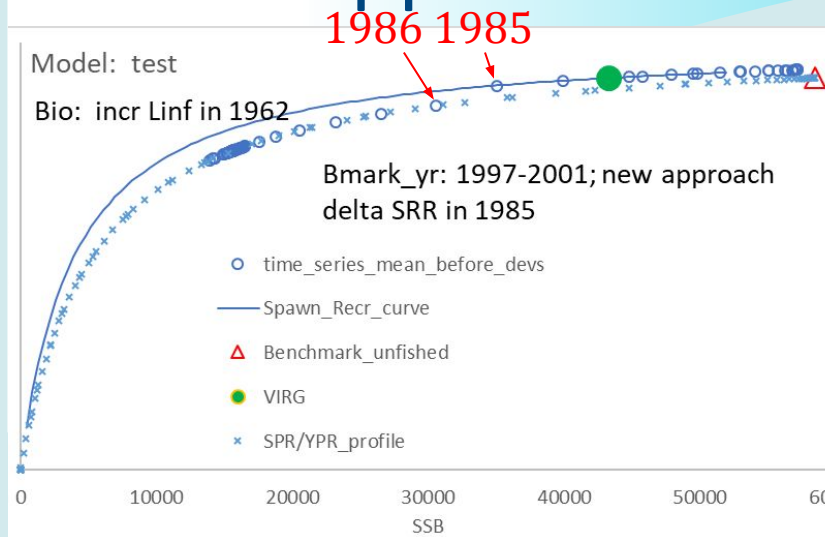
- a. Positive Blim_fraction invokes use of B_{MSY}
- b. Negative Blim_fraction invokes use of SSB_virgin, if depletion basis equals 1
- c. Negative Blim_fraction invokes use of SSB_unf, if depletion basis $\neq 1$

Note that if there is TVB and Bmark_years \neq startyr, then Bmsy and SSB_unf are consistent in both using the benchmark biology

What happens if R_0 or h changes?

- SS3 will use the biology in the year of the change to save a revised value for SSB/R_0
- The remainder of the time series, then the projection will use a spawner-recruitment curve calibrated with that SSB/R_0
- The benchmark can also use that revised SSB/R_0 , see `Bmark_years` `beg_SRparm` and `end_SRparm`
- If you try this, examine detailed outputs closely!

What happens when a SR parameter changes?

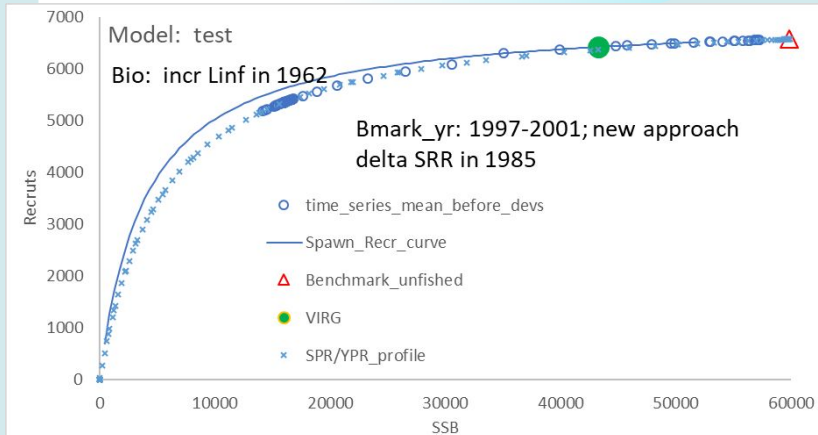


- R_0 change of 0.0 in 1985
- Triggers the logic that causes recompute of SSB/R, so new SRR equil point
- Impact shows up the following year when new curve calcs the 1986 R
- Benchmark_unfished SSB/R on new curve
- SPR/YPR profile follows new curve, so benchmarks must also
- Reference point values all change

Be careful what you ask for!

Examine details in [forecast-report.sso](#)

What happens when a SR parameter changes?



- R_0 change of 0.02335 in 1985, which is amount needed to be the equilibrium point under the changed Φ_0
- h is same, but the early and late curves differ due to change in Φ_0
- Now the late time series aligns with the benchmark calculations, and
- MSY now matches long forecast
- NOTE: Spawn_Recr_Curve is calculated only with virgin SRR parameter values

Next Steps

- Code clean-up
- Check on implementation of Bmark_years: beg_SRparm and end_SRparm
- Update r4ss to work with the:

#New_Expanded_Spawn_Recr_report
SPAWN_RECRUIT report:19

- Recruit some beta-testers
- Update the User Manual
- Release as SS3.30.24