

# Age Structured Production Models using Integrated Analysis

# Outline

**Goal: create age-structured, integrated models for data-poor problems for which biomass dynamic models are typically applied**

- **Example : Schaefer model**
- **Conclusions**

# Example: Schaefer model

- Data are 24 years of catch (C) and CPUE (I) from 1965-1988 from Namibian hake (Polacheck, 1993)
- Schaefer model implemented in Excel and ADMB

$$B_{y+1} = B_y + r B_y (1 - B_y / K) - C_y$$

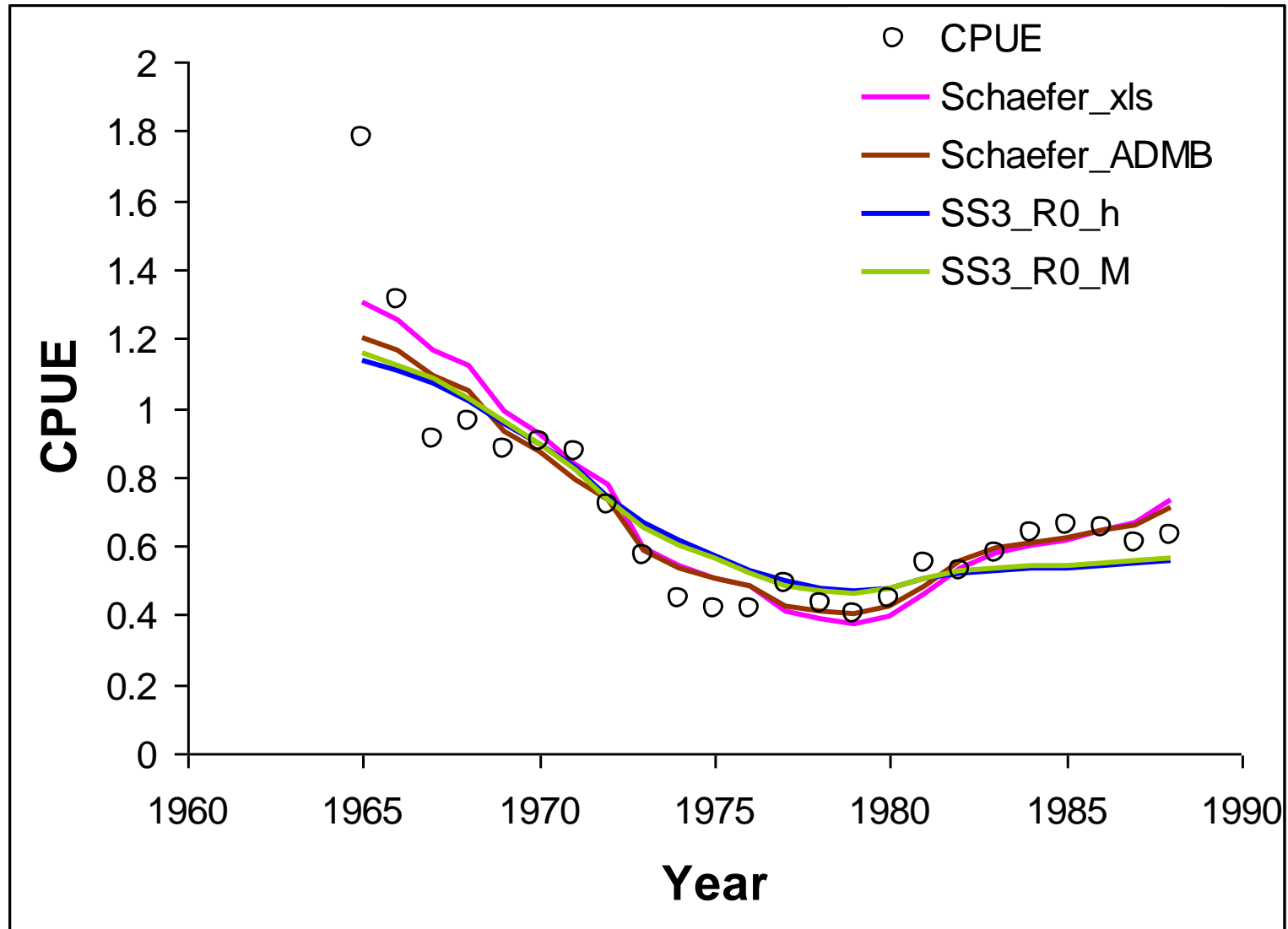
$$\hat{I}_y = q \hat{B}_y$$

- Estimated parameters are
  - $r$  (maximum population growth rate)
  - $K$  (equilibrium biomass)
  - $q$  (catchability)

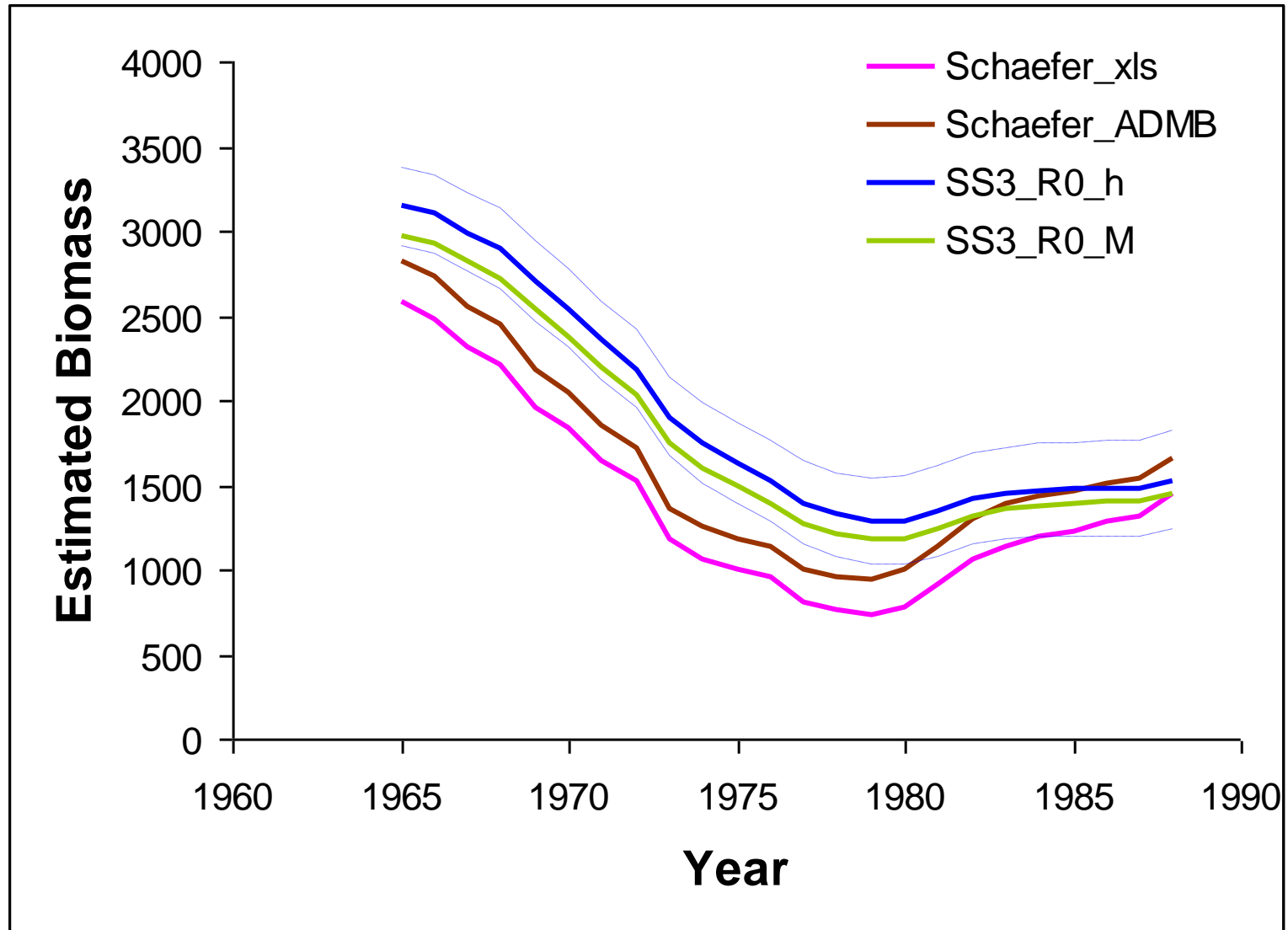
# Stock Synthesis Model

- Fully age structured (plus group = age 10, with arbitrary inputs for growth, maturity, and fecundity)
- All ages fully selected
- All ages mature
- No recdevs
- Estimated parameters are
  - $R_0$  (equilibrium recruitment)
  - either  $M$  (natural mortality) or  $h$  (steepness)
  - catchability as derived quantity

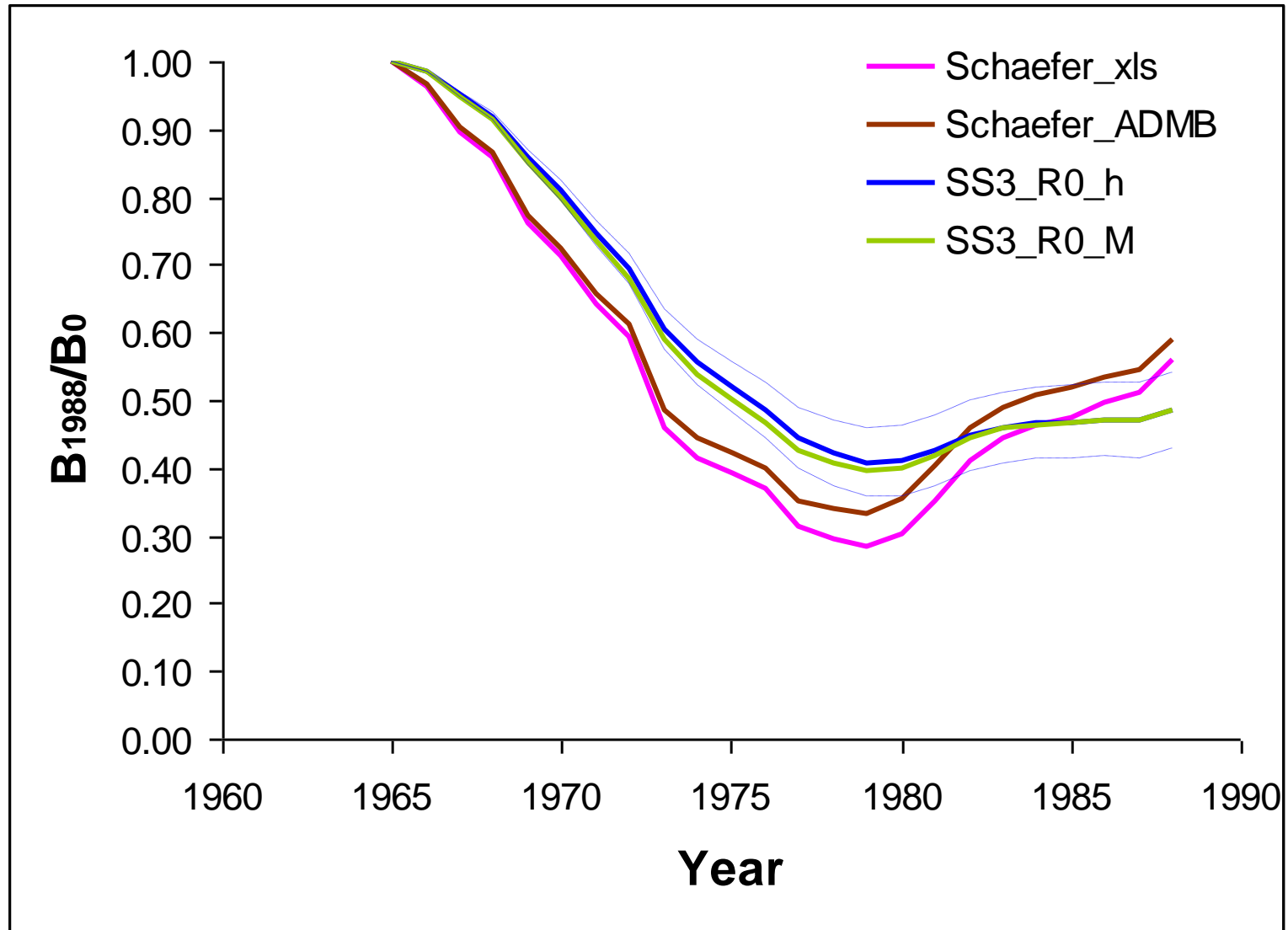
# Comparing model results



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# Comparing model results

	<b>MSY</b>	<b>B<sub>0</sub></b>	<b>B<sub>1988</sub></b>	<b>B<sub>1988</sub>/B<sub>0</sub></b>
<b>Schaefer_xls</b>	267	2575	1442	0.56
<b>Schaefer_ADMB</b>	261	2820	1660	0.59
<b>SS3_R0_h</b>	233	3145	1523	0.48
<b>SS3_R0_M</b>	230	2976	1441	0.48



# Conclusions from Schaefer example

- Age structured production model requires no more estimated parameters than Schaefer model
- Fit to CPUE data is similar
- Model output is similar
- SS allows additional flexibility in many directions

# General conclusions on age structured production models

- More options than simpler biomass dynamic models
  - provides greater ability to explore alternative scenarios and uncertainty
  - but requires more thinking about choices made
- Parameters have more direct biological interpretations
- Allows increase in complexity (and realism) through incorporation of additional data types
  - data on growth and maturity (or external estimates)
  - a single length or age composition would allow estimation of selectivity
  - priors based on biological parameters from similar species