What to do once you've fitted a model
or, *What can we do with these models?*

Predict trajectory of biomass through time

Derive absolute and relative growth rates

Correlate parameter estimates or growth rates with other things, like seed size, or functional traits

Determine which aspects of growth are most affected by model parameters

Useful model outputs

Parameter values - eg, asymptotic size, beta, etc

Biomass at particular times

Absolute or relative growth rates

In all cases, must account for uncertainty in parameter estimates!

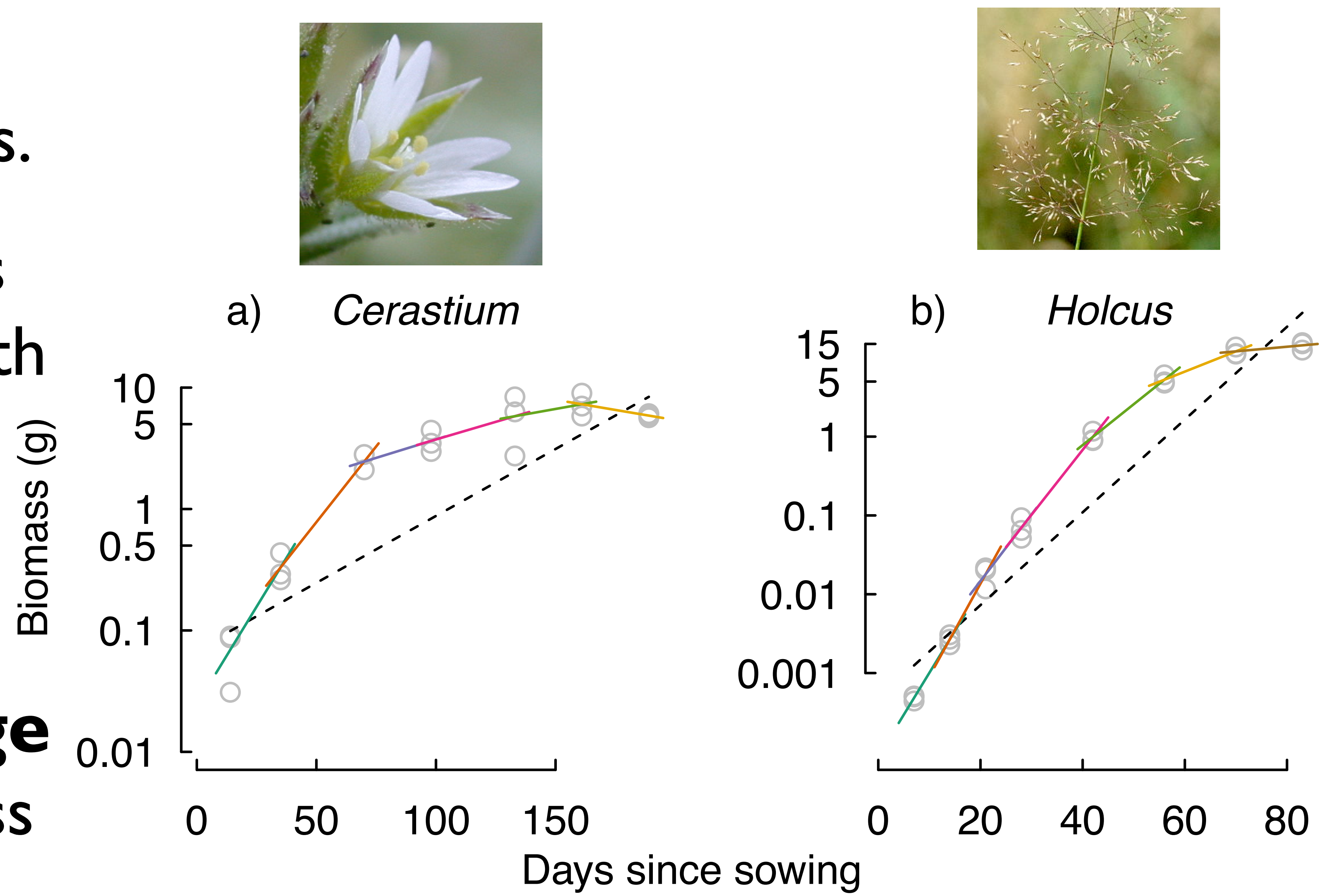
Inferences on relative growth rate (RGR)

Traditionally, $RGR = \dfrac{\ln(M_{t+1}) - \ln(M_t)}{\Delta t}$

Assumes RGR is constant through time, which it never is.

Thus, this approach is **invalid** unless growth is perfectly exponential, which is unusual

Growth rates **change** with time and biomass

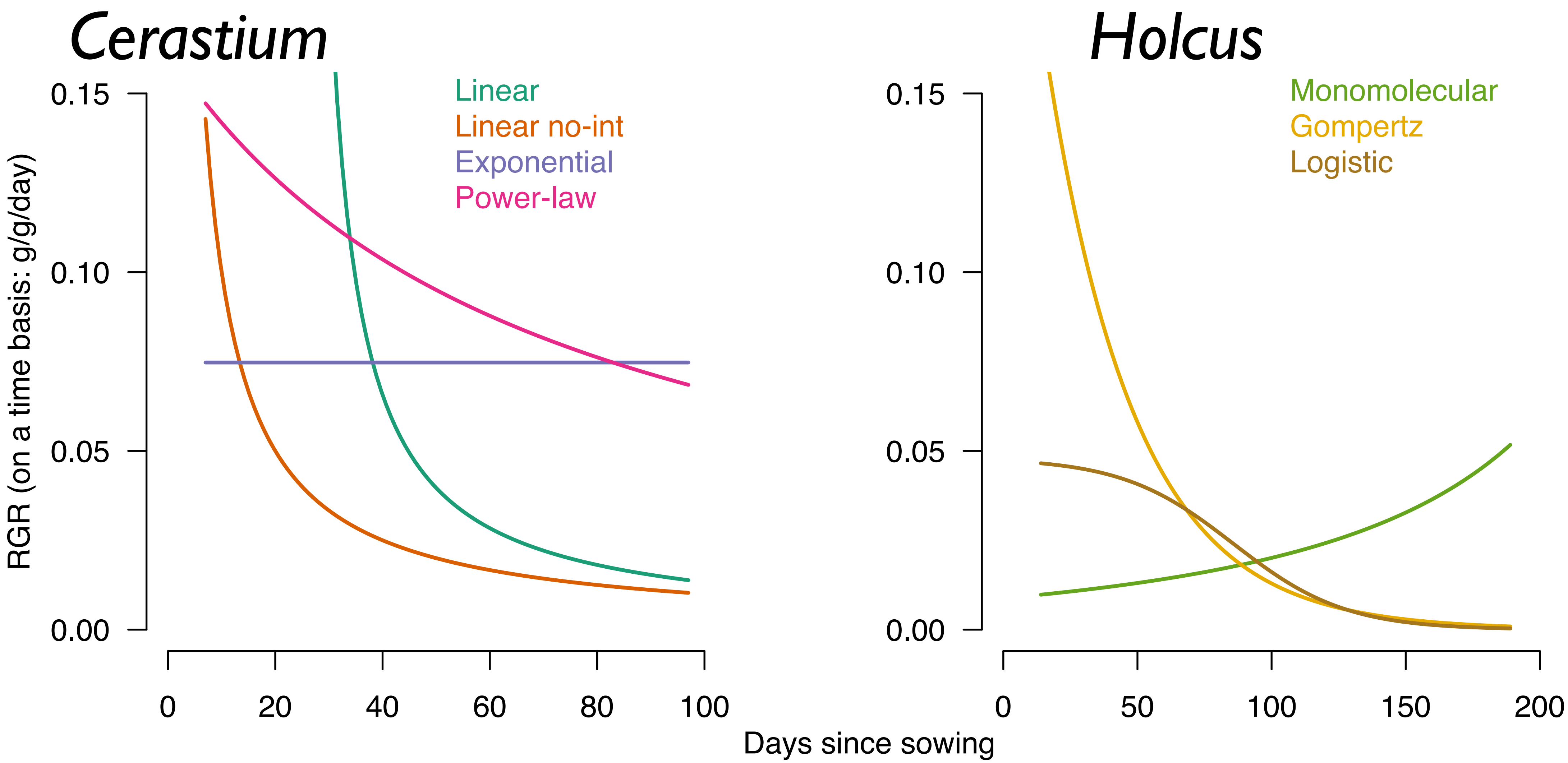


Function-derived growth rates are **better**

How to use them?

- Measure sizes at multiple times
- Fit a function
- Take derivative of that function to obtain growth rates
  - Absolute growth rate: dM/dt
  - Relative growth rate: 1/M * dM/dt

With a function, $RGR = \frac{1}{M}\frac{dM}{dt}$

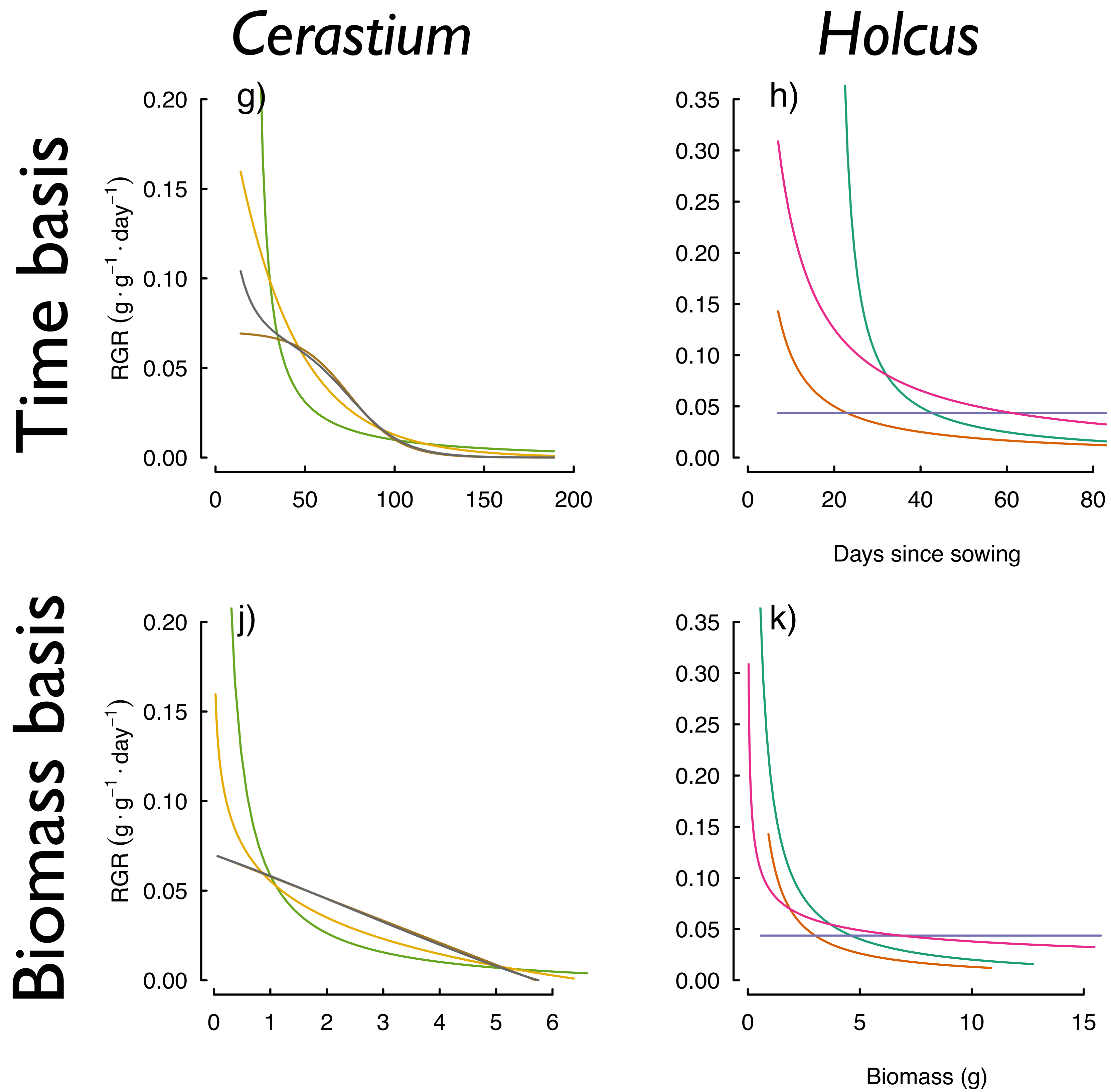


Important, since **growth slows** as non-photosynthetic biomass accumulates

Choice of form affects the temporal pattern of RGR that you infer

RGR

Deriving rates from functions also affects the pattern of RGR vs biomass - which differs from the temporal pattern, unless biomass and time are linearly related (which they're not)



Calculation of AGR

Name	**Model** dM/dt	**Biomass** M time basis	**AGR** dM/dt time basis
Linear	a	$M_0 + at$	a
Exponential	rM	$M_0 e^{rt}$	$rM_0 e^{rt}$
Power-law	rM^{β}	$\left(M_0^{1-\beta} + rt(1-\beta)\right)^{1/(1-\beta)}$	$r\left(M_0^{1-\beta} + rt(1-\beta)\right)^{\beta/(1-\beta)}$
Monomolecular	$r(K - M)$	$K - e^{-rt}(K - M_0)$	$re^{-rt}(K - M_0)$
Logistic	$rM\left(1 - \frac{M}{K}\right)$	$\frac{M_0 K}{M_0 + (K - M_0)e^{-rt}}$	$\frac{rM_0 K e^{-rt}(K - M_0)}{\left(M_0 + e^{-rt}(K - M_0)\right)^2}$
Four-parameter logistic	$rM\left(1 - \left(\frac{M}{K}\right)^{1/xmid}\right)$	$M_0 + \frac{K - M_0}{1 + e^{xmid - t/r}}$	$\frac{(K - M_0)e^{xmid - t/r}}{r\left(1 + e^{xmid - t/r}\right)^2}$
Gompertz	$rM\left(\ln\frac{K}{M}\right)$	$K\left(\frac{M_0}{K}\right)^{e^{-rt}}$	$rKe^{-rt}\left(\frac{M_0}{K}\right)^{e^{-rt}} \ln\frac{K}{M_0}$

Looks ugly, but any AGR can be calculated by substitution, once solution to differential equation is known

Calculation of RGR

Name	**Model** dM/dt	**RGR** $(dM/dt)/M$ time basis	**RGR** $(dM/dt)/M$ mass basis
Linear	a	$\frac{a}{M_0 + at}$	$\frac{a}{M}$
Exponential	rM	r	r
Power-law	rM^{β}	$r\left(M_0^{1-\beta} + rt(1-\beta)\right)^{-1}$	$rM^{\beta-1}$
Monomolecular	$r(K - M)$	$\frac{r(K - M_0)}{M_0 + K(e^{rt} - 1)}$	$\frac{r(K - M)}{M}$
Logistic	$rM\left(1 - \frac{M}{K}\right)$	$\frac{re^{-rt}(K - M_0)}{M_0 + e^{-rt}(K - M_0)}$	$r\left(1 - \frac{M}{K}\right)$
Four-parameter logistic	$rM\left(1 - \left(\frac{M}{K}\right)^{1/xmid}\right)$	$\frac{(K - M_0)e^{xmid - t/r}}{r\left(1 + e^{xmid - t/r}\right)^2} \Big/ M_0 + \frac{K - M_0}{1 + e^{xmid - t/r}}$	$r\left(1 - \left(\frac{M}{K}\right)^{1/xmid}\right)$
Gompertz	$rM\left(\ln\frac{K}{M}\right)$	$re^{-rt}\ln\frac{K}{M_0}$	$r\ln\frac{K}{M}$

RGR on a biomass basis is often cleaner to deal with, as well as often being more appropriate.

RGR on a biomass basis

Often the more appropriate way to compare RGR among groups

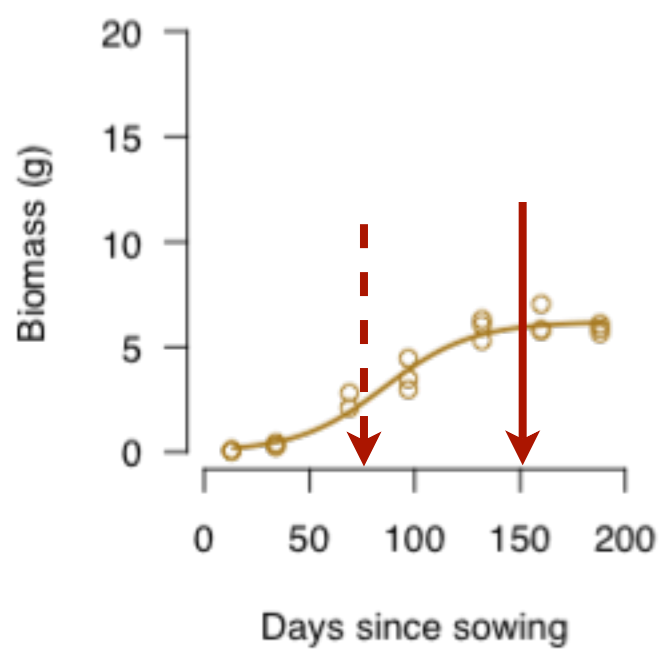
Makes RGR independent of M_0

Compare groups at a certain reference mass, rather than a reference time.

Choice of reference mass or reference time also affects comparisons

= Fert. matters

= Or it doesn't

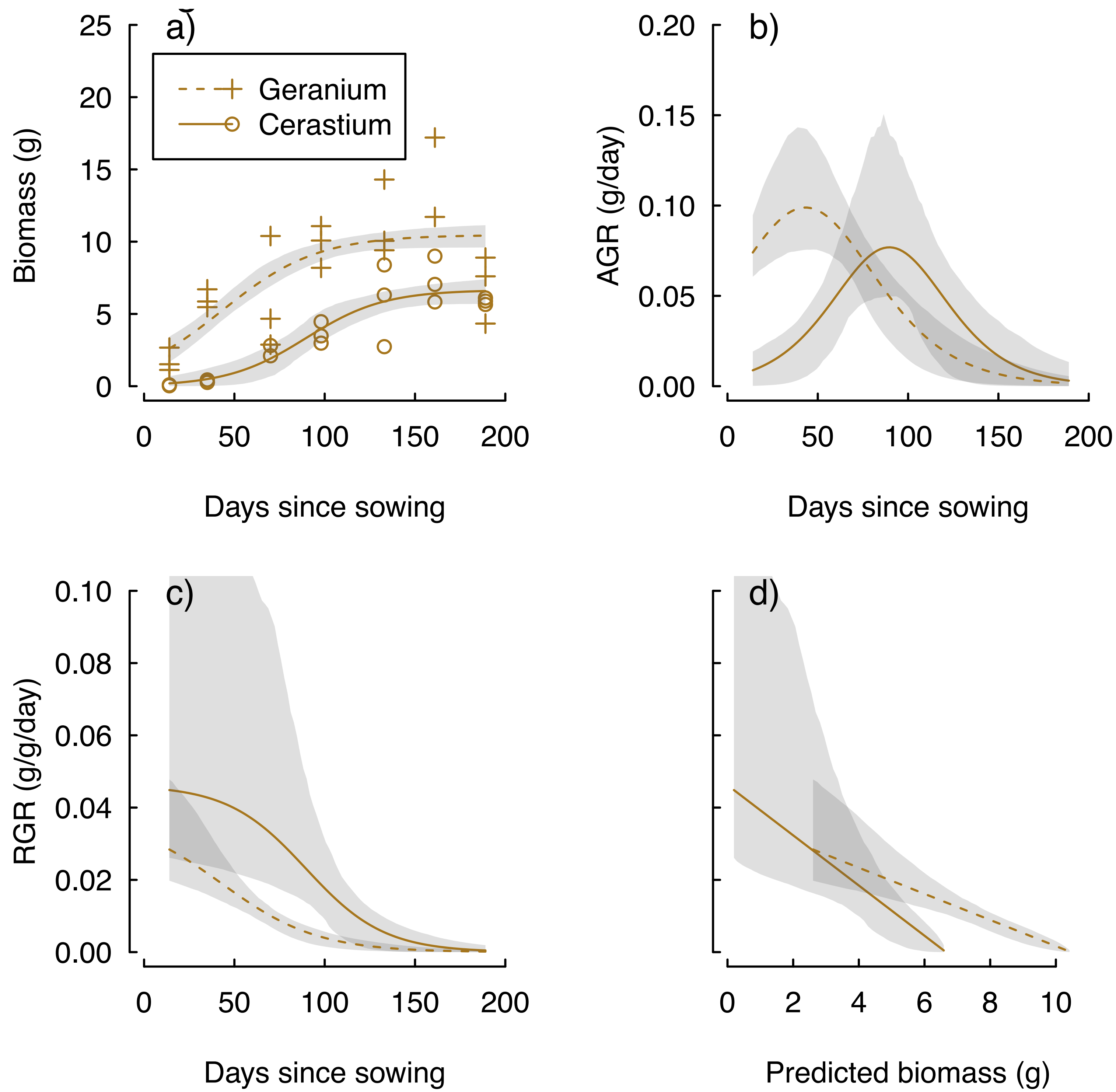


Use
natural history
to choose times/masses for comparison

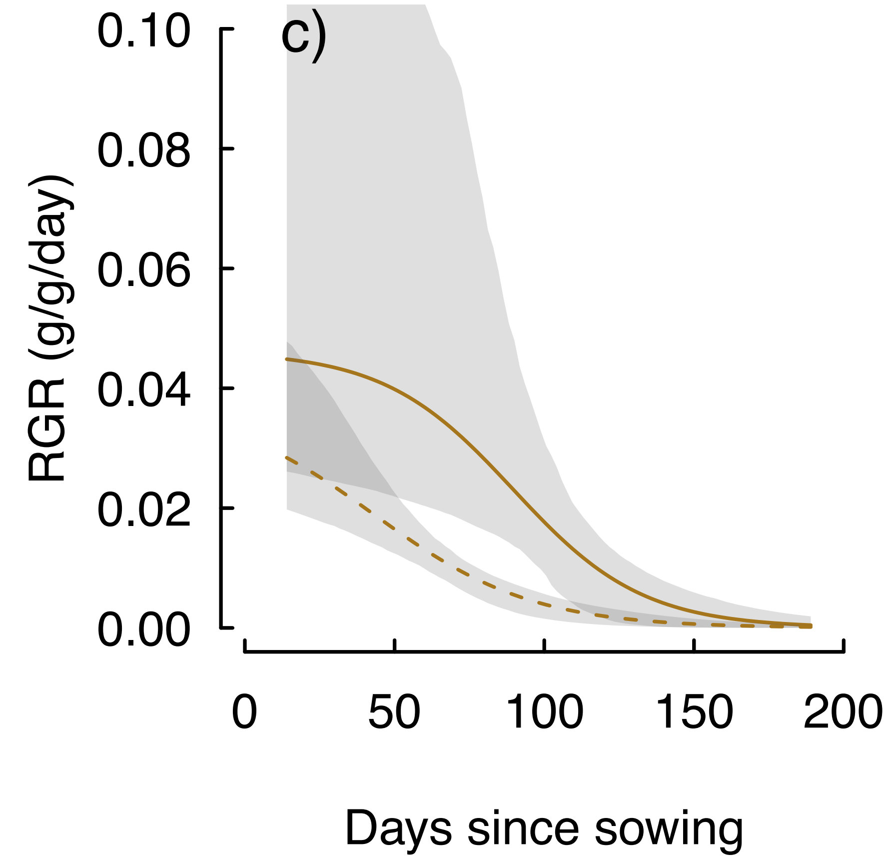
Propagation of uncertainty

We estimate parameter values. We do not know them exactly.

That uncertainty needs to be dealt with when making inferences on growth rates



Propagation of uncertainty- Population Prediction Intervals



General approach:

Obtain means and variance-covariance matrix for parameter estimates for each group of interest (here, two species).

Draw ~1000 random deviates from the multivariate normal distribution defined by those means & var-cov matrix.

Use those deviates to calculate 1000 RGR's, using the appropriate function. Take the 0.025^{th} and 0.975^{th} percentiles of the distribution of RGRs at every biomass (or time)