Hit n’ run in numerical ecology

Maps F

Parent G

Record N

Plourde S

UNIVERSITÉ LAVAL

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BIGELOW LABORATORY FOR OCEAN SCIENCES

Québec OCÉAN

Pêches et Océans Canada

Fisheries and Oceans Canada

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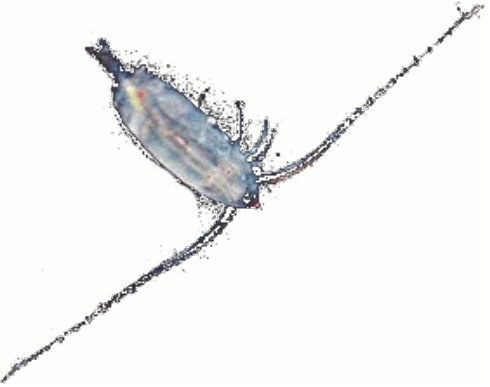
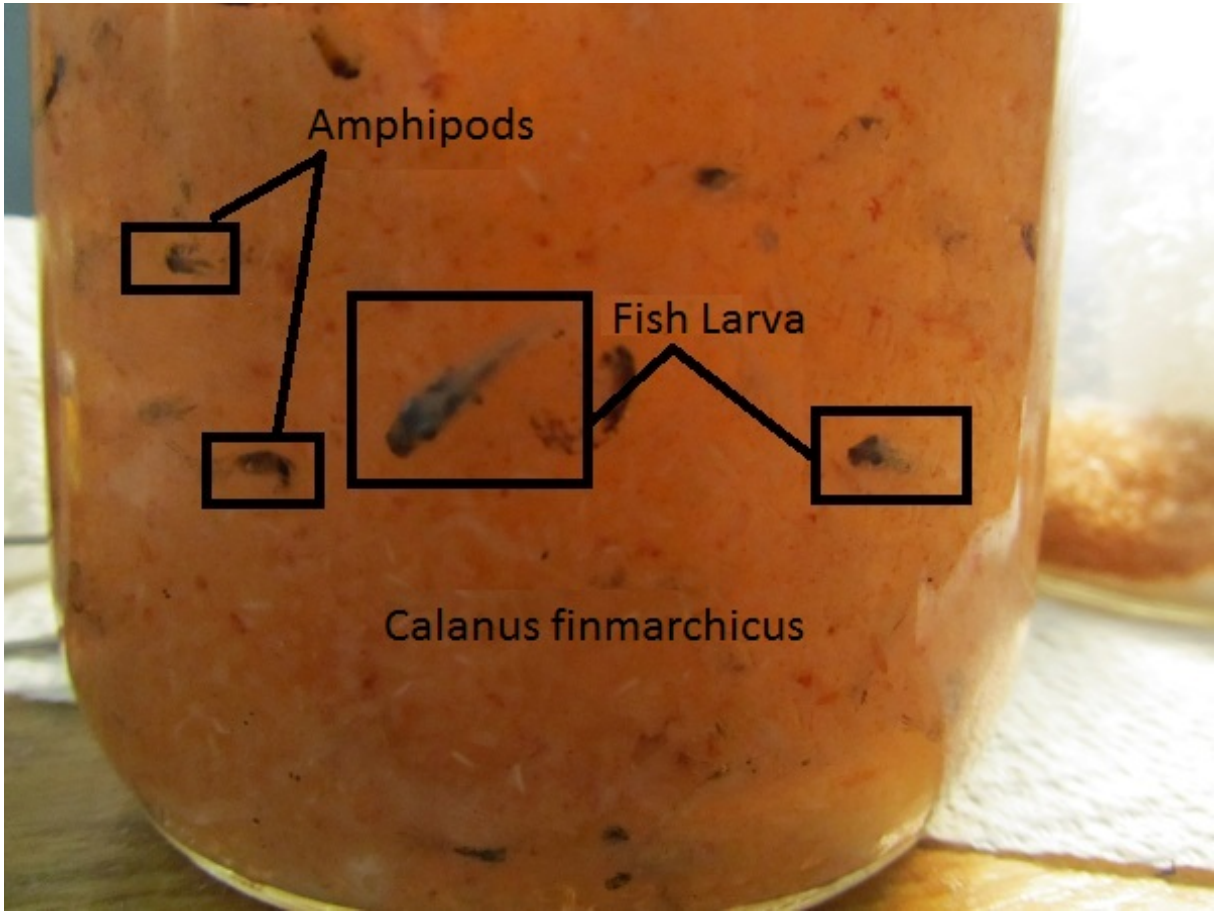


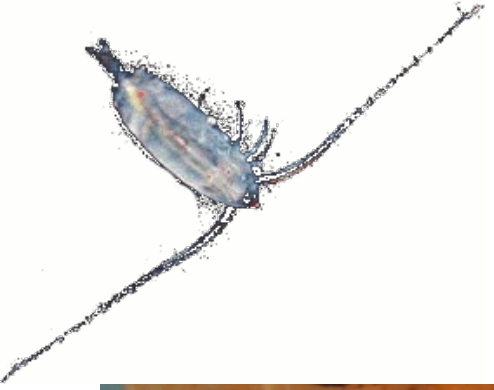
Presentation outline

- Pelagic copepods (that matter) ≈ *Calanus* spp
- Parameterization of *Calanus* models
- “Hybrids” ?... in trait-based models ?
- Prospective: ecological implications + approaches

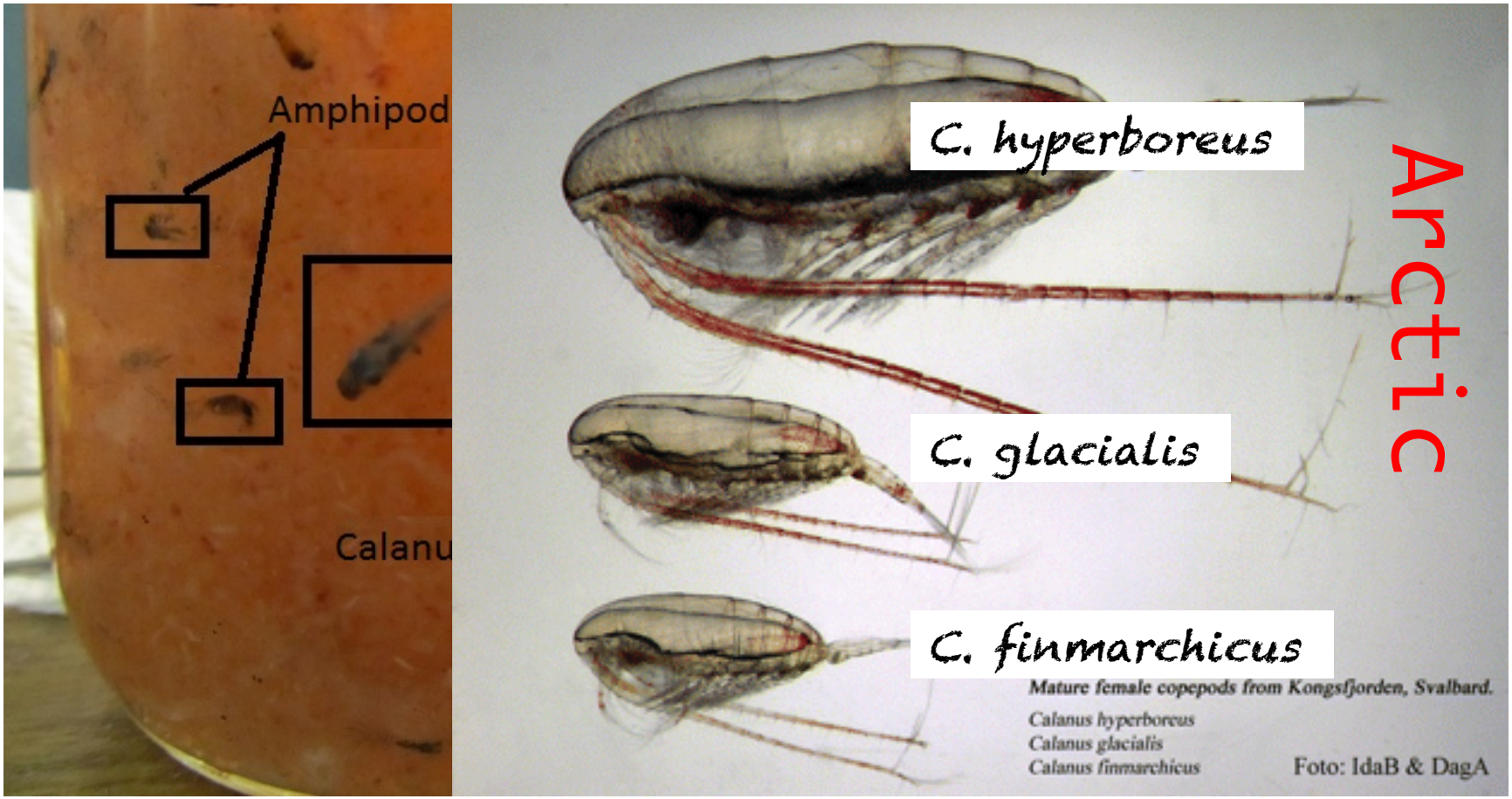
Pelagic copepods ≈ *C. finmarchicus*

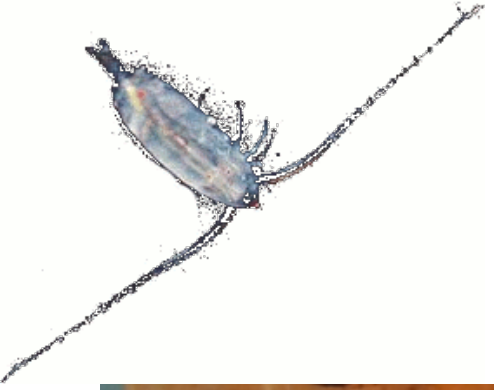


North Atlantic

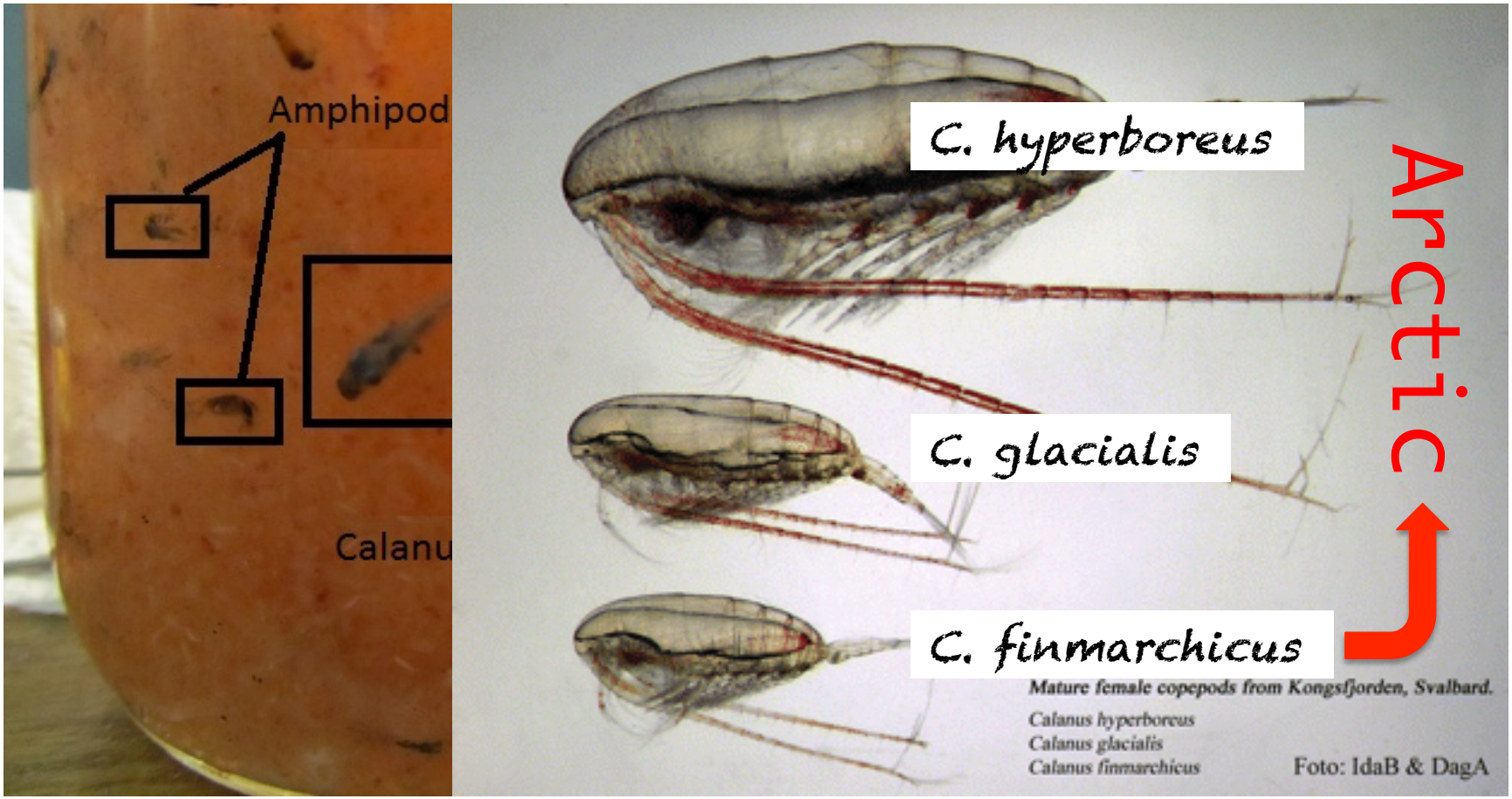


Pelagic copepods ≈ *Calanus* spp



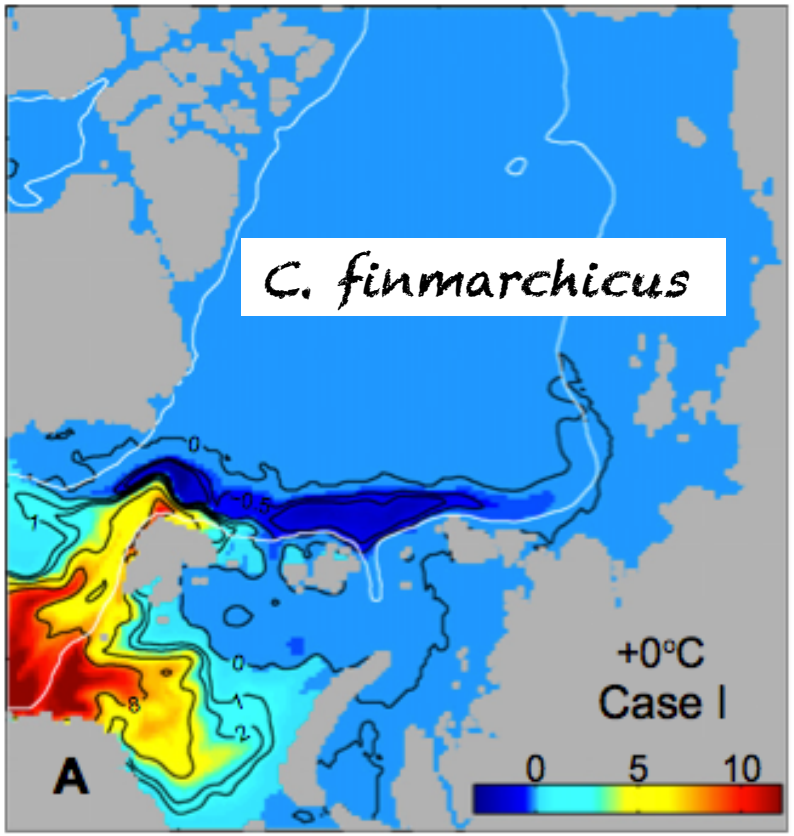


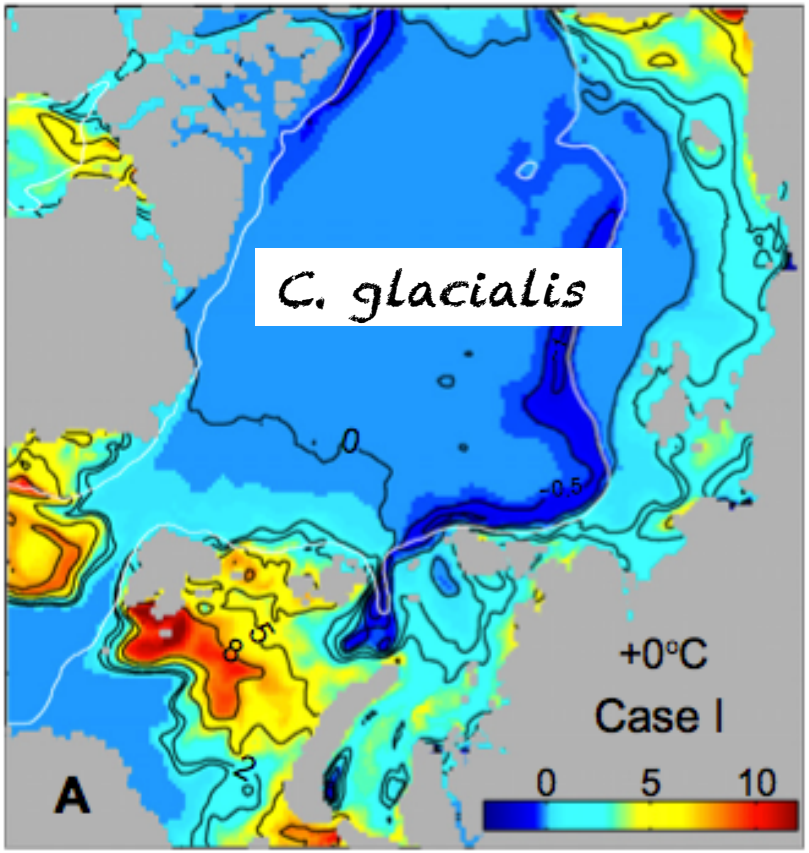
Pelagic copepods ≈ *Calanus* spp

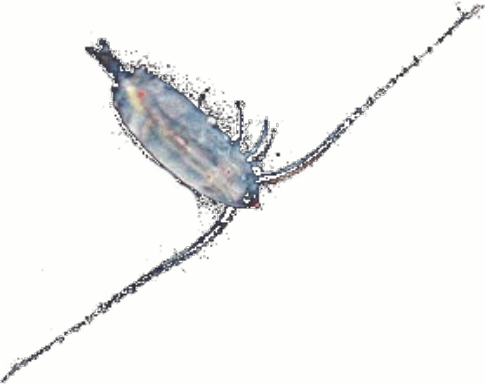


Parameterization of *Calanus* models

From Slagstad *et al.* 2011 (doi:10.1016/j.pocean.2011.02.009) their fig. 9 & 11





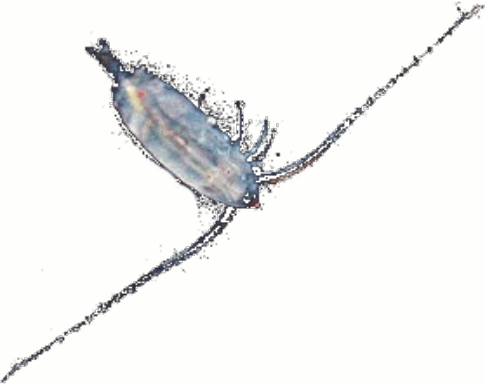


Parameterization of *Calanus* models

[...]

The *C. finmarchicus* model is stage distributed, implying that the naupliar and copepodite stage distribution is resolved.

[...]



Parameterization of *Calanus* models

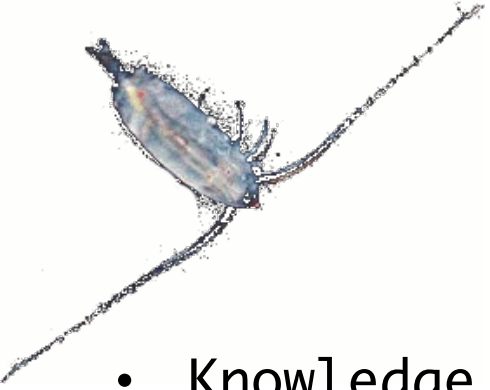
[...]

The *C. finmarchicus* model is stage distributed, implying that the naupliar and copepodite stage distribution is resolved.

[...]

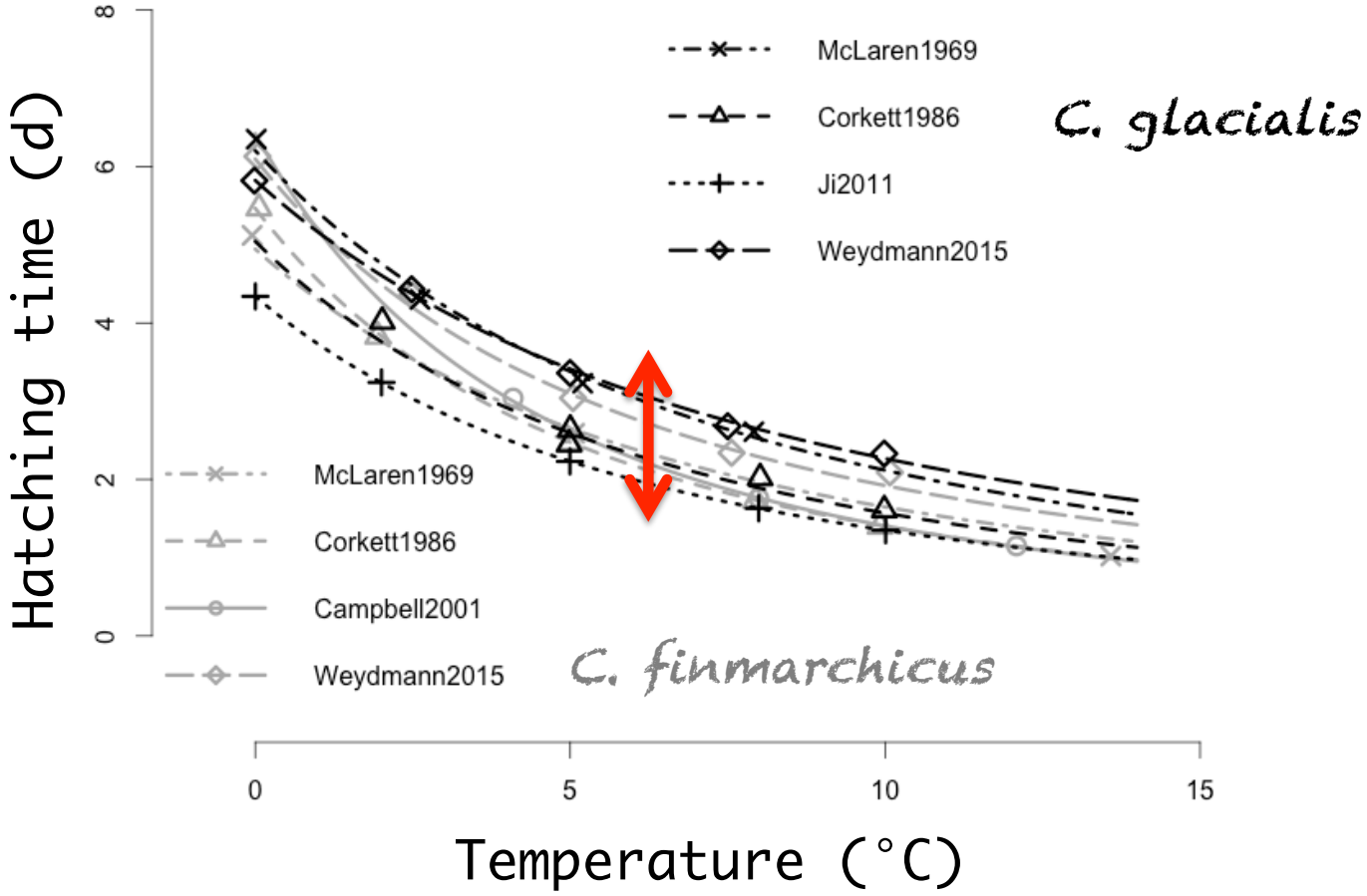
Insufficient knowledge of the stage duration of *C. glacialis* model makes the parameterization of a stage structured model unreliable and a box model (one state variable) has been chosen to represent this species.

[...]



Parameterization of *Calanus* models

- Knowledge is insufficient... or confusing !



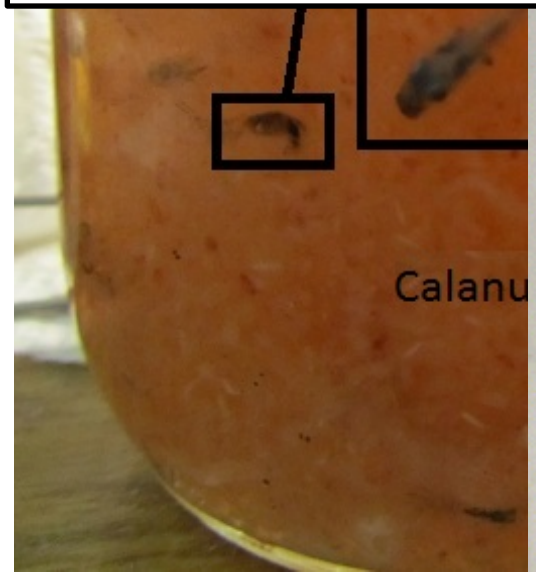
“Hybrids” ?… in models ?

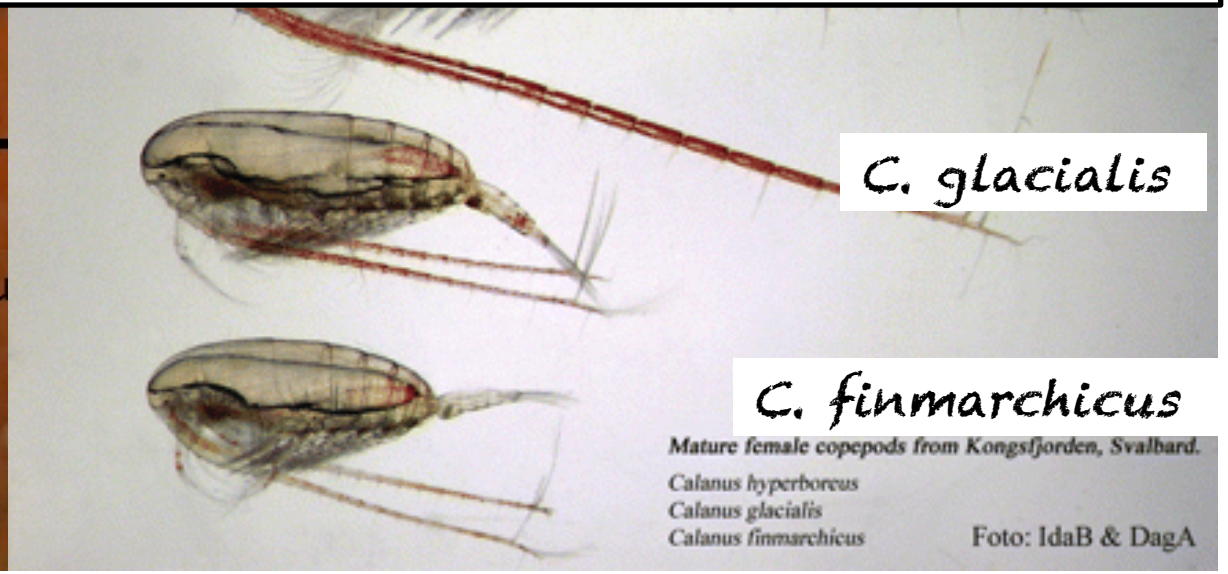
Limnol. Oceanogr., 57(4), 2012, 1057–1066

doi:10.4319/lo.2012.57.4.1057

Natural hybridization between *Calanus finmarchicus* and *C. glacialis* (Copepoda) in the Arctic and Northwest Atlantic

Geneviève J. Parent,[a,*] Stéphane Plourde,[b] and Julie Turgeon [a]





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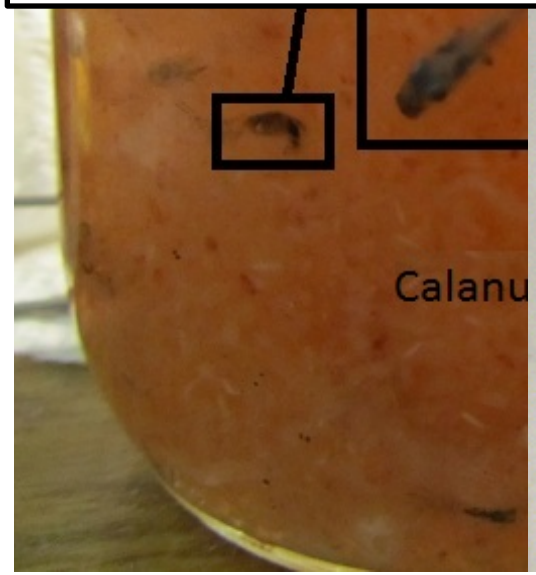

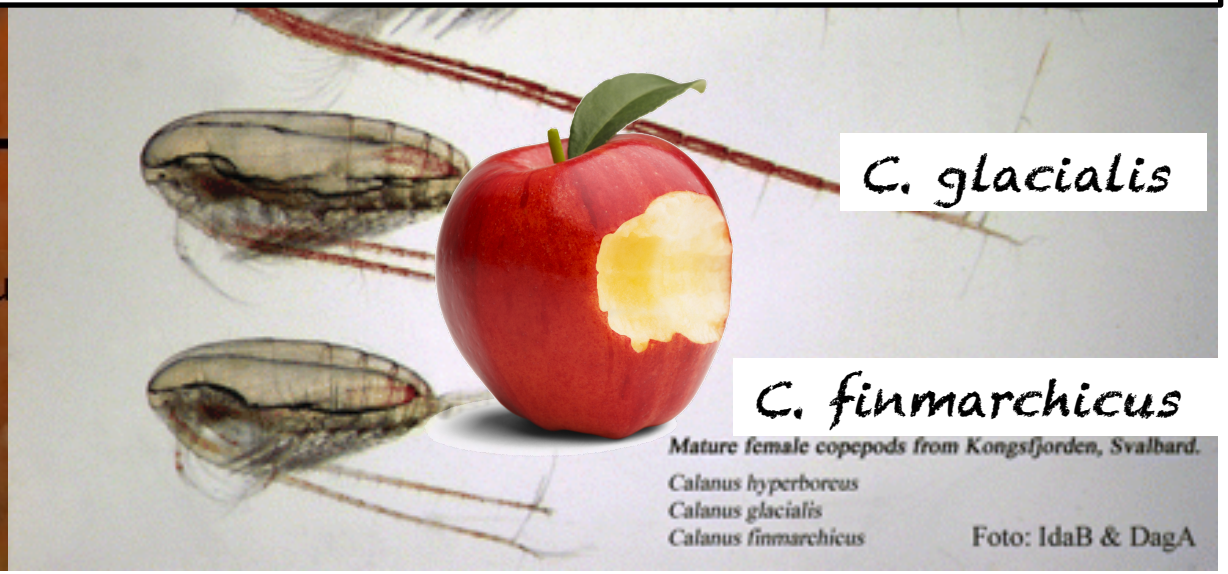

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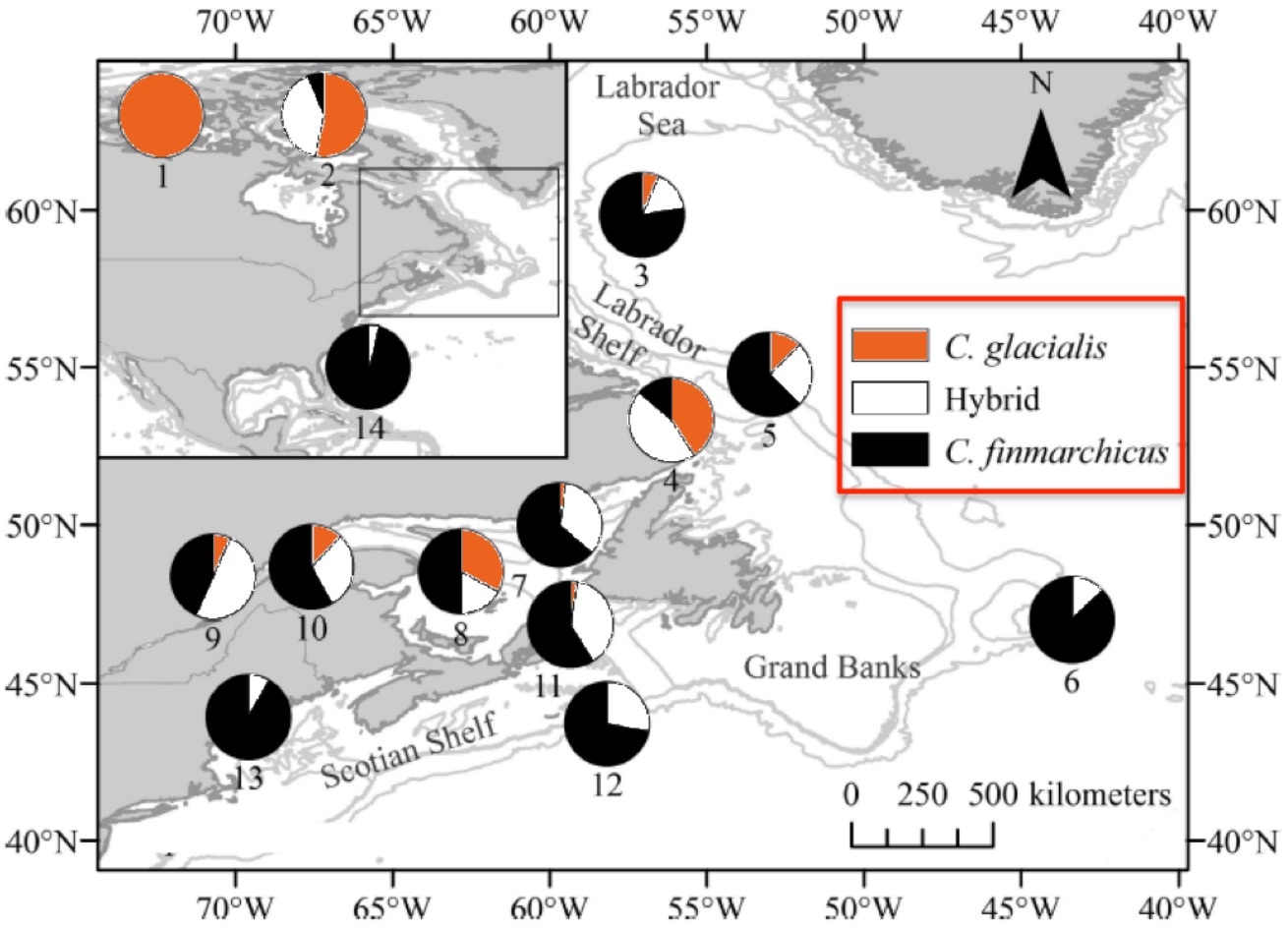
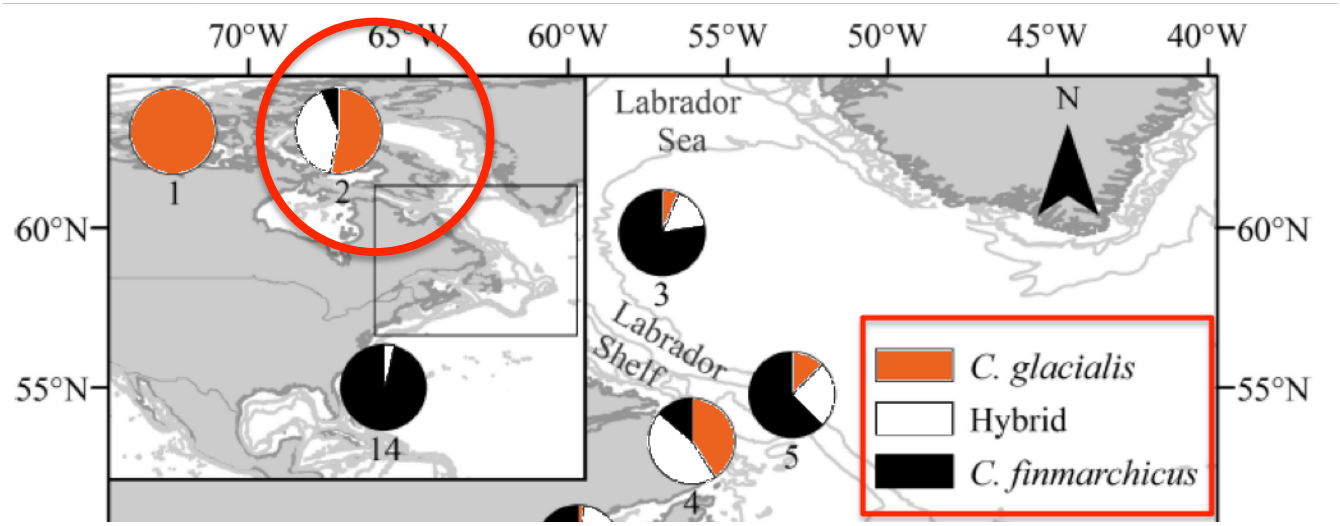


Fig. 1. Map of the Arctic and North Atlantic Oceans showing the frequency of parental species and hybrids (as determined with mtDNA and nucDNA markers) at each station.

“Hybrids” ?… in models ?



- Add more confusion since the only true Arctic stage development data published for *C. glacialis* = McLaren 1969 in Frobisher Bay (ᐃᖃᓗᐃᑦ) …

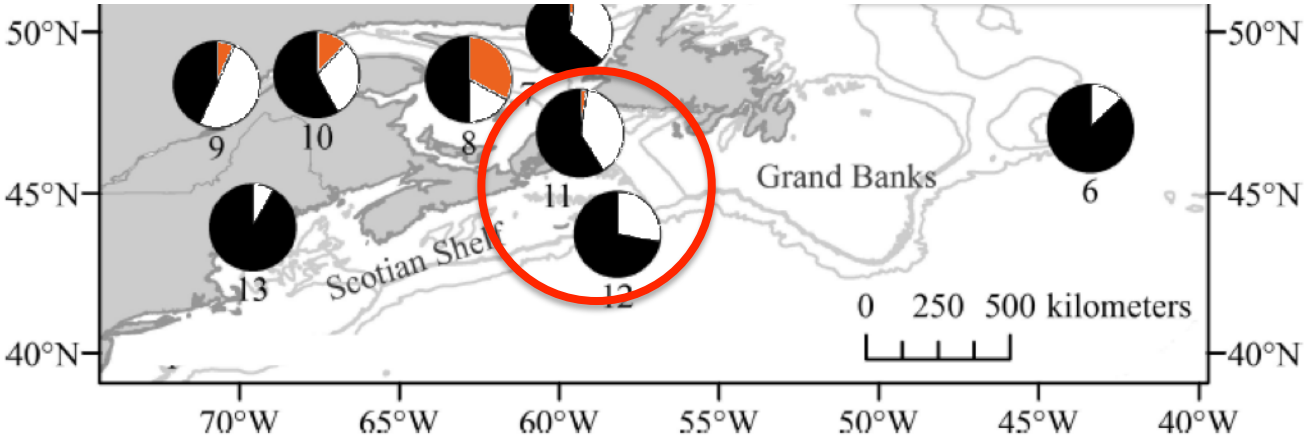
70°W 65°W 60°W 55°W 50°W 45°W 40°W

Fig. 1. Map of the Arctic and North Atlantic Oceans showing the frequency of parental species and hybrids (as determined with mtDNA and nucDNA markers) at each station.

“Hybrids” ?… in models ?

70°W 65°W 60°W 55°W 50°W 45°W 40°W

- … but all current models based (at least in part) on Corkett et al. 1986 who sampled down there:



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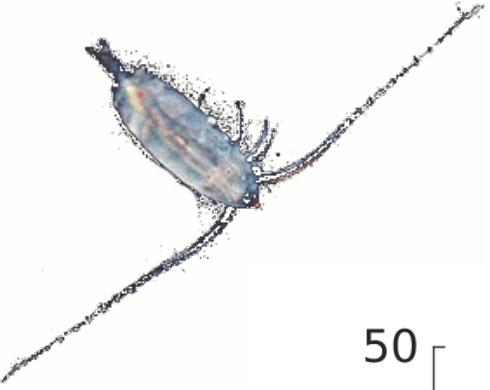
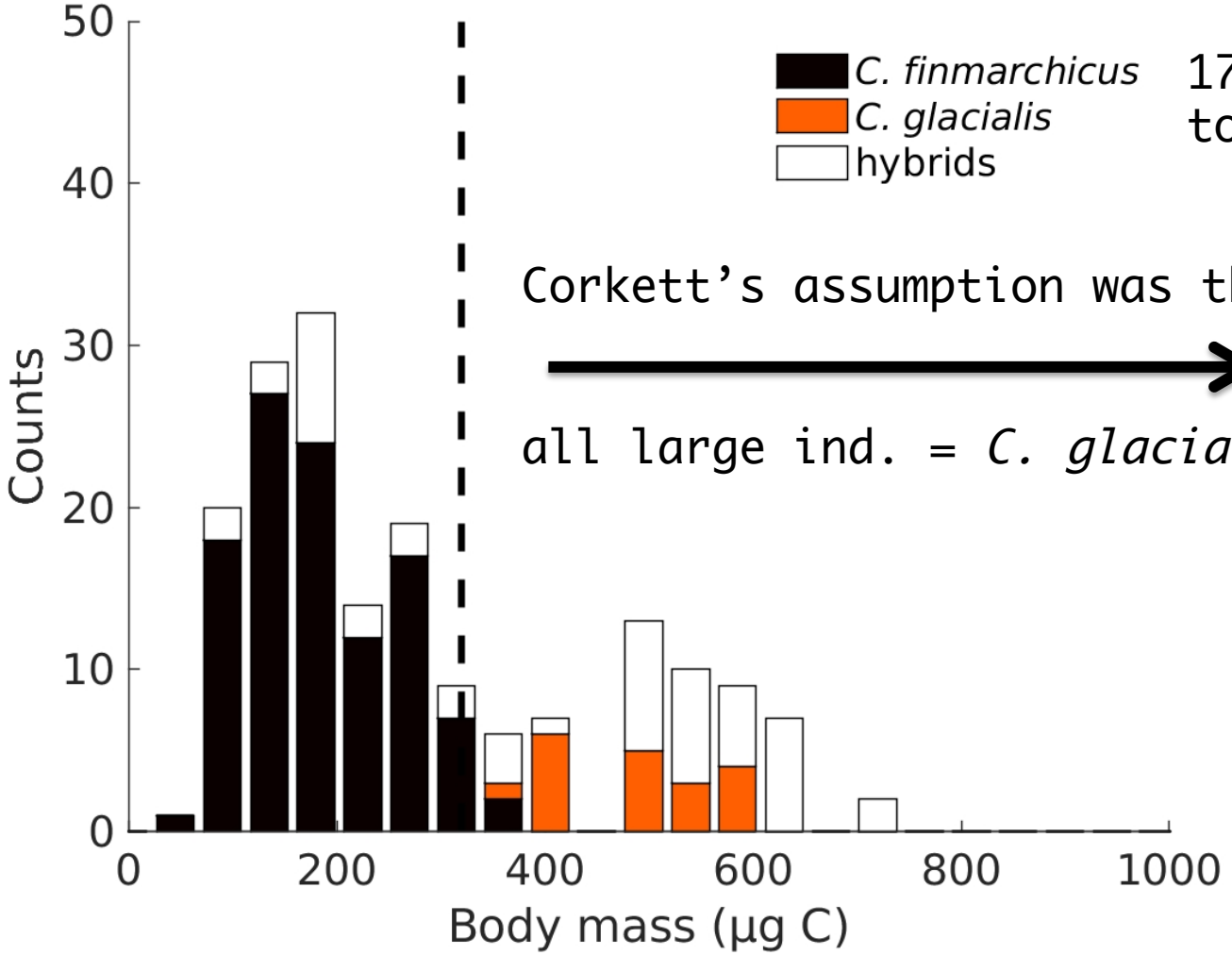
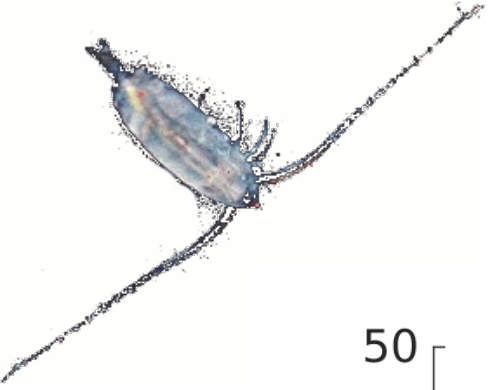


“Hybrids” ?… in models ?





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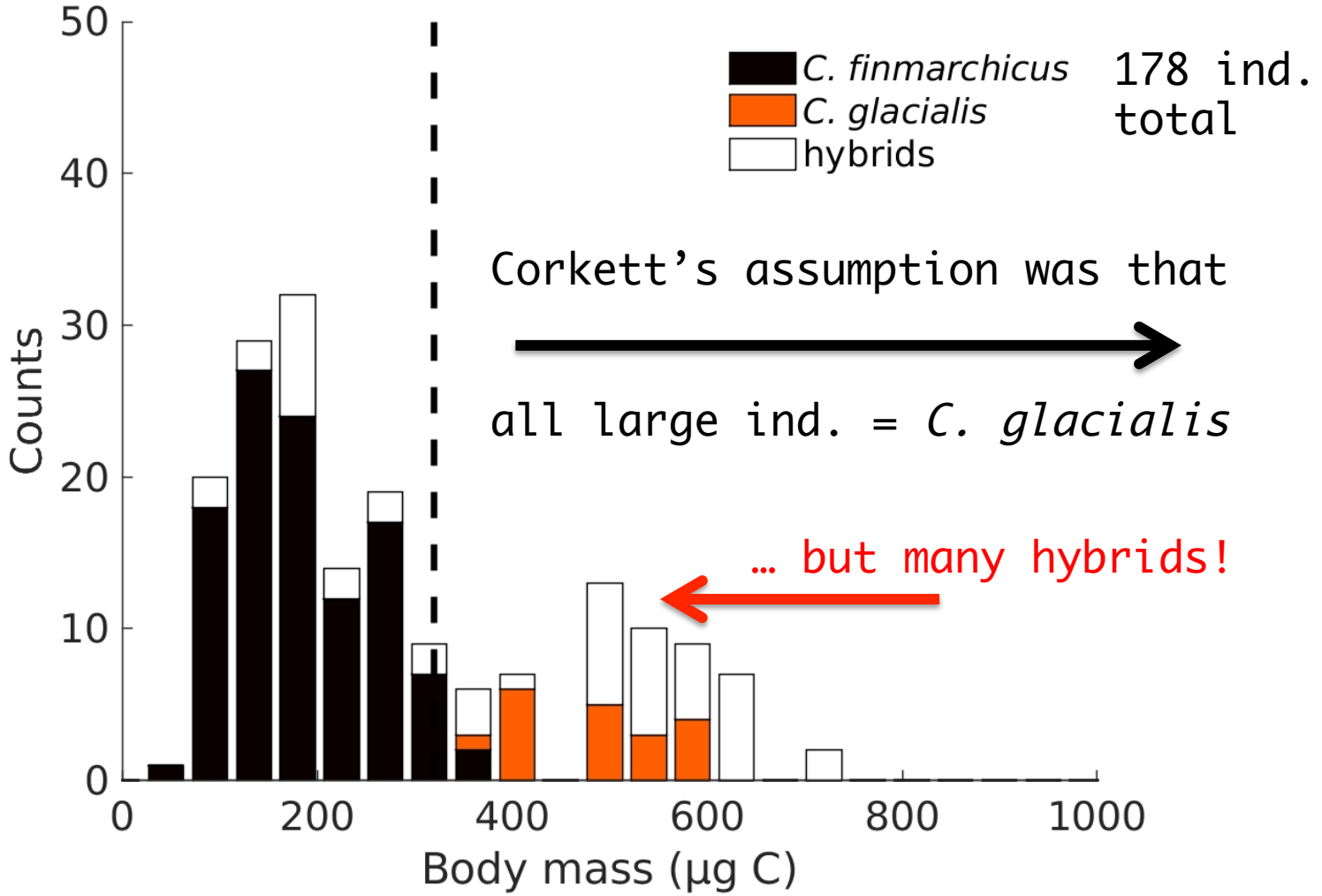
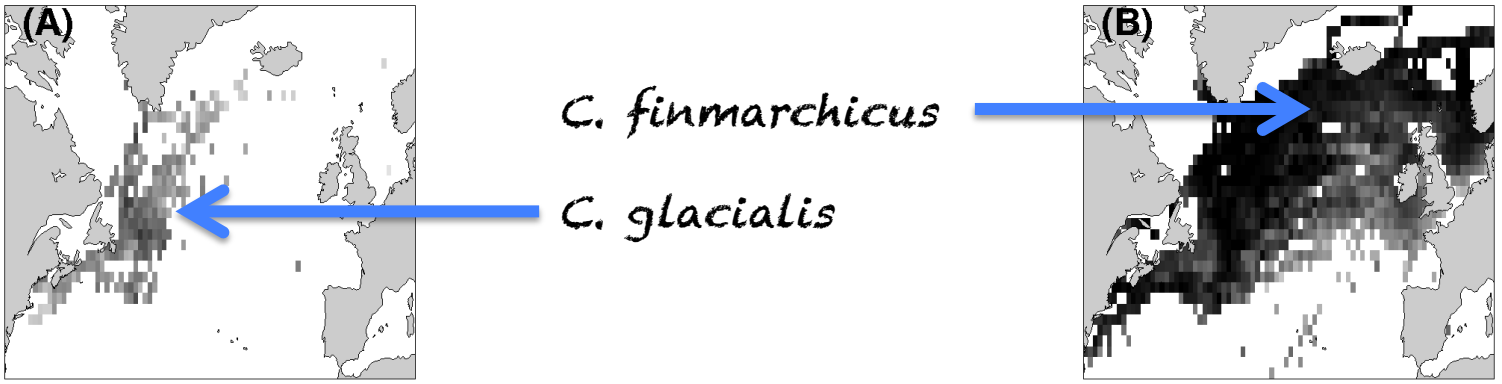
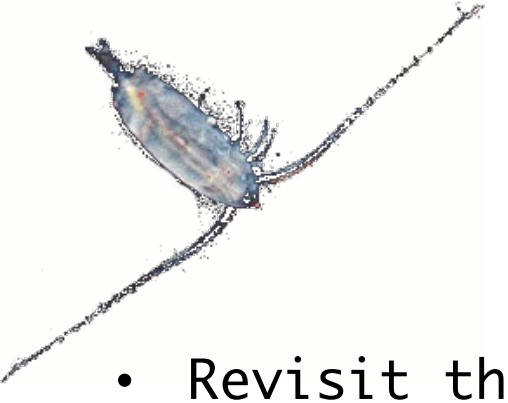


“Hybrids” ?… in models ?

- Revisit the morphologically-based biogeography ?



CPR data; species abundance estimated according to the categories “large Calanus” and “*C. finmarchicus*”



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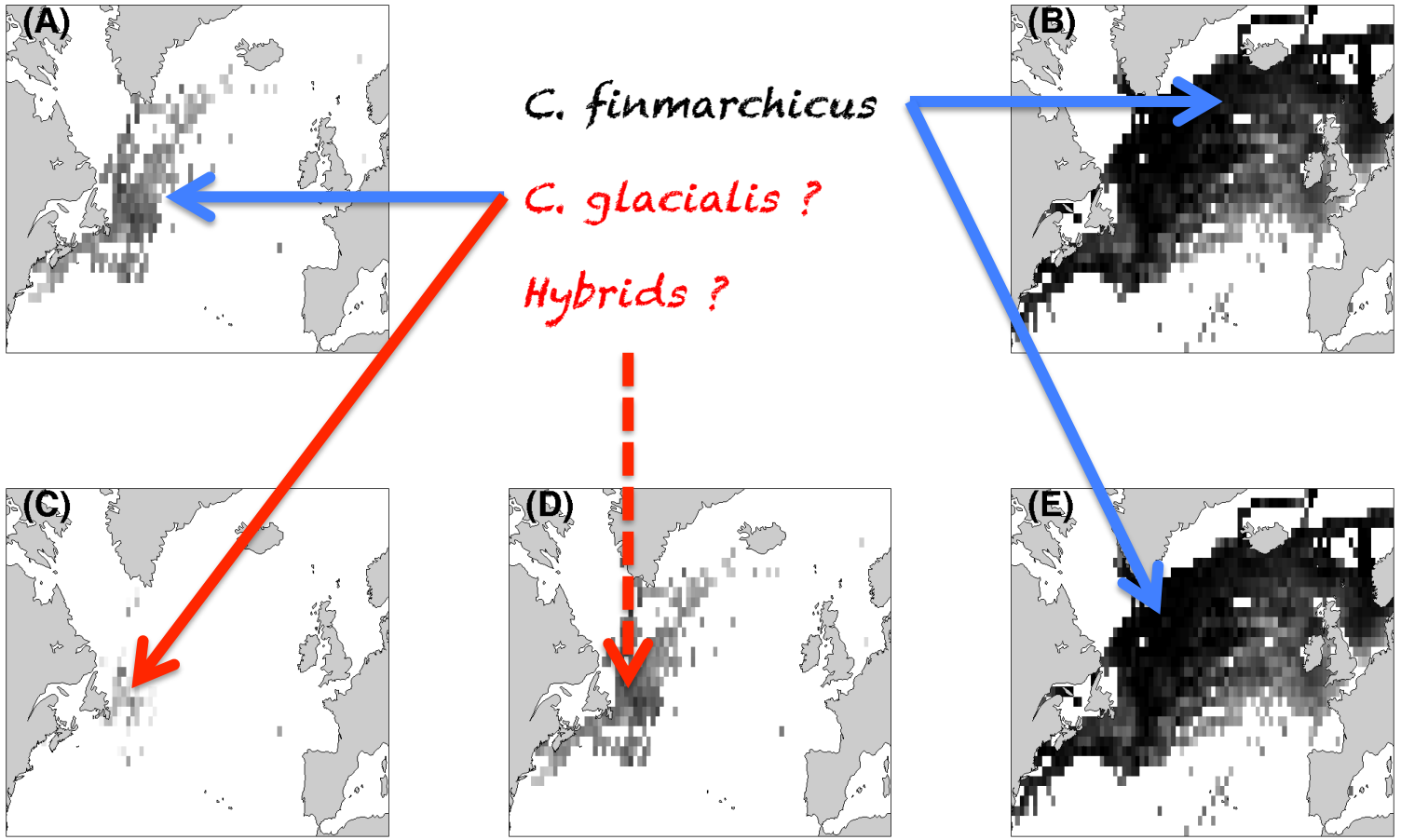
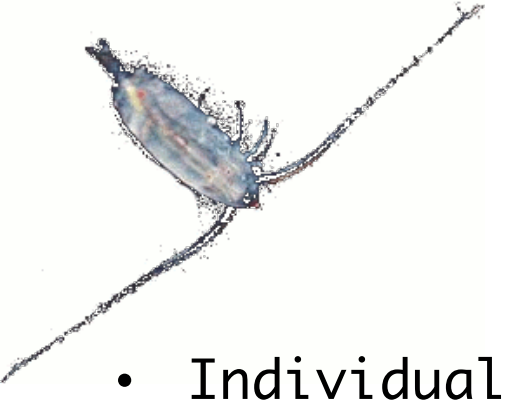
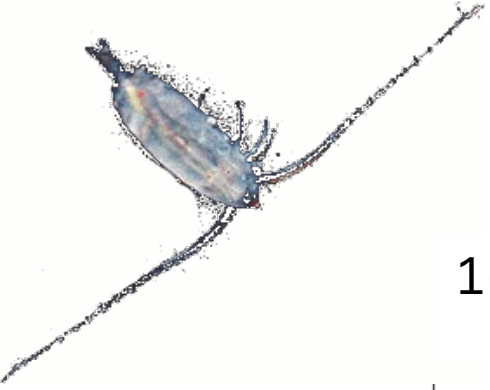




“Hybrids” ?… in models ?

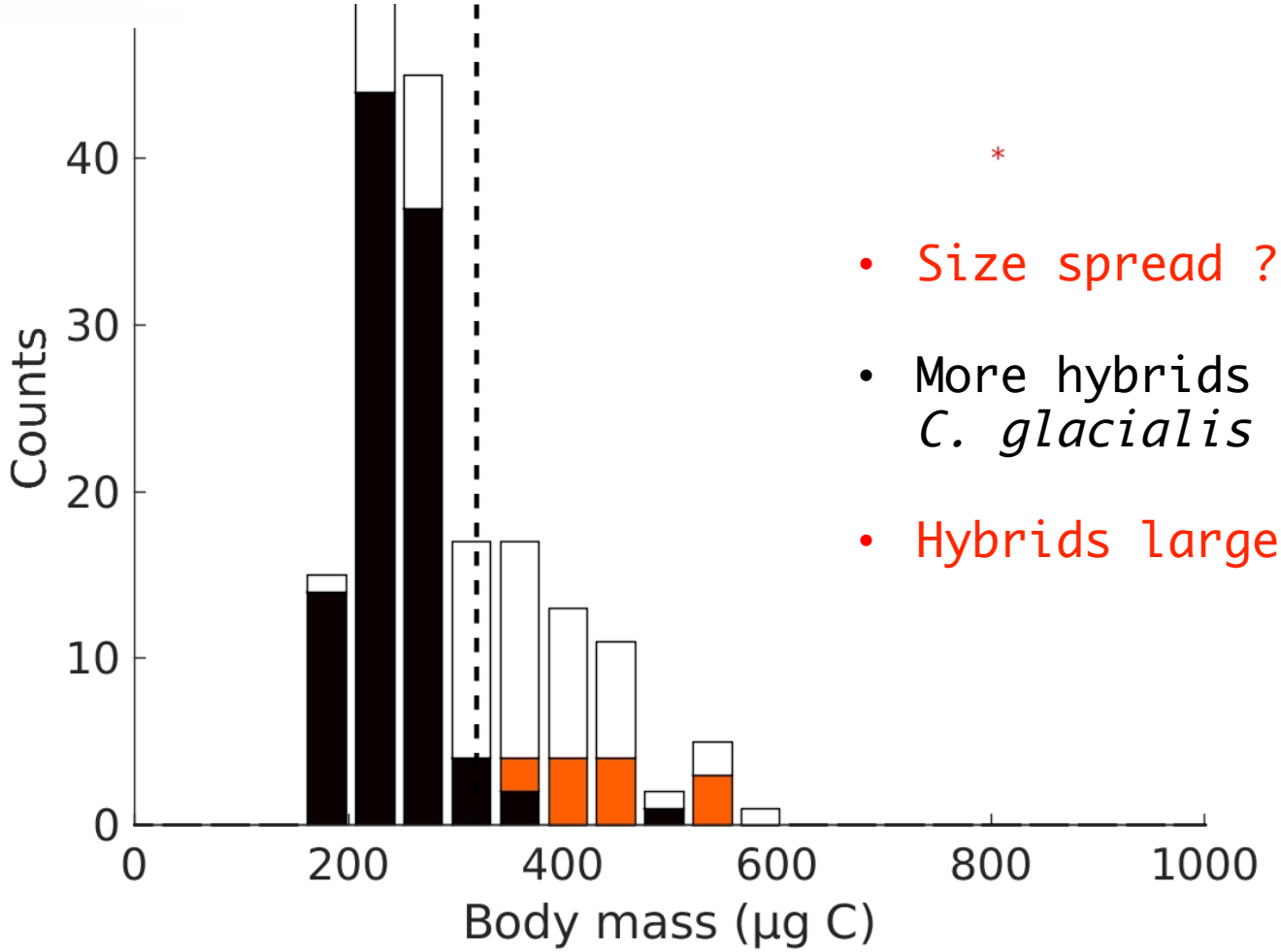
- Individual-based model with probabilities of encounter (mating) based on relative abundances
- Traits vary with a CV=3% from the species-specific canonical “paramosome” (vector of parameters)
- Hybridization strategies:

1. Average of parameters from each parent (“mean”)
2. Simple exchange of parameters (“cross”)
3. 1 or 2 + maternal effect (“mom” = values inherited as is)

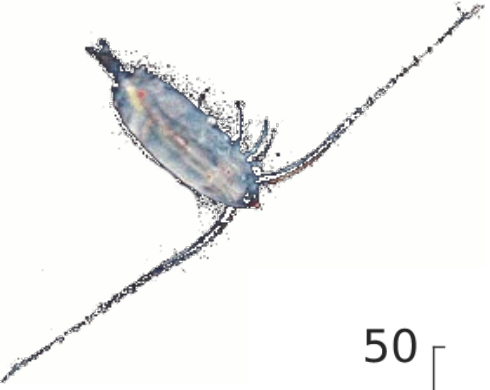


“Hybrids” ?… in models ?

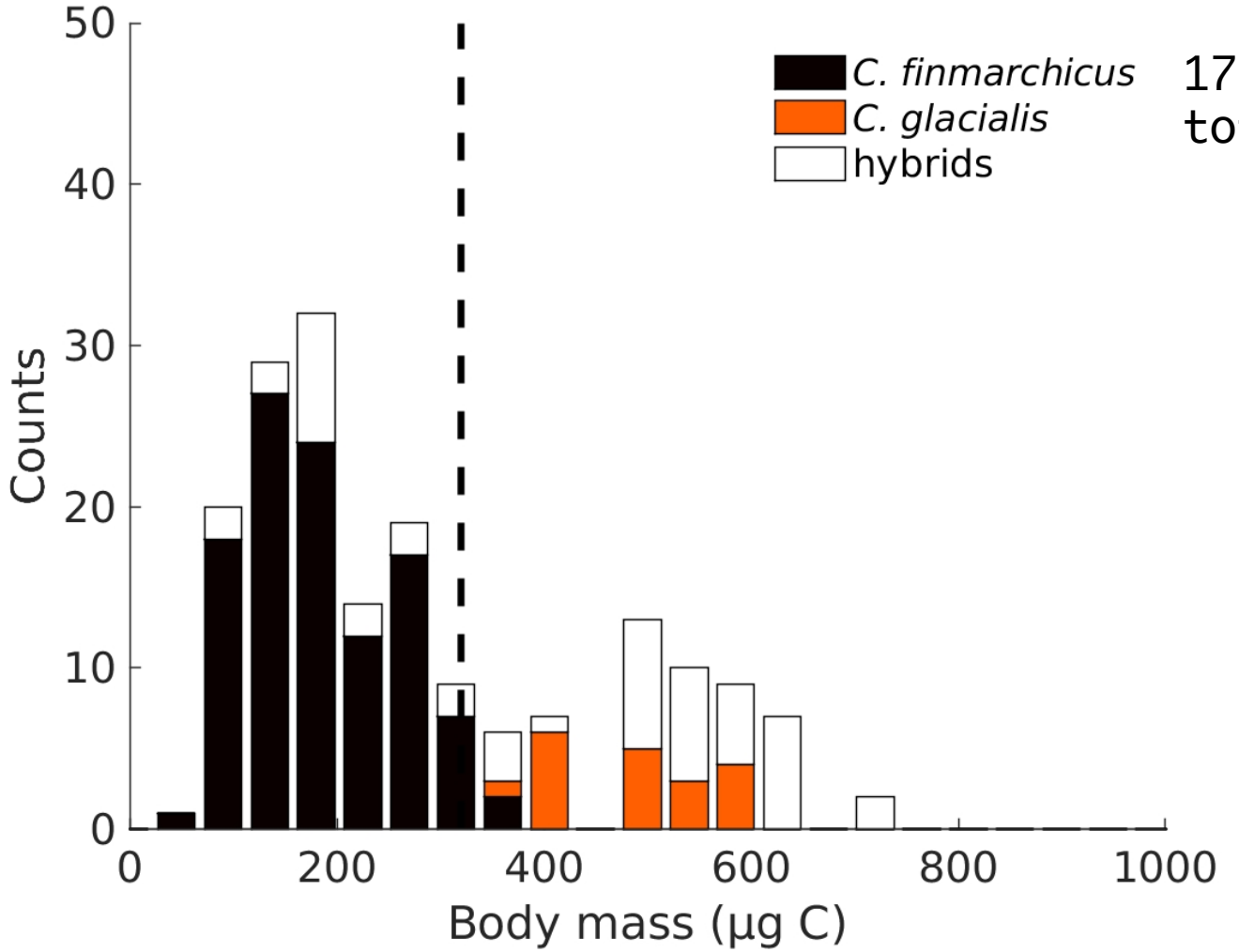
1- Results from the “mean” scenario

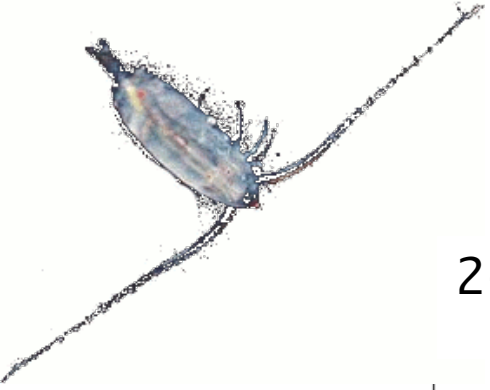


- Size spread ?
- More hybrids in *C. glacialis* range
- Hybrids larger ?



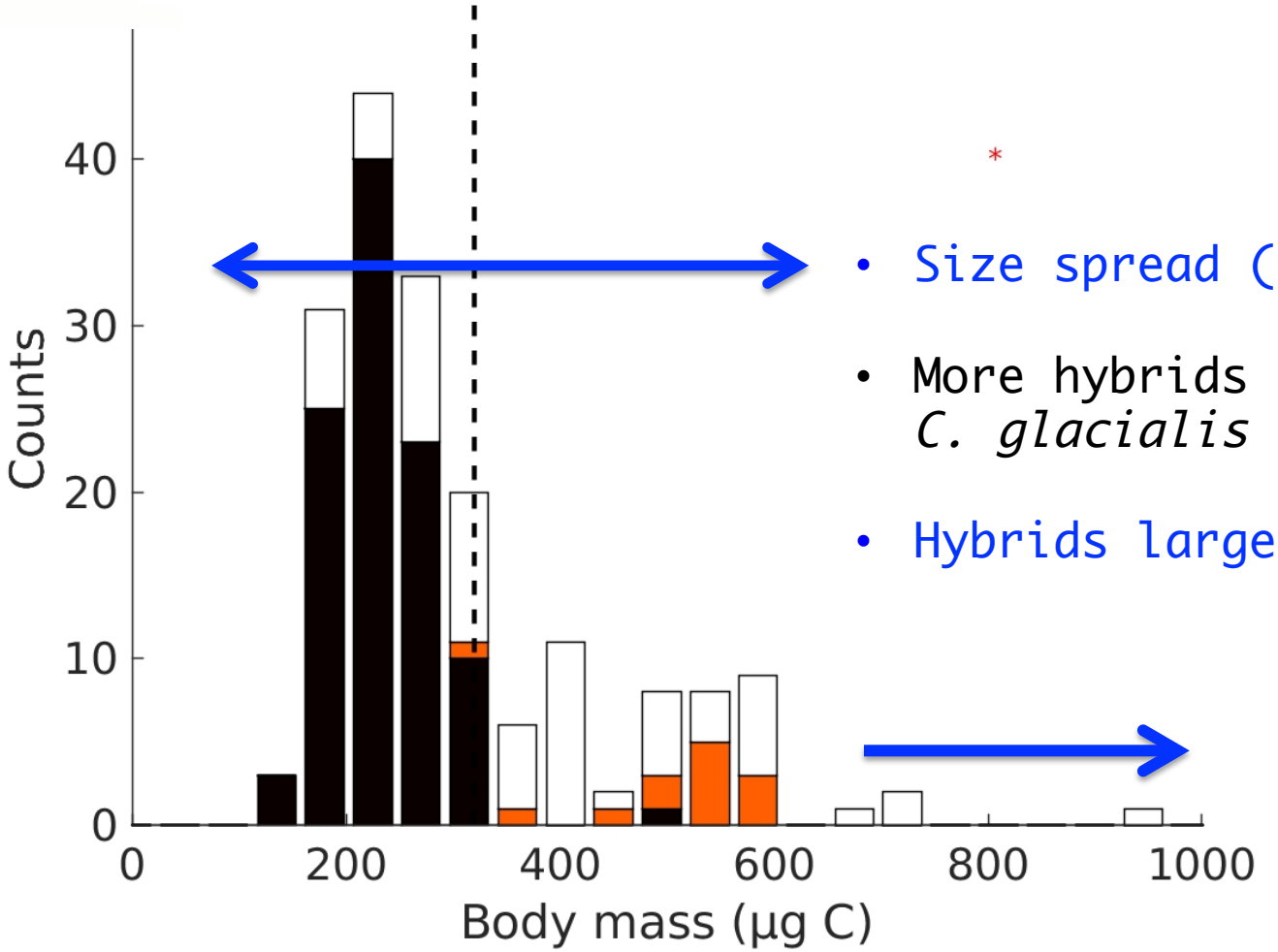
“Hybrids” ?… in models ?



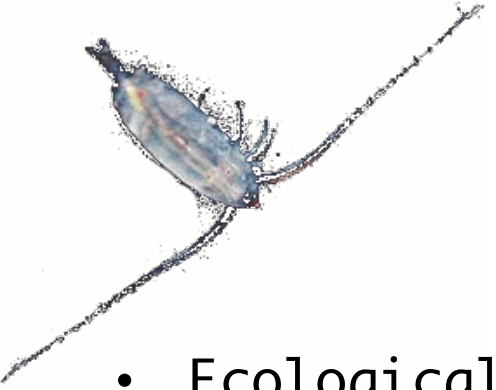


“Hybrids” ?… in models ?

2- Results from the “cross” scenario

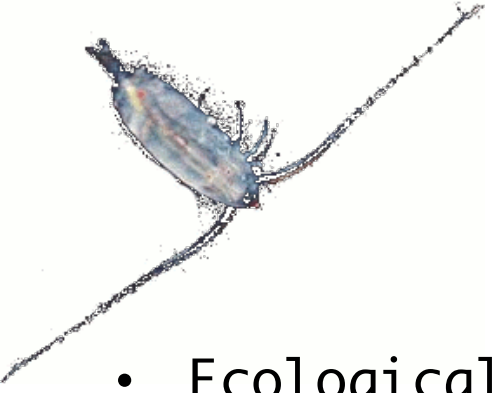


- Size spread (?)
- More hybrids in *C. glacialis* range
- Hybrids larger



Prospective

- Ecological implications
- This was just about size...
- Biogeography & boundaries between species affected by climate change
- Hybridization an issue within the contact zone of the species that is their respective biogeographical margins!
- Investigate phenotypical response and plasticity of hybrids + re-invest in underappreciated lab experiments



Prospective

- Ecological implications

Vol. 524: 1–9, 2015
doi: 10.3354/meps11240

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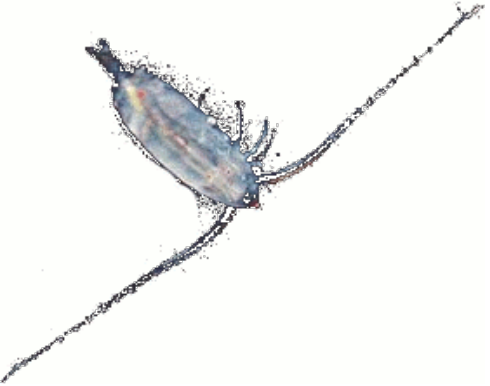
FEATURE ARTICLE

Phenology and fitness of *Calanus glacialis*, *C. finmarchicus* (Copepoda), and their hybrids in the St. Lawrence Estuary

Geneviève J. Parent[1,*], Stéphane Plourde[2], Pierre Joly[2], Julie Turgeon[1]


Takk!



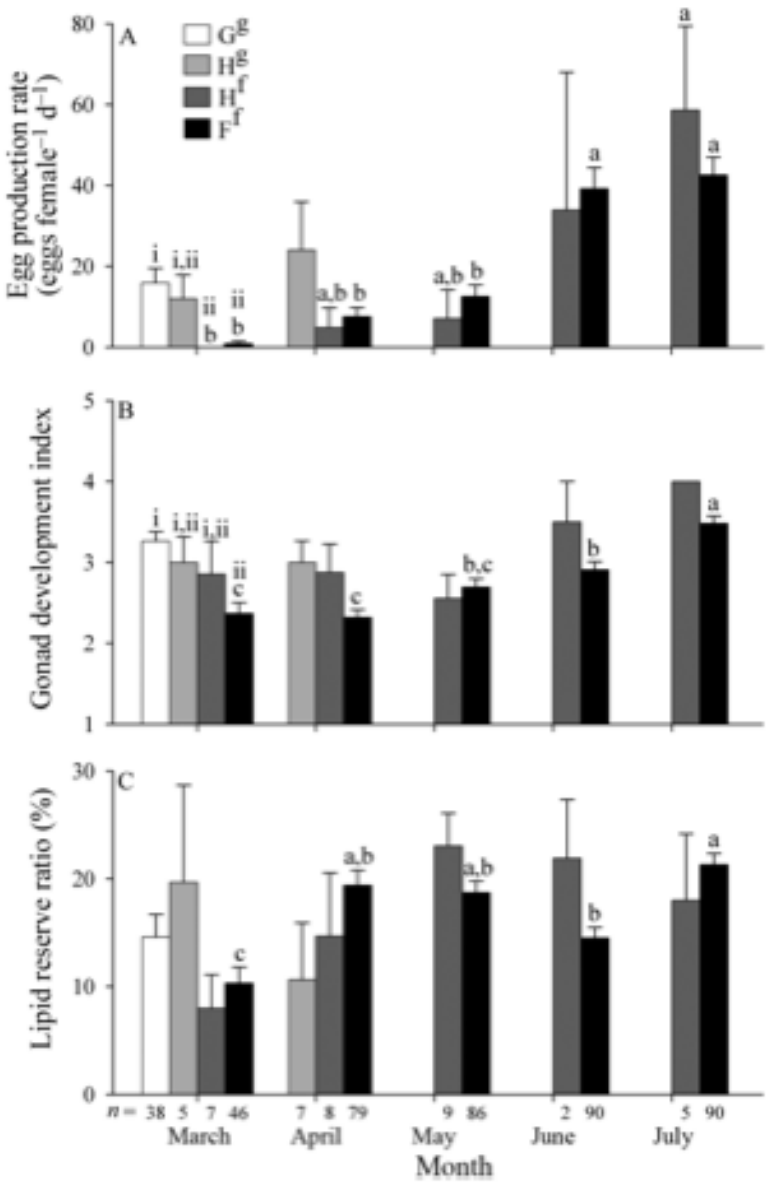


Fig. 3. Temporal variability of reproductive output at Rimouski Station in 2010 (mean ± SE). Genotypes are identified as in Table 1. Different small letters above bars indicate values that are significantly different from one another within a month (e.g. i, ii) or across months (e.g. a, b) (Tukey-Kramer, $p < 0.05$). Only samples with size ≥ 3 are considered for statistical analyses

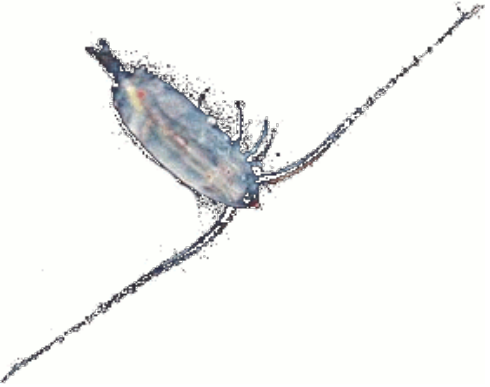
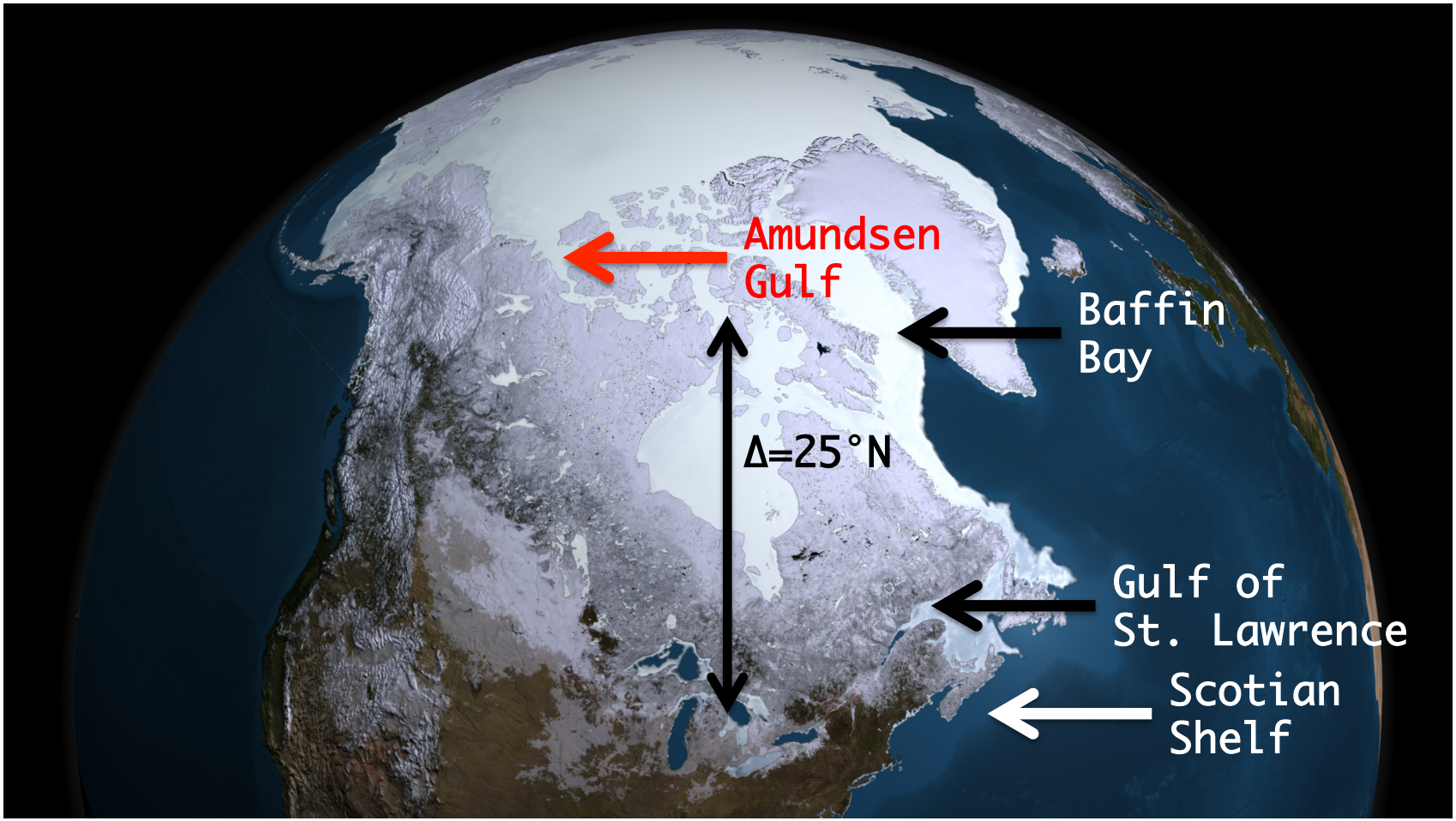


Table 1. Mean development time ($\overline{DT}_i$) and standard deviation (σ_{DT_i}) and mean stage duration ($\overline{SD}_i$) and standard deviation (σ_{SD_i}) calculated from laboratory data in Campbell *et al.* (2001) for *C. finmarchicus* held under constant temperatures (4°, 8°, and 12°C) and food conditions (high, medium, and low). Also shown is the coefficient of variation (*C.V.*).

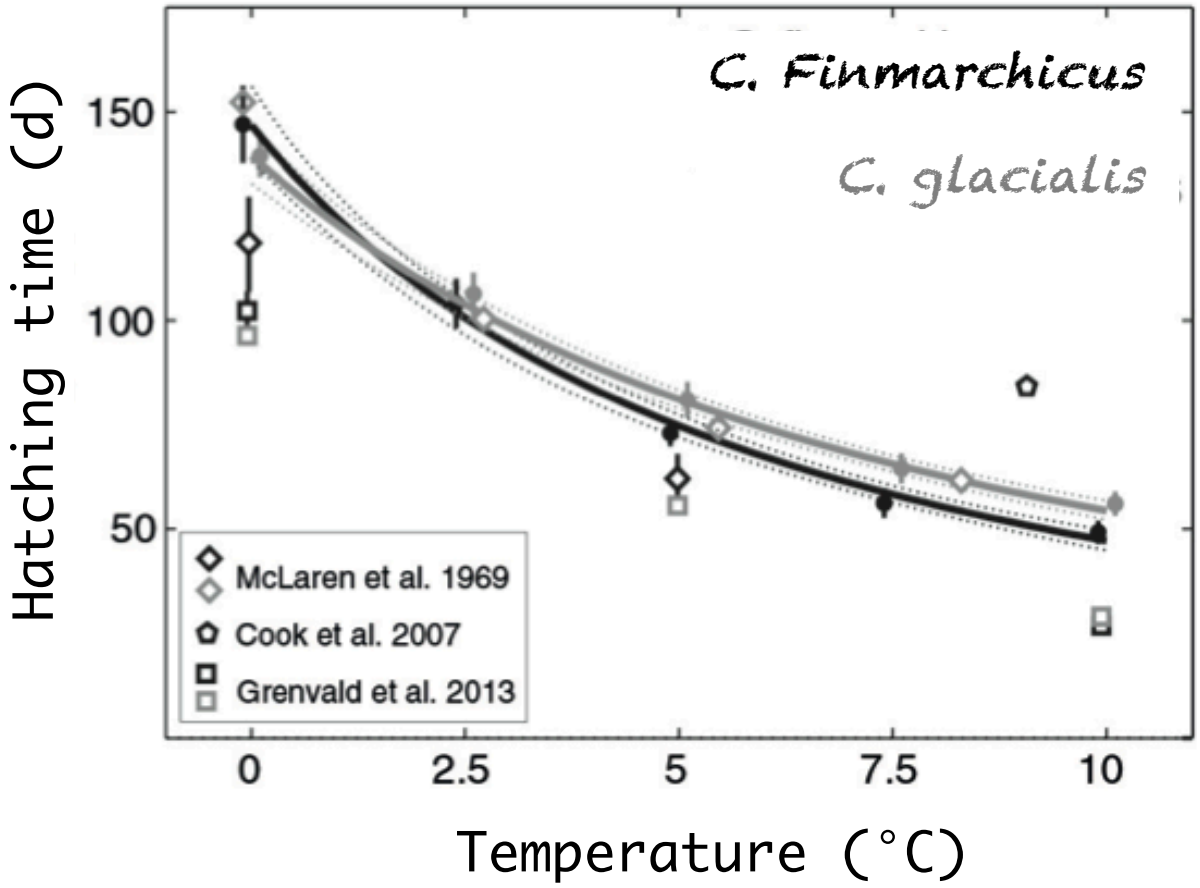
Temperature (°C)/food level	*i*	4°C/high		8°C/high		12°C/high		8°C/medium		8°C/low	
		Mean ± s.d. (d)	*C.V.* (%)	Mean ± s.d. (d)	*C.V.* (%)	Mean ± s.d. (d)	*C.V.* (%)	Mean ± s.d. (d)	*C.V.* (%)	Mean ± s.d. (d)	*C.V.* (%)
DT_i(d)	NI	3.0 ± 0.3	10	1.8 ± 0.4	20	1.1 ± 0.3	23	1.8 ± 0.4	20	1.7 ± 0.4	20
	NII	5.0 ± 0.5	9	2.9 ± 0.4	14	2.0 ± 0.3	17	2.8 ± 0.4	14	2.9 ± 0.4	14
	NIII	7.9 ± 0.6	8	4.8 ± 0.5	10	3.1 ± 0.4	13	4.6 ± 0.5	10	4.6 ± 0.5	10
	NIV	15 ± 0.8	5	8.9 ± 0.5	6	5.7 ± 0.5	8	10 ± 2.3	22	13 ± 5.0	39
	NV	19 ± 1.0	5	11 ± 0.6	5	7.0 ± 0.5	7	15 ± 2.8	19	19 ± 5.4	28
	NVI	23 ± 1.1	5	13 ± 0.7	5	8.5 ± 0.6	7	18 ± 3.3	18	23 ± 5.9	26
	CI	27 ± 1.3	5	16 ± 0.7	5	10 ± 0.6	6	21 ± 3.7	17	27 ± 6.3	23
	CII	32 ± 1.5	5	18 ± 0.7	4	12 ± 0.7	6	26 ± 4.2	16	33 ± 6.7	20
	CIII	37 ± 1.6	5	22 ± 0.9	4	15 ± 0.8	5	31 ± 4.6	15	38 ± 7.1	19
	CIV	45 ± 1.8	4	26 ± 0.9	4	18 ± 0.9	5	37 ± 5.1	14	44 ± 7.5	17
	CV	56 ± 2.0	3	32 ± 1.0	3	22 ± 0.9	4	45 ± 5.6	12	58 ± 7.9	14
	CVI	91 ± 19	21	44 ± 4.9	11	30 ± 4.4	15	62 ± 8.9	14	80 ± 15	18

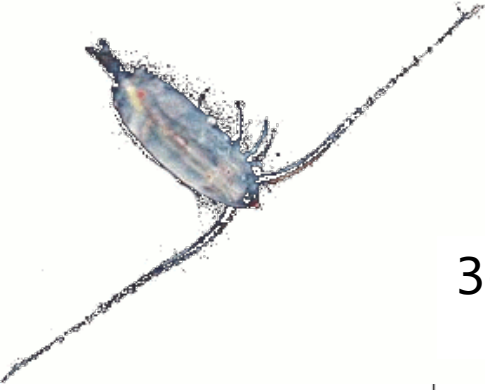
Some new results



Parameterization of *Calanus* models

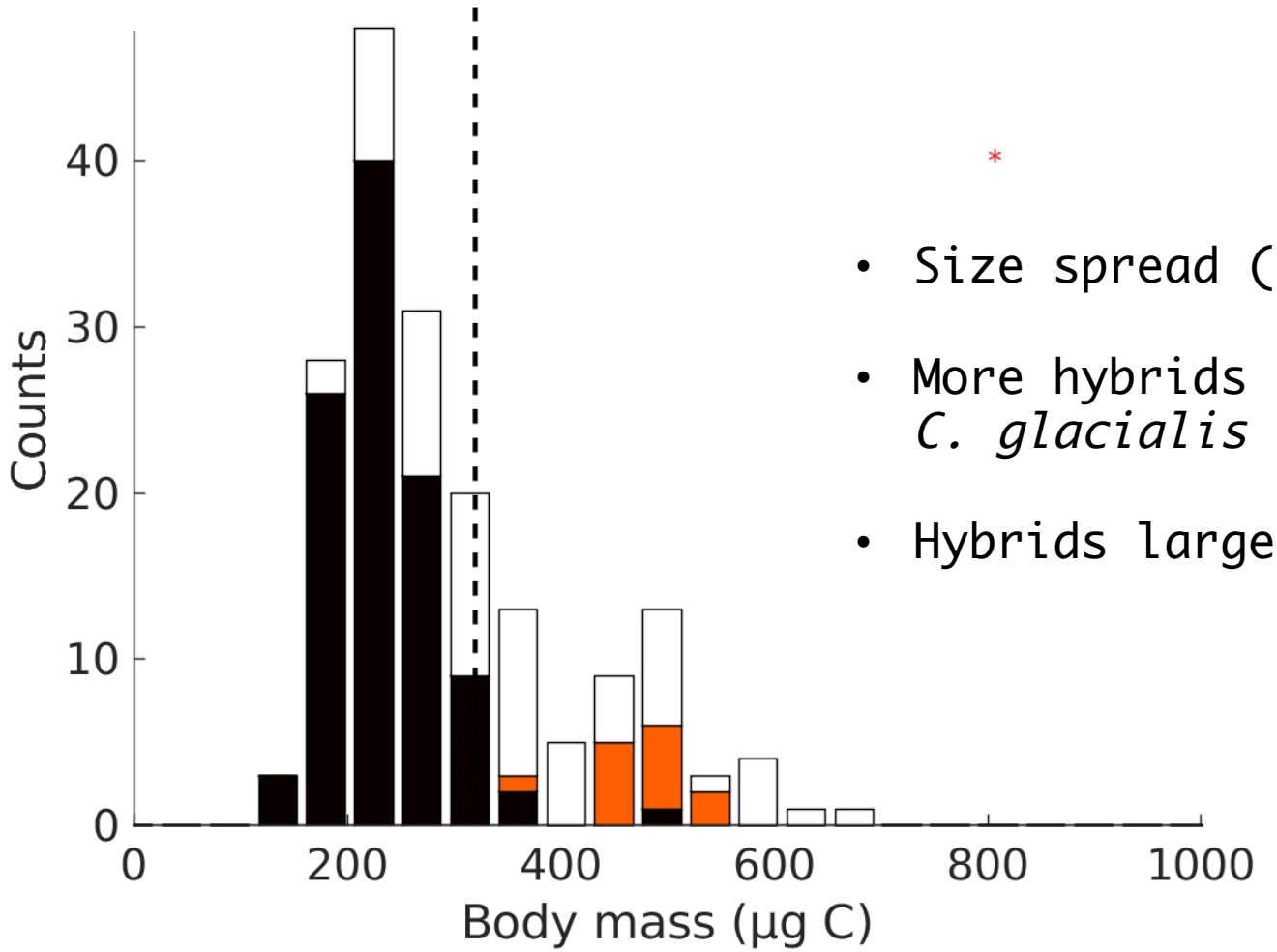
- Effect size matters





“Hybrids” in trait-based models?

3- Results from the “mom” scenario



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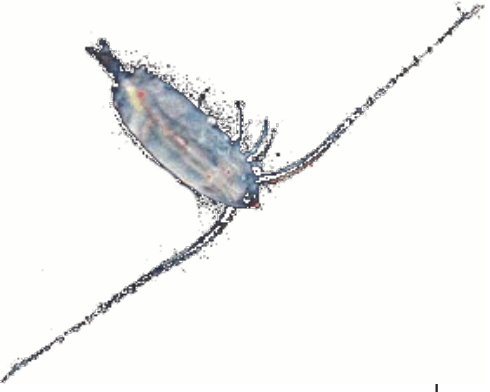
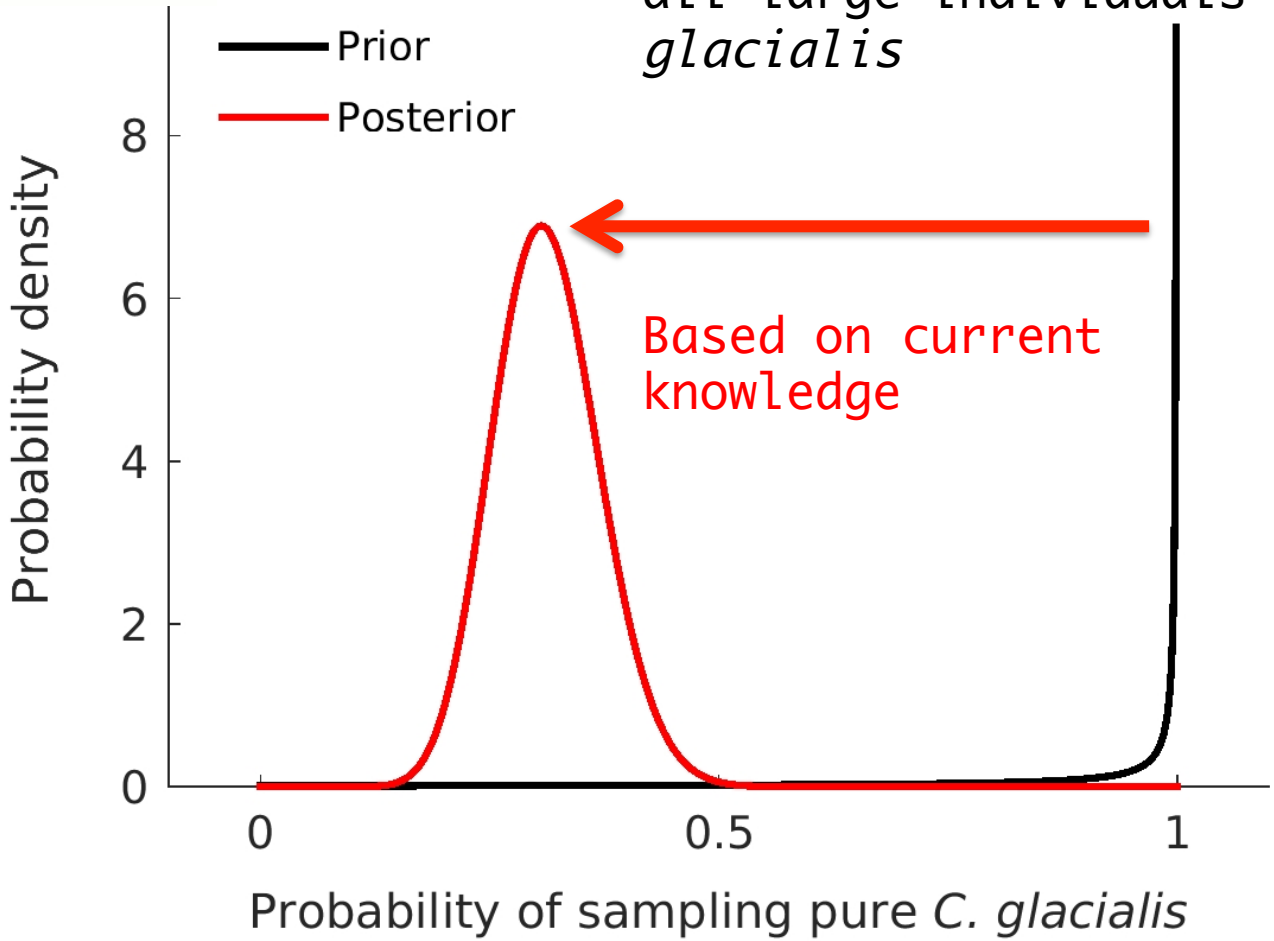
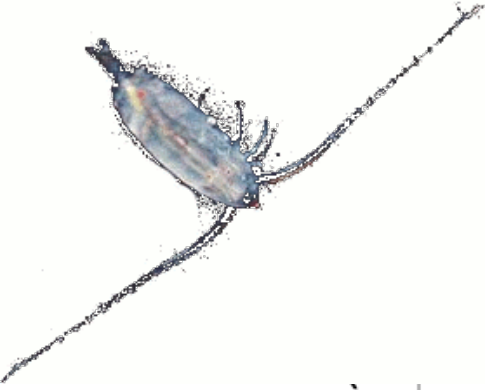


“Hybrids” ?… in models ?

Prior = strong belief that all large individuals are *glacialis*



Based on current knowledge



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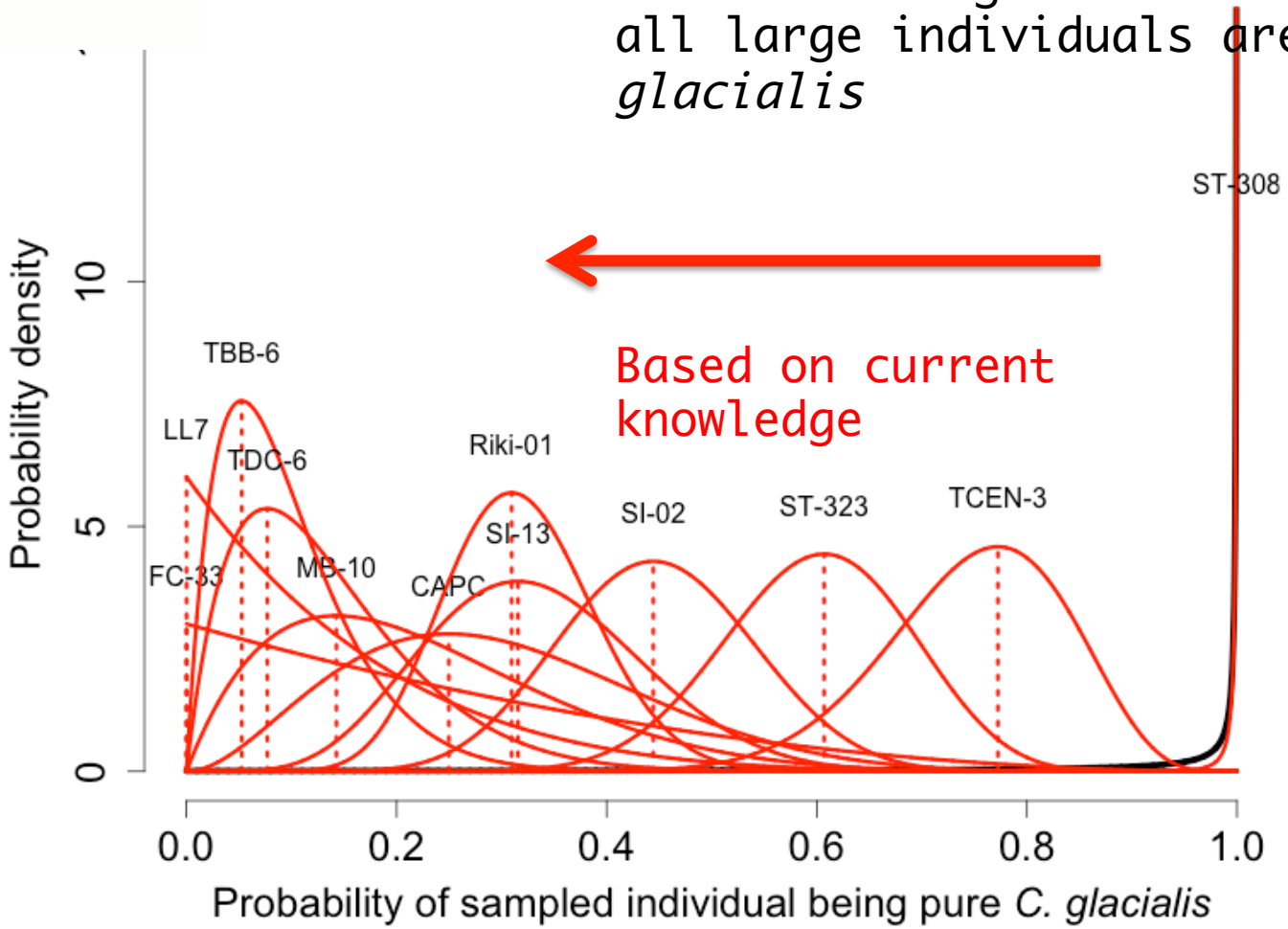
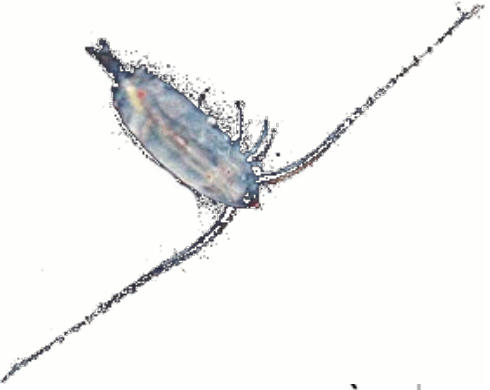
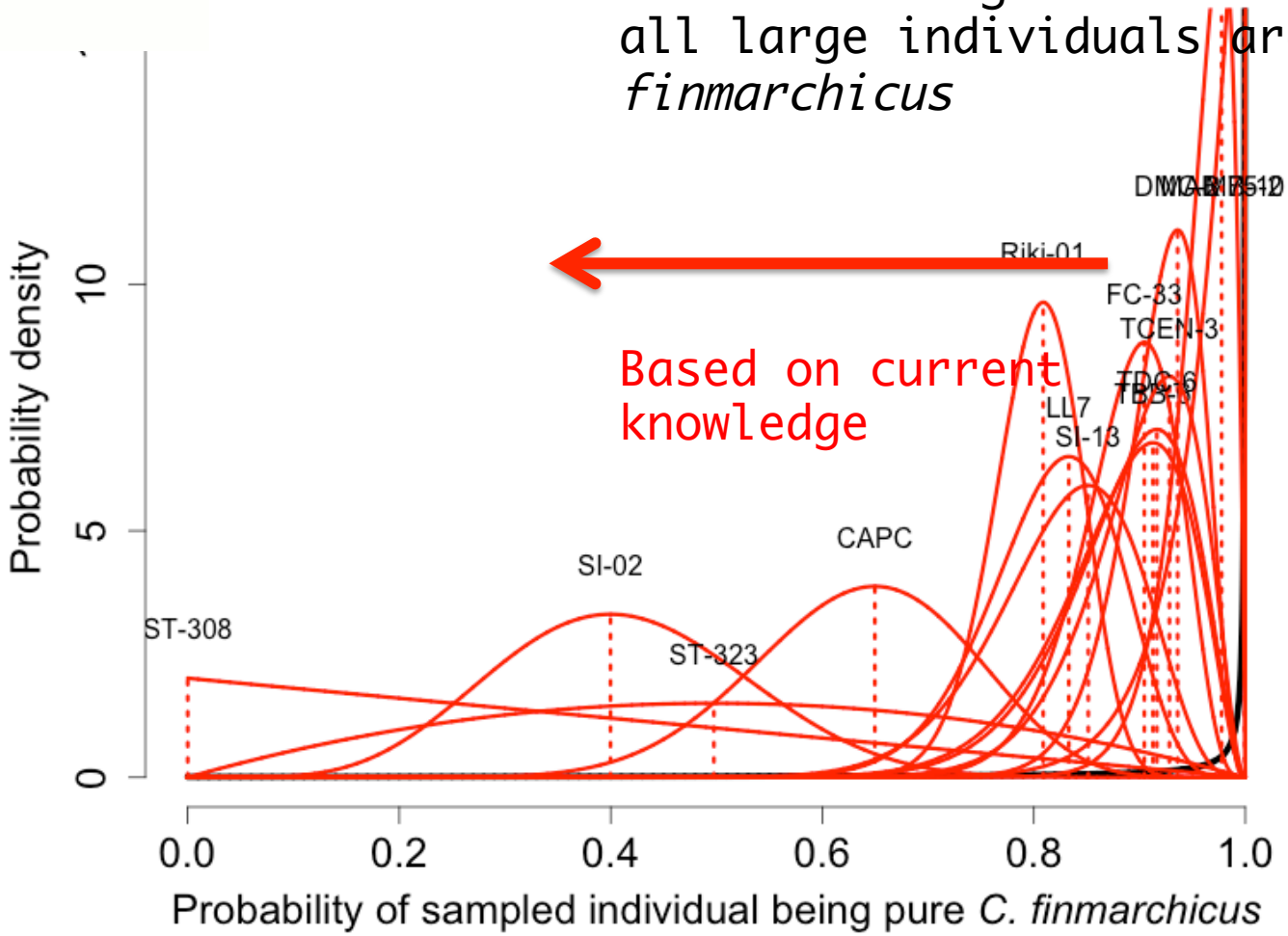
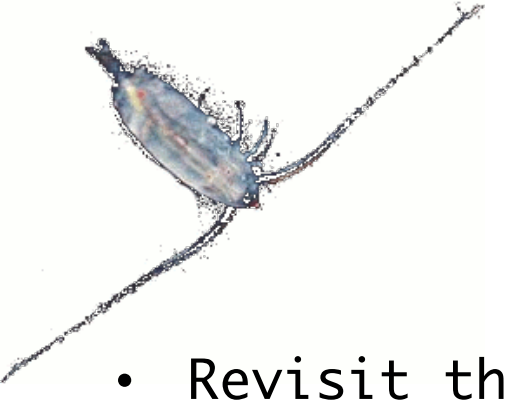




“Hybrids” ?… in models ?

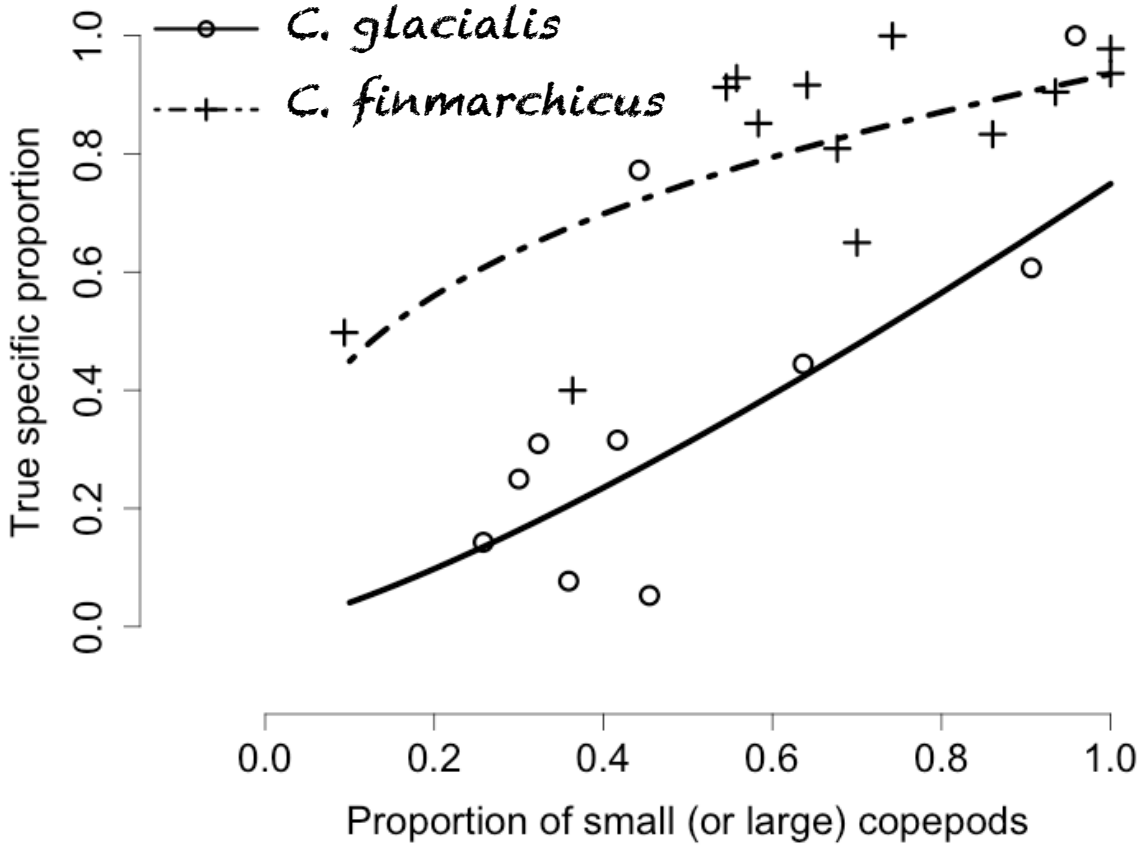
Prior = strong belief that all large individuals are *finmarchicus*

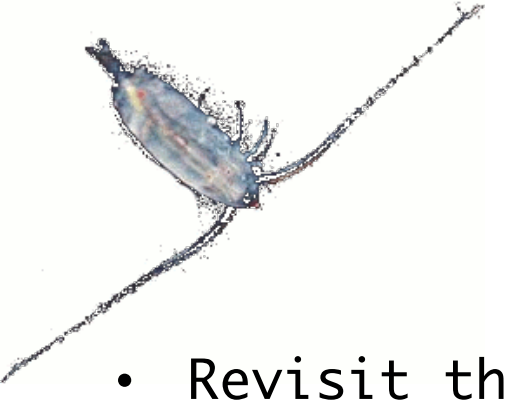




Parameterization of *Calanus* models

- Revisit the morphologically-based biogeography ?





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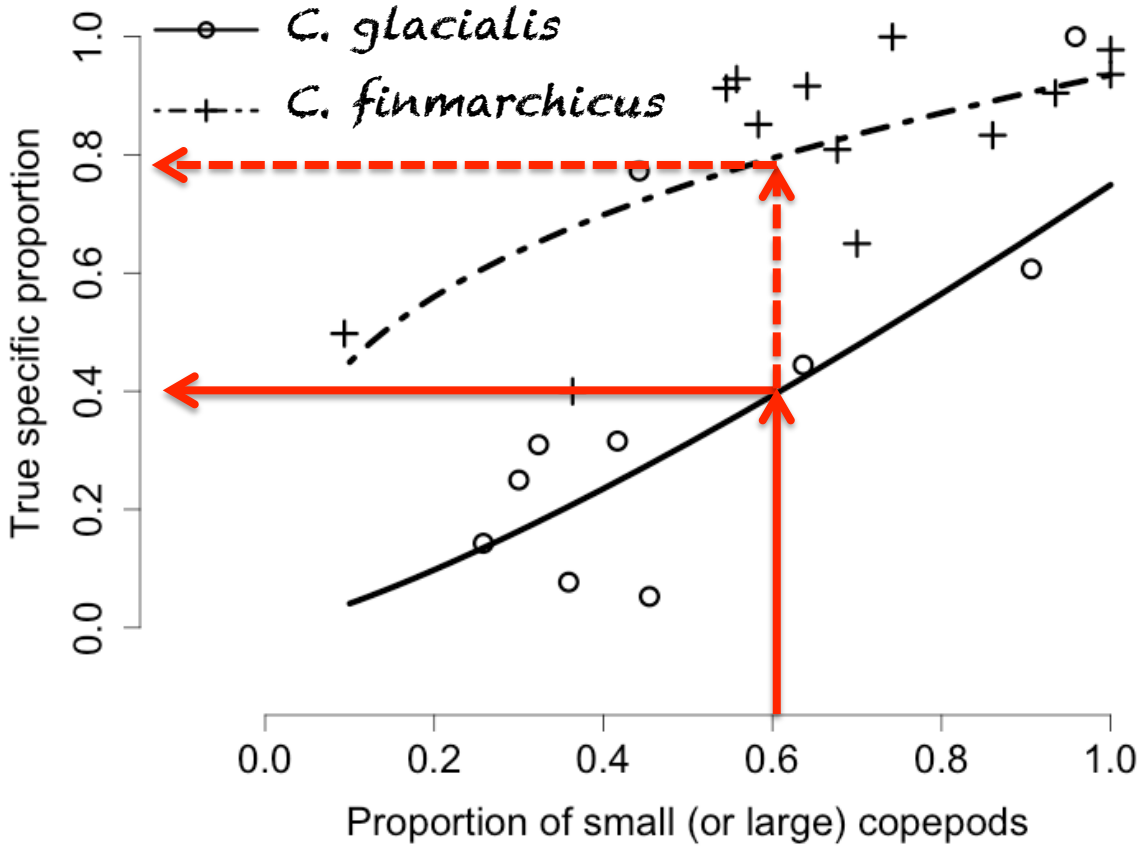
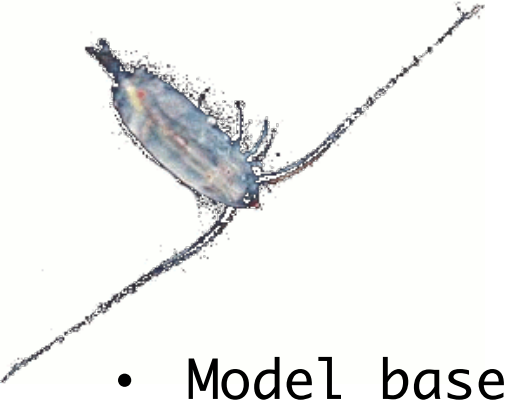
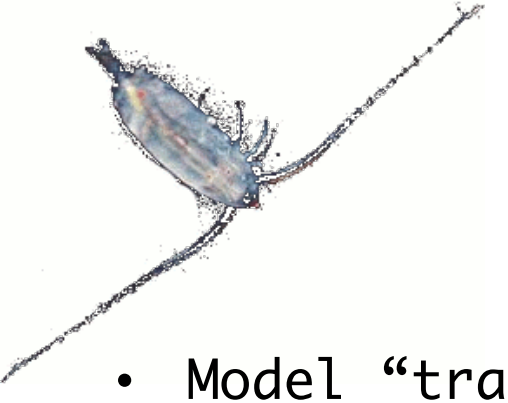




“Hybrids” ?… in models ?

- Model based on first principles of biology and physiology (Arrhenius, allometry, Holling type...)
- Allow the decoupling between growth & development = variable individual size
- Now model the whole life cycle of 3 (sub)Arctic *Calanus* congeners + different strategies (use McLaren 1969 for *C. glacialis* development)
- Hybridization ?



“Hybrids” ?… in models ?

- Model “traits” = clusters of parameters used for a specific process / life-cycle strategy

```
%   cluster(1)  : param(1)     -> ME     : Mass of the egg (ug C)
%   cluster(2)  : param(2)     -> Eb     : Activation energy for metabolism (eV K^-1)
%   cluster(3)  : param(3)     -> B0(1)  : Metabolism constant for active individuals
%   cluster(4)  : param(4)     -> B0(2)  : Metabolism constant for diapausing individuals
%   cluster(5)  : param(5)     -> Ed     : Activation energy for development (eV K^-1)
%   cluster(6)  : param(6:18)  -> SD0    : Stage-specific stage duration coefficients (d)
%                                          generation time varies, not the equiproportional schedule
%   cluster(7)  : param(19)    -> A      : Assimilation efficiency = 1-egestion(~.3)-excretion(~.1)
%   cluster(8)  : param(20:21) -> F0     : Food limitation coefficient for nauplii|copepodid
%   cluster(9)  : param(22:23) -> K0     : Kernel prey encounter coefficient
%   cluster(10) : param(24:25) -> H0     : Handling time of food unit (s)
%   cluster(11) : param(26)    -> Ei     : Activation energy for ingestion (eV K^-1)
%   ...
```

- 9 groups belong to metabolism, development, feeding