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MACROSEA

WP4 MARINE MODELLING

ANNUAL MEETING, TRONDHEIM, OCTOBER 26, 2017

Ole Jacob Broch

WP4 Marine modelling

- Oliver Evans (U. Akron, OH)
- Shane Rogers
- Solveig Foldal
- Sanna Matsson
- Ole Jacob Broch (++)
- … and all the rest in

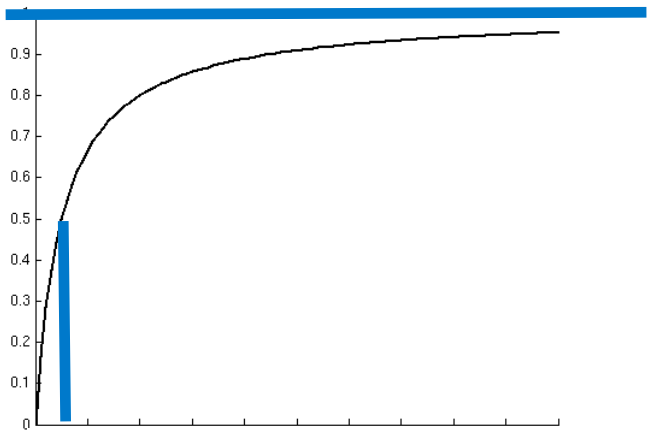
Goals

- Implement the results and research from the other WPs in growth models for kelp (eg. *S.latissima*) and other macroalgae
- Growth models are coupled with 3D hydrodynamic-ecosystem model system SINMOD (www.sintef.no/sinmod)
- Study growth and production potential, constraints etc

WP4

Original tasks

- T4.1 Tune growth model for *S. latissima* and *A. esculenta*
- T4.2 Develop growth model for *P. palmata*
- T4.3 Develop model for mechamincal interactions, light and nutrient shading

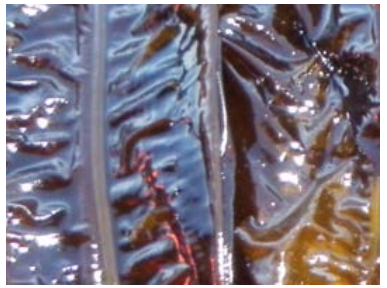


uptake, growth, pohto rates

external conc, internal status, light field

Specification of tasks

- **ST4.1 Develop and implement *general* individual based seaweed model**
- ST4.2 Tune *S. latissima* model for general model
- ST4.3 Develop growth model for *A. esculenta*
- ST4.4 Develop growth mode for *P. palmata*
- **ST4.5 Develop a population sub-model for light (self) shading**
- ST4.6 Develop a population sub-model for nutrient shading
- ST4.7 Develop population sub-model for individual interactions
- ST4.8 Effects of fouling
- ST4.9 Farm scale model with realistic constraints for production



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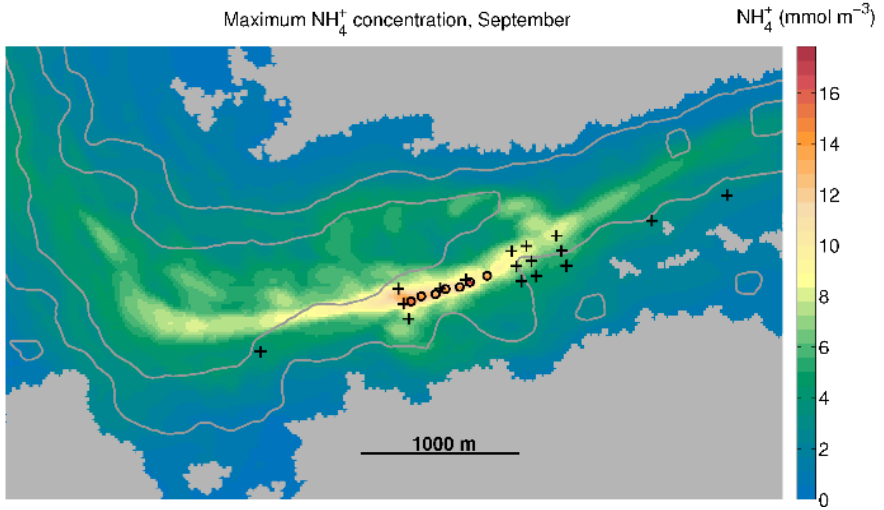
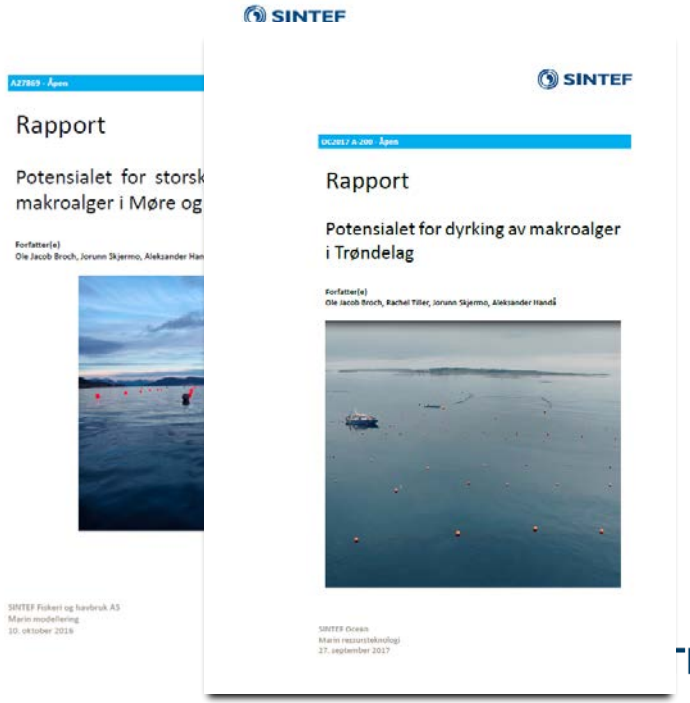
Plans for 2017

- Finish implementation of light shading
  - Simulations and testing
- Mortality and morphology
  - "Population model" and individual *S. latissima* model
- Physiology (input from WP2, WP5, WP6)
- Production modelling - synergies
  - KELPRO project – environmental effects of seaweed cultivation
  - TAREAL – Mapping good locations for kelp cultivation in Norway



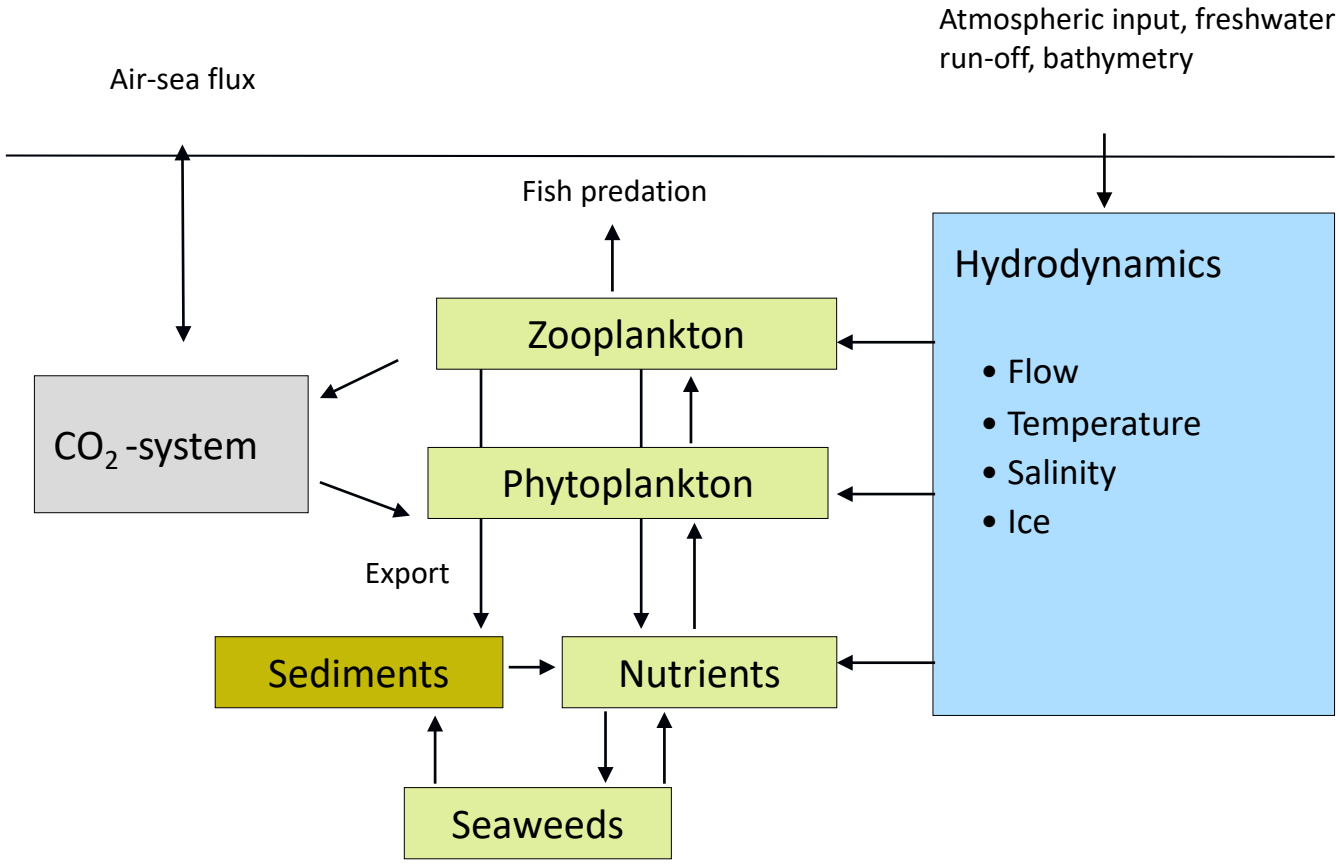


Plan today

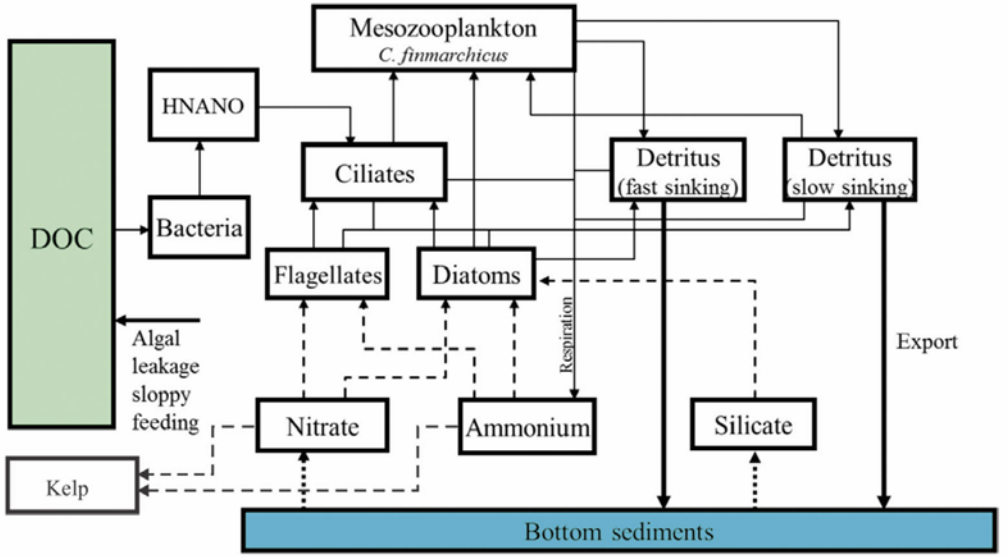
- General seaweed model framework (individual level)
- "Population" model – Individual Based Model – mortality, interactions
- Light shading - Oliver Evans (Uakron), Shane Rogers (Clarkson)
- Morphology and biomass development - Solveig Foldal, NTNU

Marine modelling – 3D model system SINMOD

Overall model structure



Simpliefied food web model



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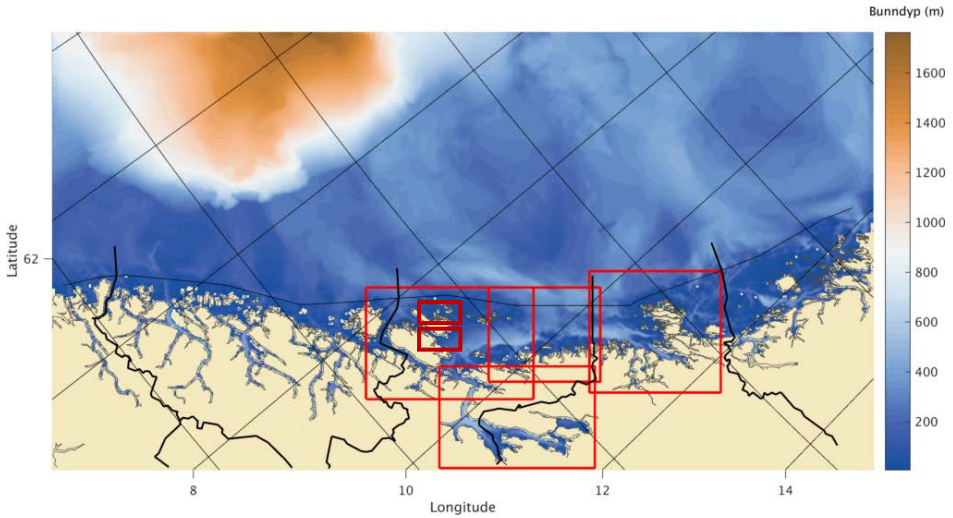
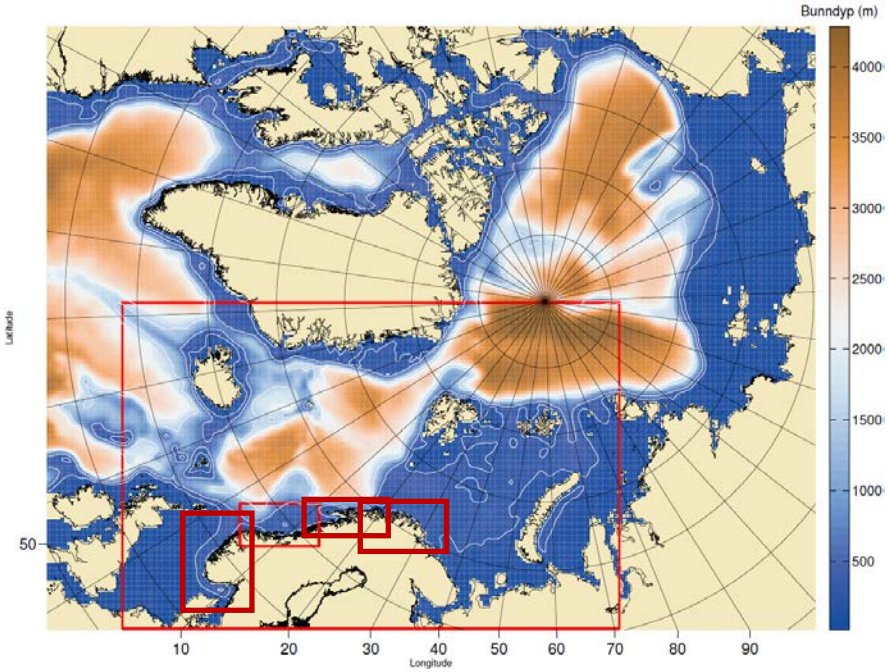
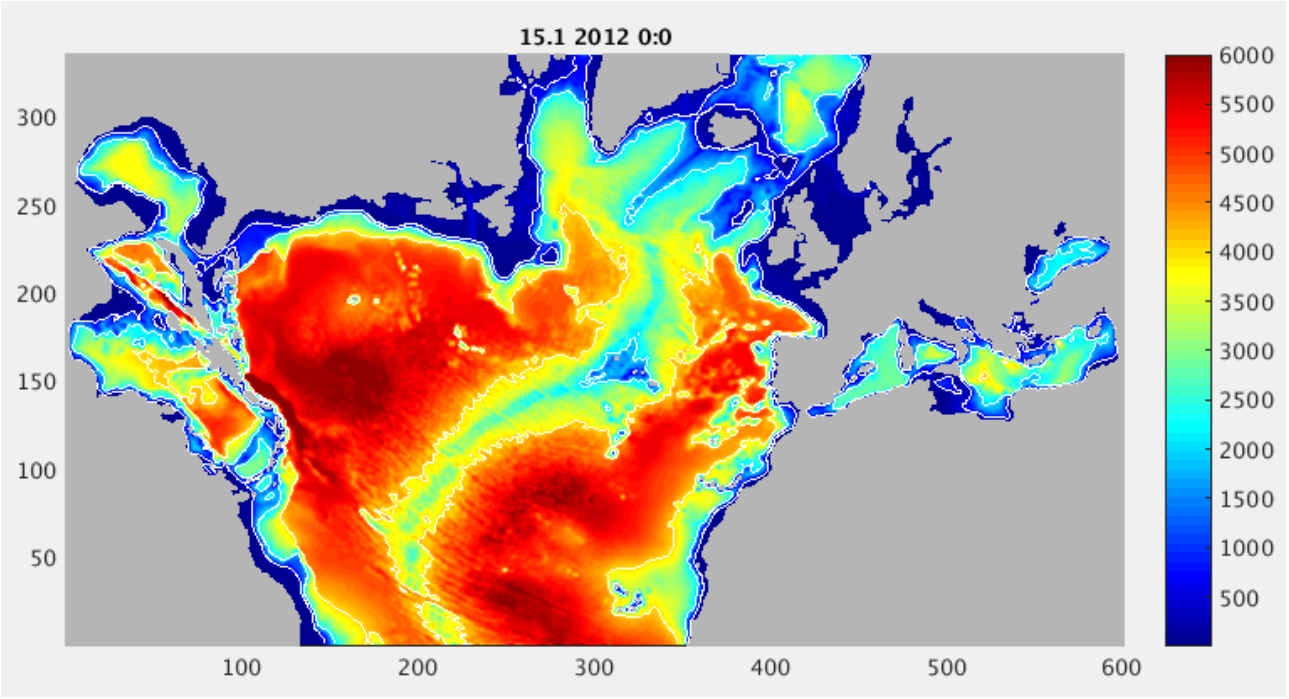
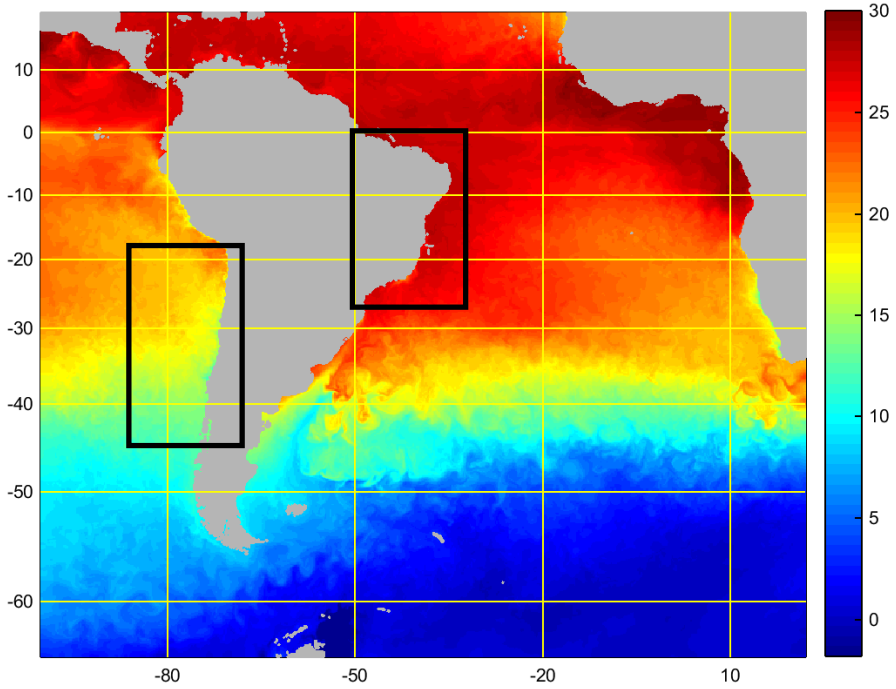
Model domains









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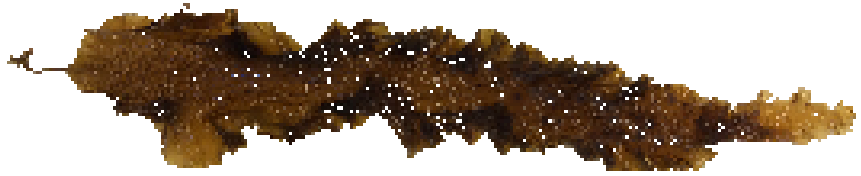
Seaweed model framework (computer code)

- Model implemented in Fortran 90 (applause!)
  - Main reason is to talk easily with SINMOD (and possibly other ocean models); still very efficient language 60 years on!
- Code has been compartmentalized
  - Physiological processes (uptake, photosynthesis etc) are called separately
  - Allows for uses of the same process **and code** for different species
- More efficient parametrization
  - Variable parameters

```
subroutine Uptake_mm_int(upt_field, &
     ext_conc, &
     curr_speed, &
     salinity, &
     int_res, &
     maxupt, &
     halfsat, &
     minint_res, &
     maxint_res, &
     t_step, &
     rate_step)

  use setup_module
  use saccharina_module
  use depth_module
  use swd_main_module

  implicit none
  real, dimension(sac_nsi, sac_nsu, sac_klev), intent(inout) :: upt_field
  real, dimension(sac_nsi, sac_nsu, sac_klev), intent(in) :: &
       ext_conc, &
       curr_speed, &
       salinity, &
       int_res, &
       maxupt, &
       halfsat, &
       minint_res, &
       maxint_res

  real(KIND_DB), intent(in) :: t_step, rate_step
  ! integer, intent(in) :: &
  !     t_step, &
  !    rate_step
  ! Rate_step: is uptake given in "per hour" or per day?
  ! Rate step is the number of seconds of the time unit, e.g. if per hour t_
p is
  ! divided by 3600

  real, dimension(sac_nsi, sac_nsu, sac_klev):: f_s, f_curr
  integer :: i, j, k
```

Individual Based Population Model

Original *S. latissima* model

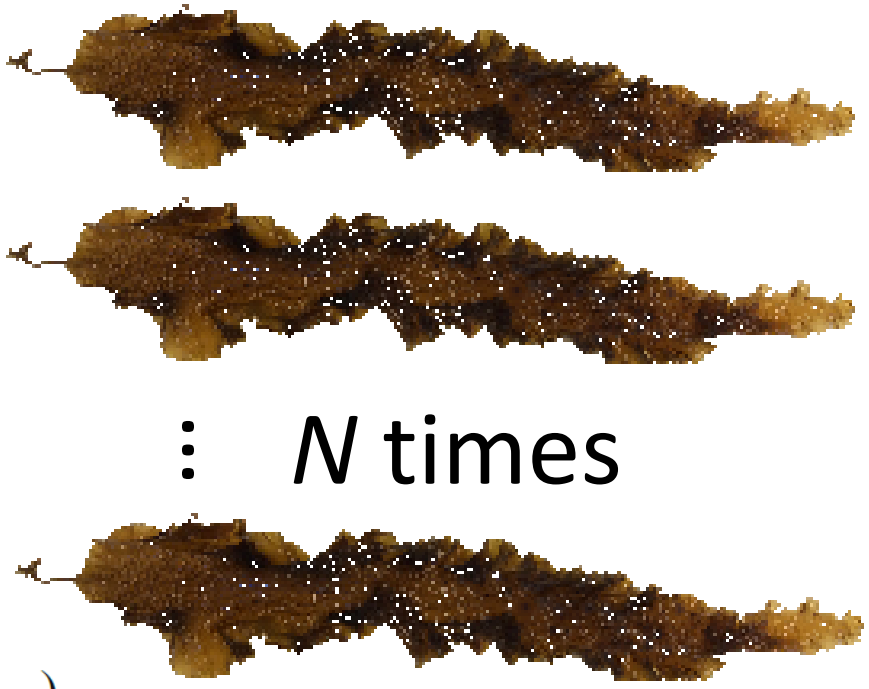


$$\frac{dA}{dt} = [\mu(A, N, C, T, t) - \nu(A)]A$$

$$\frac{dN}{dt} = k_A^{-1} J - \mu\,(N + N_{\text{struct}})$$

$$\frac{dC}{dt} = k_A^{-1}[P(I, T)(1 - E(C)) - R(T)] - \mu(C + C_{\text{struct}})$$

Upscaling to dropper, longline, or farm level



⋮ *N* times

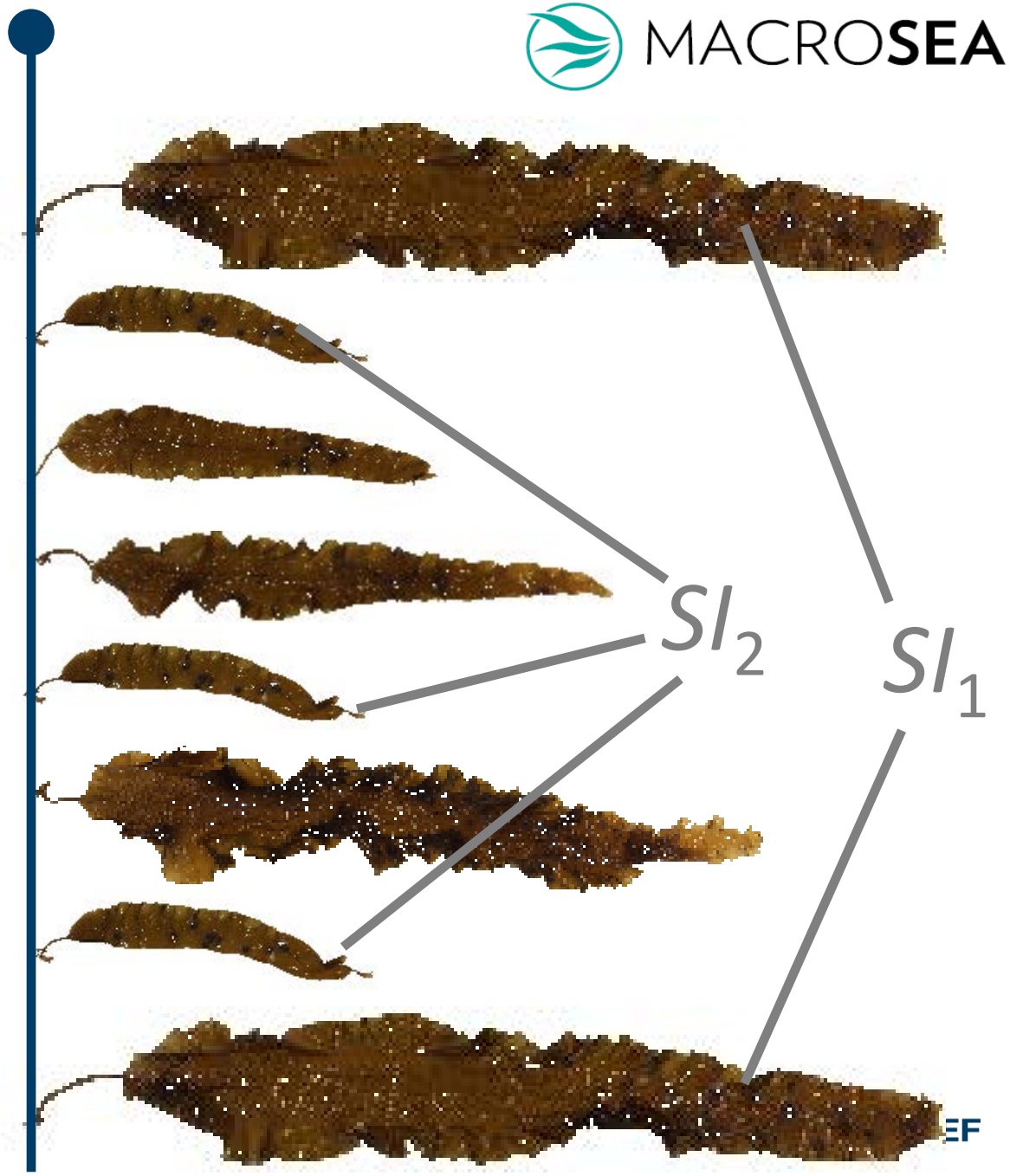
Individual Based Population Model

- Reality is more like this:

- For large farms we cannot expect to resolve all individuals in any reasonable way – could even be computationally limiting (~ millions of individuals)
- We would still like to be able to estimate biomass, uptake of nutrients etc.
- A well established compromise is to use **super individuals** (e.g. Scheffer et al. 1995)

IBM: super individuals

- The population is represented by several distinct individuals, but not as many as the total population
- For example, to the right, a total of 8 individuals is represented by 5 super individuals, each, respectively, representing 2, 3, 1, 1 and 1 individuals
- All the individuals "within" each super-individual have the same **state values**, e.g. the same frond size, the same nitrogen content etc.

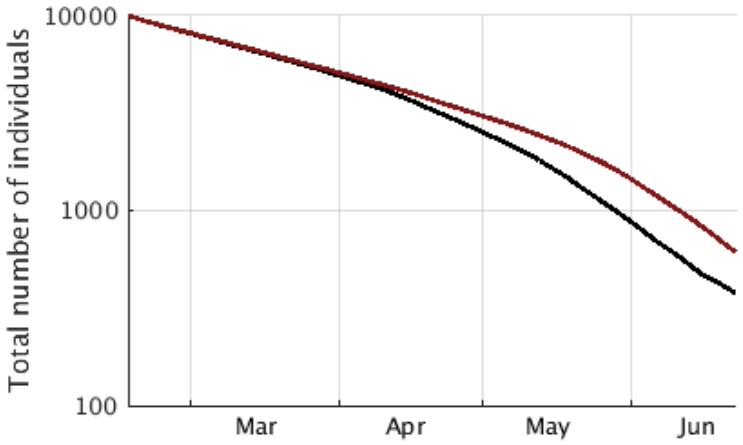


Why is this useful?

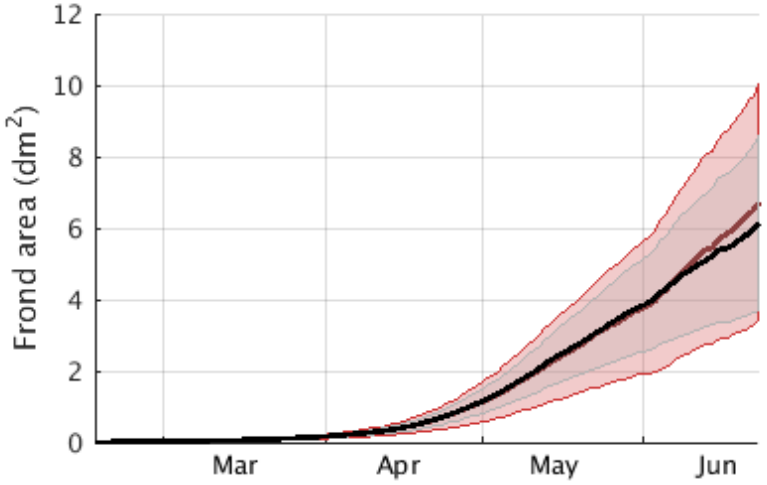
- SIs may have different mortality rates, depending on state values
- Interactions between individuals (mechanical interactions, light and nutrient shading etc)
- Thinning effects – punish the culture for having been seeded too densely
- Different parameters for different SIs
- Of course not a proper population model – no birth effects

Example results
Flåtegrunnen, Sogn og Fjordane (IMTA)

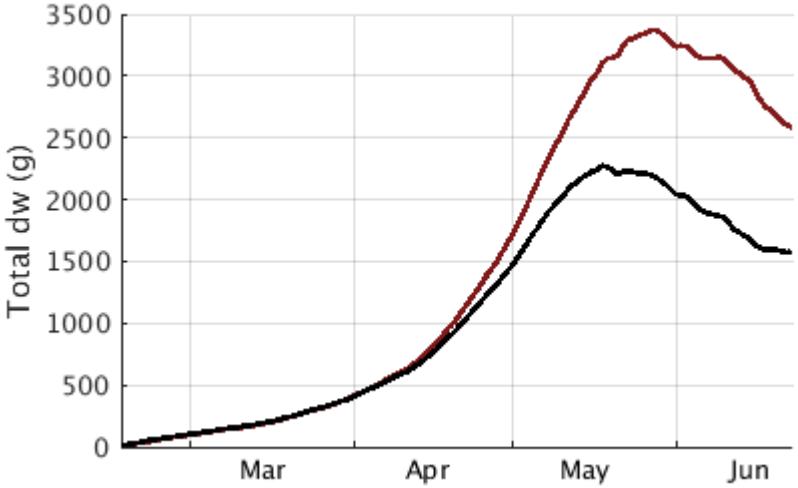
Number of individuals



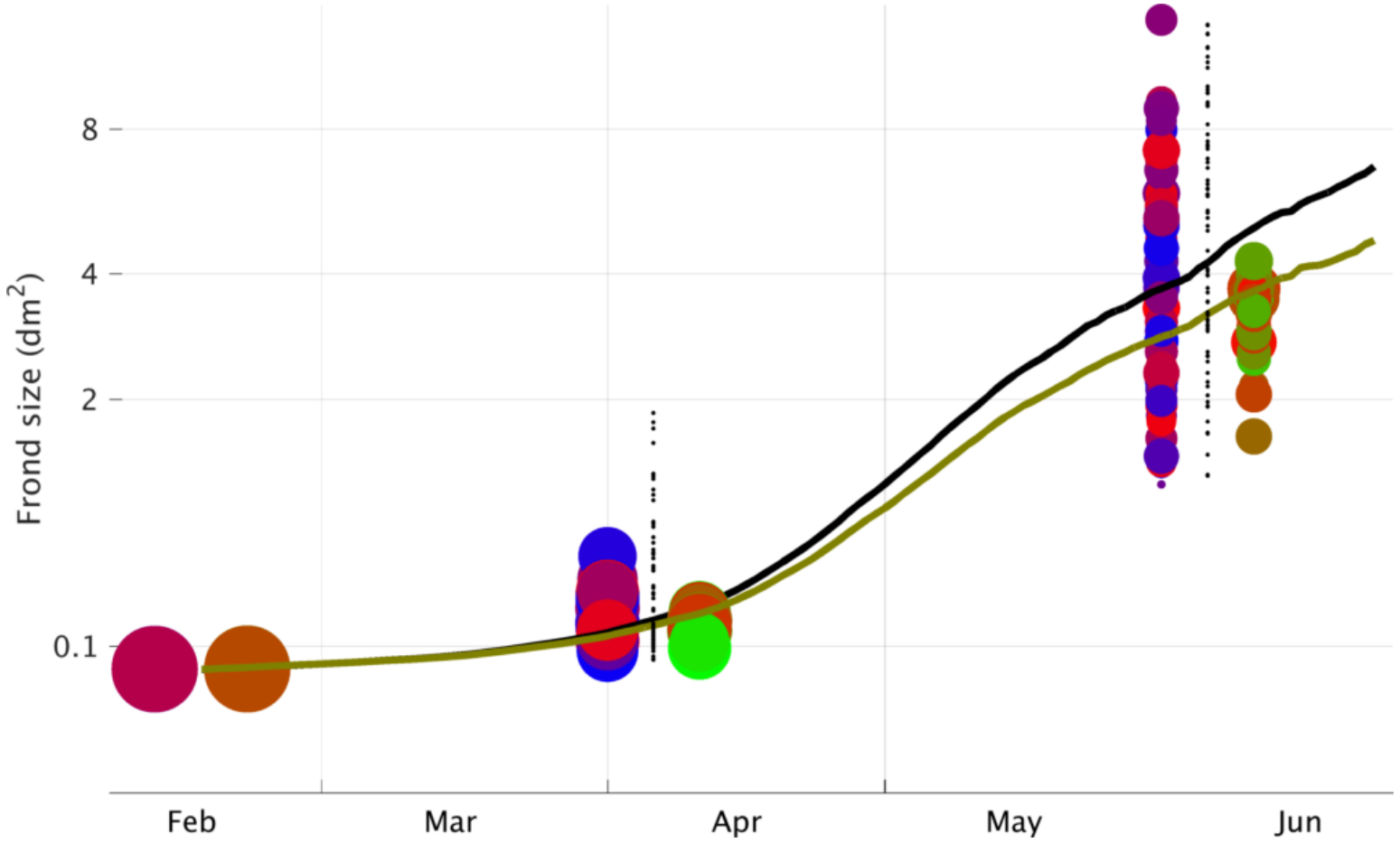
Mean frond area and SD



Biomass development



Example results



Light and light shading effects

- Presentation made by Oliver Evans

Morphology (also related to WP2)

Solveig Foldal (MSc-student NTNU)

- Trying to understand more about how the kelp biomass develops
  - Further useful for model development and / or improvement
- Looking into
  - Number of plants / substrate unit (length of rope)
  - Frond areas, lengths, widths
  - Total dry weight
  - Frond Thickness
  - **Relations between these variables and how they develop in time**

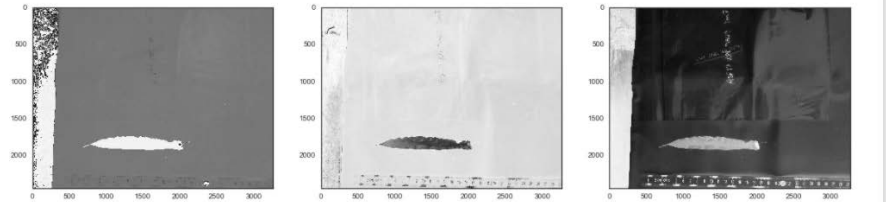
Sampling in monitoring progamme

- Stations
  - ASF april, may, june
  - SES april, may, june
  - APN may, june
- 5 droppers, 2 depths, 10 plants from each (total 800)
- Individually photographed, measured (length, tissue thickness) and weighed (dry weight)

Image processing

```
In [3]: img = imread('C:/MACROSEA/Morfologi/testbilder/IMG_7760.JPG')
        fig, ax = plt.subplots(figsize=(16, 10))
        plt.imshow(img)
```

```
In [16]: #Convert to  HSV representation
         imghsv = color.rgb2hsv(img)
         fig, ax = plt.subplots(1, 3, figsize=(20, 10))
         for i in range(3):
             ax[i].imshow(imghsv[:,:,i])
```



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WP4 project plan updates

		2016				2017				2018				2019			
		Q1	Q2	Q3	Q4	Q1	Q2	Q3	Q4	Q1	Q2	Q3	Q4	Q1	Q2	Q3	Q4
Task	Activity																
T4.1	ST4.1 General individual based model framework	x	x	x	x	x	x										
	ST.4.2 *S. latissima* model			x	x	x			x	x	x						
	ST4.3 *A. esculenta* model									x	x	x	x				
T4.2	ST4.4 *P. palmata* model								x	x	x	x	x				
T4.3	ST4.5 Light shading model	x	x	x	x	x	x	x									
	ST4.6 Nutrient shading model						x	x	x	x							
	ST4.7 Mechanical interactions, mortality					x	x	x	x	x							
	ST4.8 Fouling							x	x	x	x	x	x	x	x		
	ST4.9 Farm scale and production model							x	x	x	x	x	x	x	x	x	x

WP4 project plan updates updates

		2016				2017				2018				2019			
		Q1	Q2	Q3	Q4	Q1	Q2	Q3	Q4	Q1	Q2	Q3	Q4	Q1	Q2	Q3	Q4
Task	Activity																
T4.1	ST4.1 General individual based model framework	x	x	x	x	x	x										
	ST.4.2 *S. latissima* model			x	x	x			x	x	x	x					
	ST4.3 *A. esculenta* model										x	x	x	x	x		
T4.2	ST4.4 *P. palmata* model										x	x	x	x	x		
T4.3	ST4.5 Light shading model	x	x	x	x	x	x	x									
	ST4.6 Nutrient shading model									x	x	x	x				
	ST4.7 Mechanical interactions, mortality					x	x	x	x	x							
	ST4.8 Fouling									x	x	x	x	x	x		
	ST4.9 Farm scale and production model									x	x	x	x	x	x	x	x

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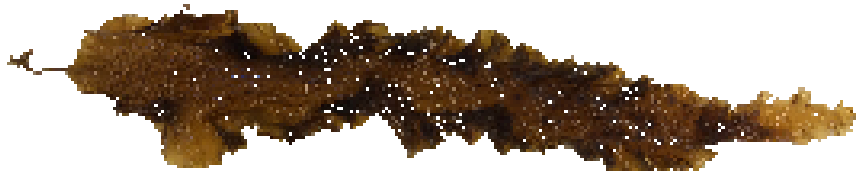
Teknologi for et bedre samfunn

Individual based "population" model

Original *S. latissima* model



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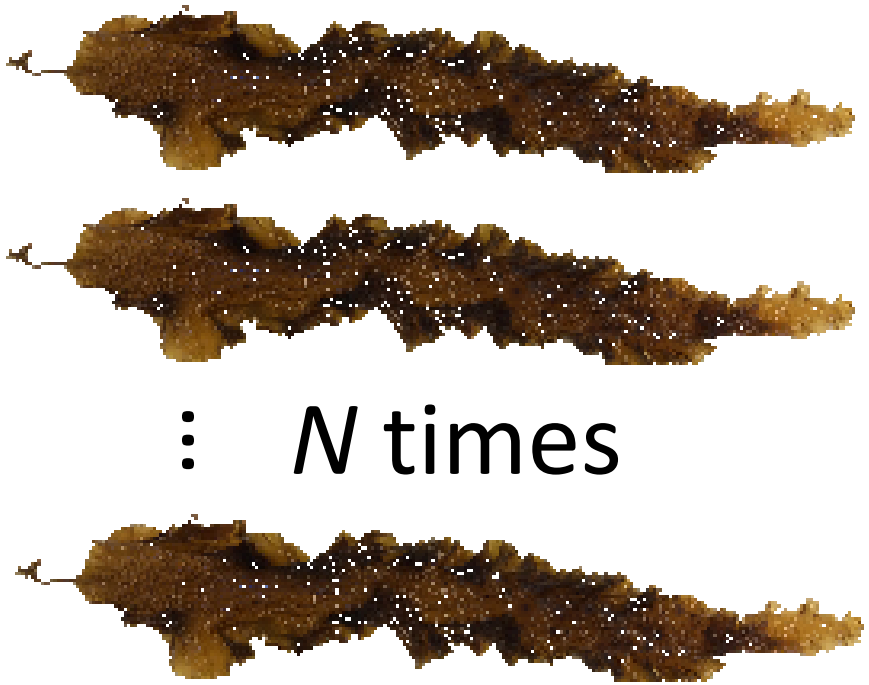

⋮ *N* times