

See discussions, stats, and author profiles for this publication at: <http://www.researchgate.net/publication/236867840>

# S41-Monday-1130-Alvarez

DATASET · MAY 2013

---

DOWNLOADS

46

---

VIEWS

72

7 AUTHORS, INCLUDING:



Jorge Díez

University of Oviedo

49 PUBLICATIONS 335 CITATIONS

SEE PROFILE



Juan José del Coz

University of Oviedo

51 PUBLICATIONS 297 CITATIONS

SEE PROFILE

# Automated classification techniques targeted to improve the precision of biomass estimates

Eva Álvarez

Ángel López-Urrutia

Enrique Nogueira

Rafael González-Quirós

Pablo González

Jorge Díez

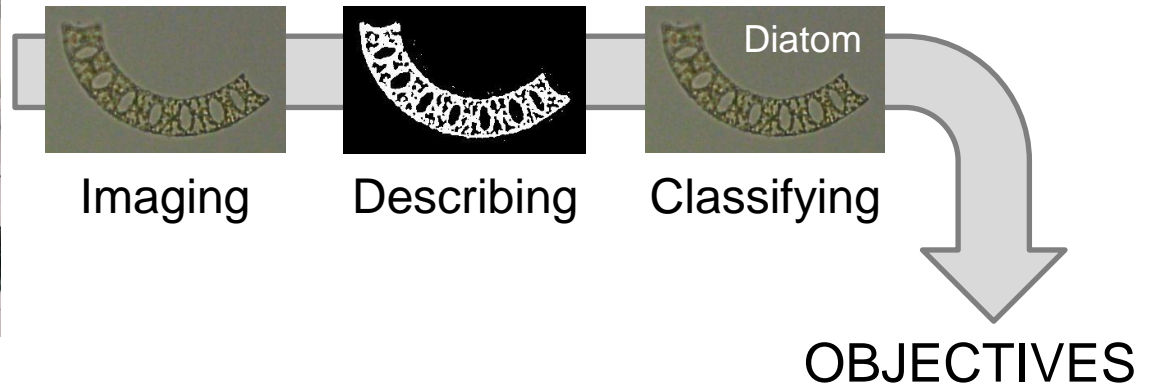
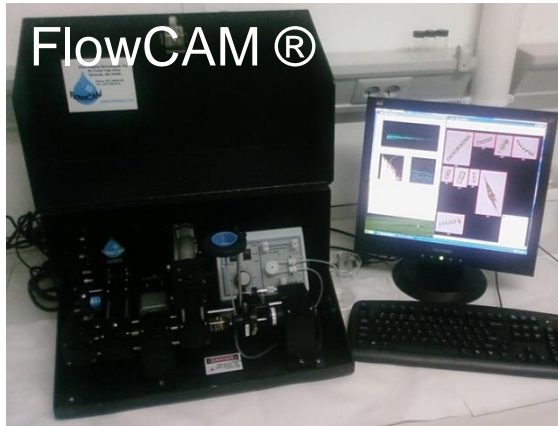
Juan José del Coz

Instituto Español de Oceanografía  
Centro Oceanográfico de Gijón  
Asturias, Spain

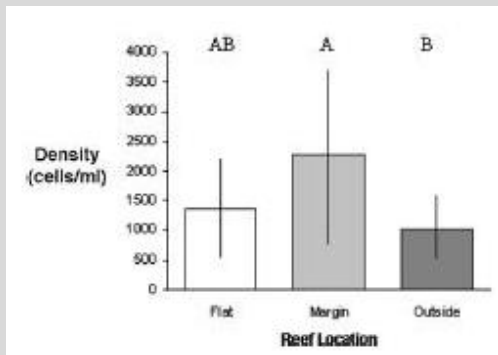
Artificial Intelligence Center  
University of Oviedo  
Asturias, Spain



# Automatic sampling and classification techniques

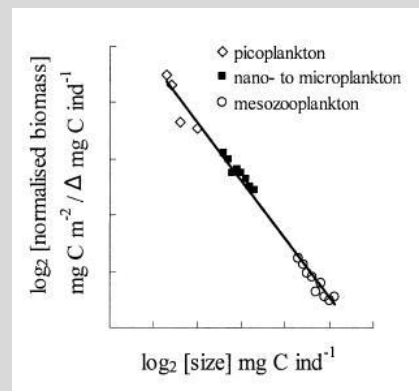


## Abundance per taxonomic group



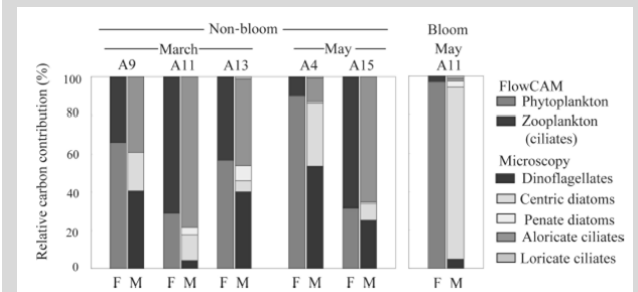
Littman, R.A. et al.  
*J. Exp. Mar. Biol. Ecol.* (2008)

## Community size-structure



San Martin, E. et al.  
*Limnol. Oceanogr.* (2006)

## Biomass per taxonomic or functional group




Ide, K. et al.  
*J. Plankton Res.* (2007)

1

Community size-structure  Improvement of the biovolume calculation

Projected area based method vs shape based method

2

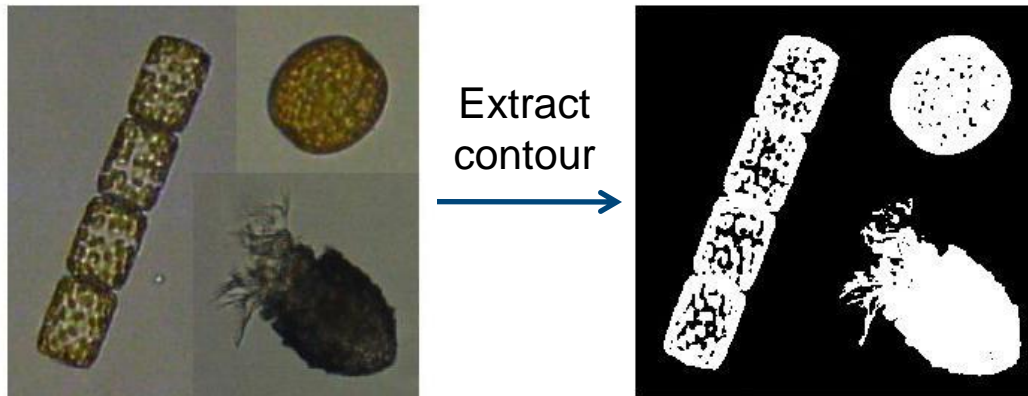
Biomass per group  Biomass-oriented formulation of the classification algorithm

Abundance oriented method vs biomass oriented method

# 1. Biovolume calculation

## Biovolume based on projected area

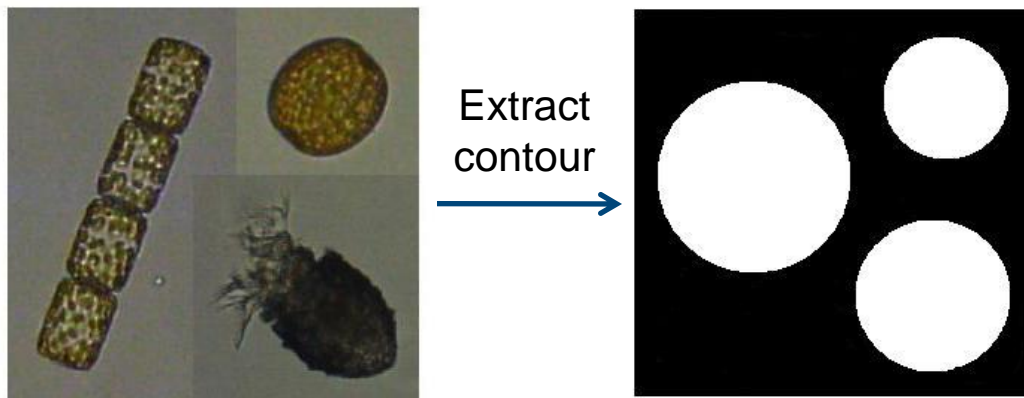
Automatic sampling devices based on image-analysis measure particle volume from the Equivalent Spherical Diameter (ESD)



# 1. Biovolume calculation

## Biovolume based on projected area

Automatic sampling devices based on image-analysis measure particle volume from the Equivalent Spherical Diameter (ESD)

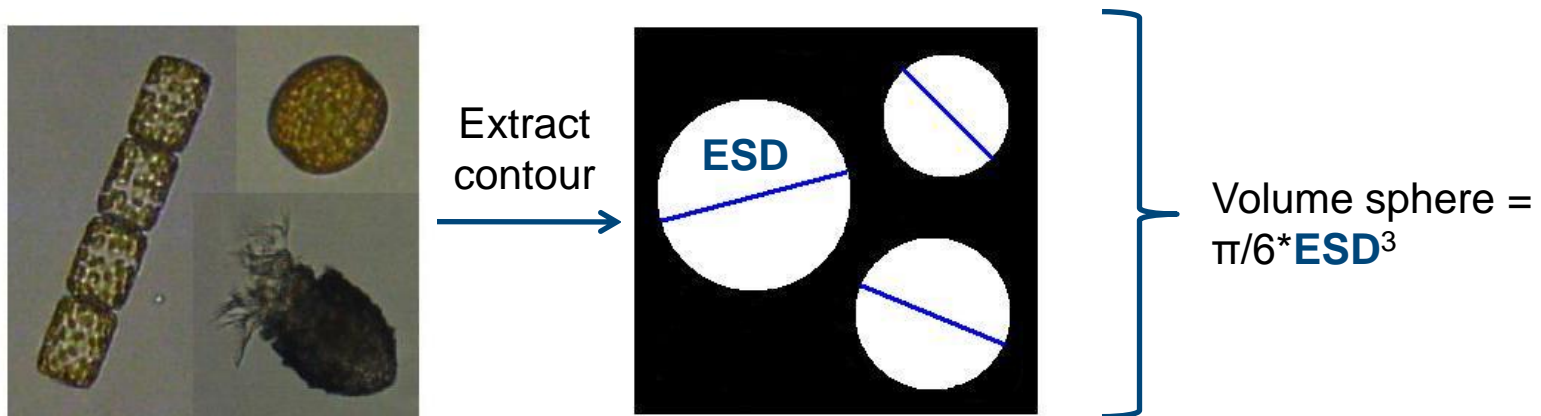


considering every particle as an sphere independently of its shape.

# 1. Biovolume calculation

## Biovolume based on projected area

Automatic sampling devices based on image-analysis measure particle volume from the Equivalent Spherical Diameter (ESD)

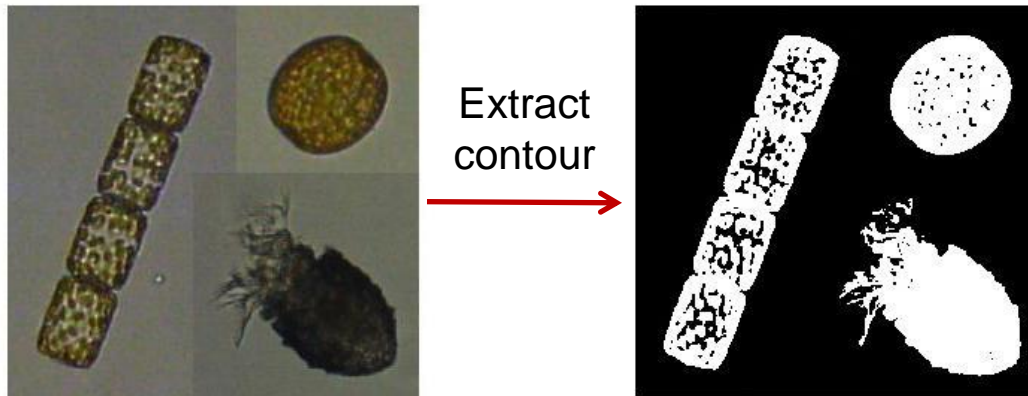


considering every particle as an sphere independently of its shape.

# 1. Biovolume calculation

## Biovolume based on shape

Traditionally biovolume has been measured assigning shape to the cells and calculating the volume accordingly.

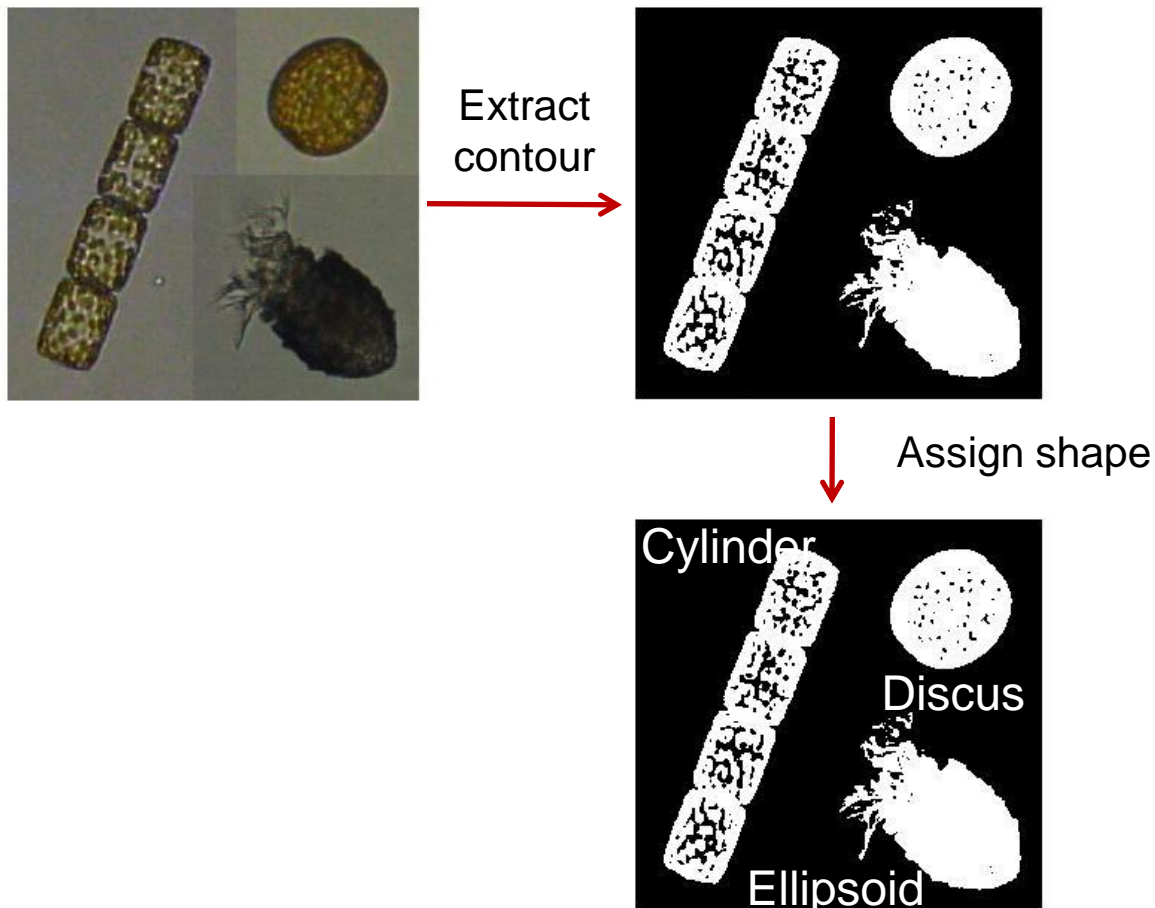




# 1. Biovolume calculation

## Biovolume based on shape

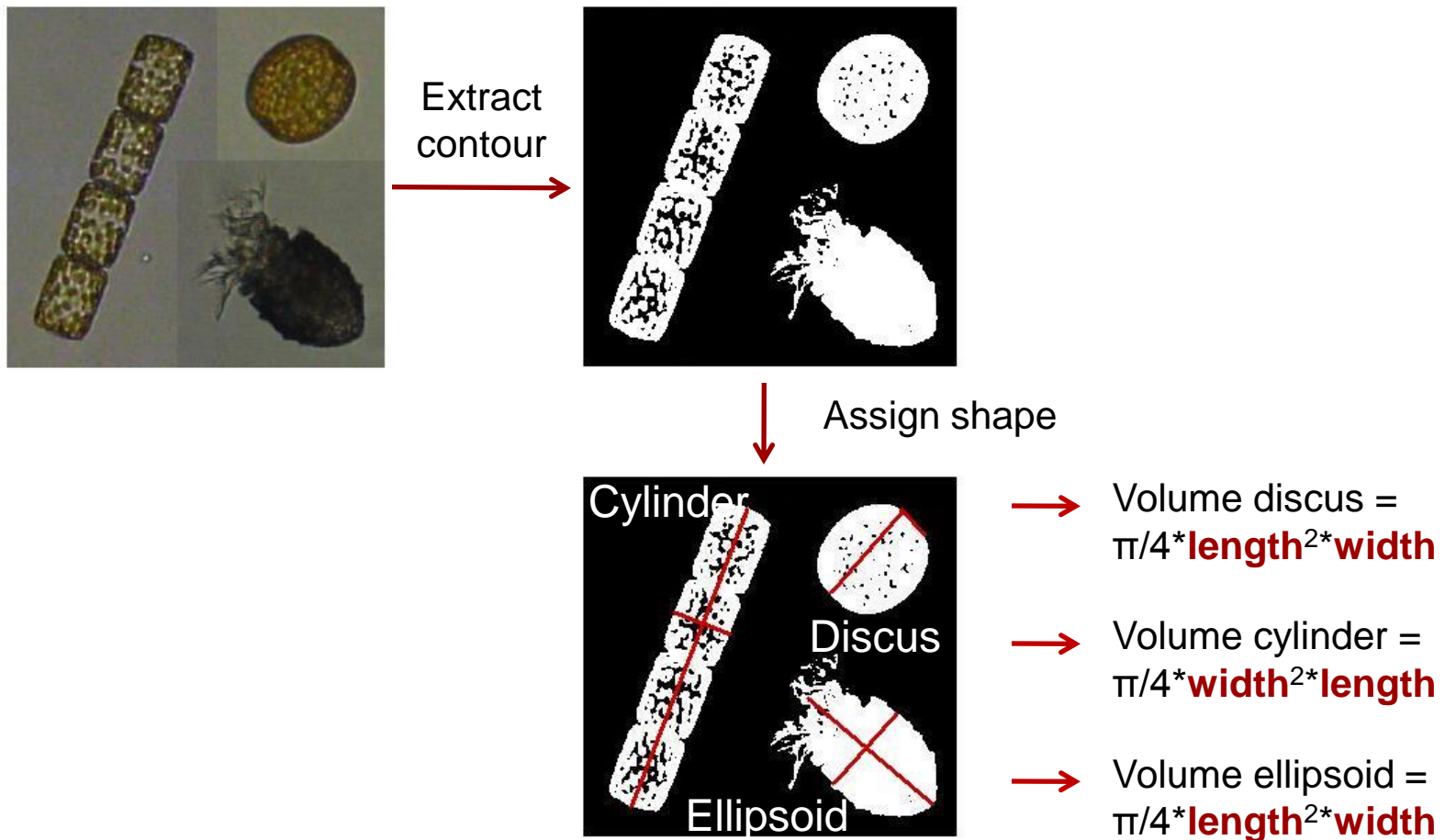
Traditionally biovolume has been measured assigning shape to the cells and calculating the volume accordingly.



# 1. Biovolume calculation

## Biovolume based on shape

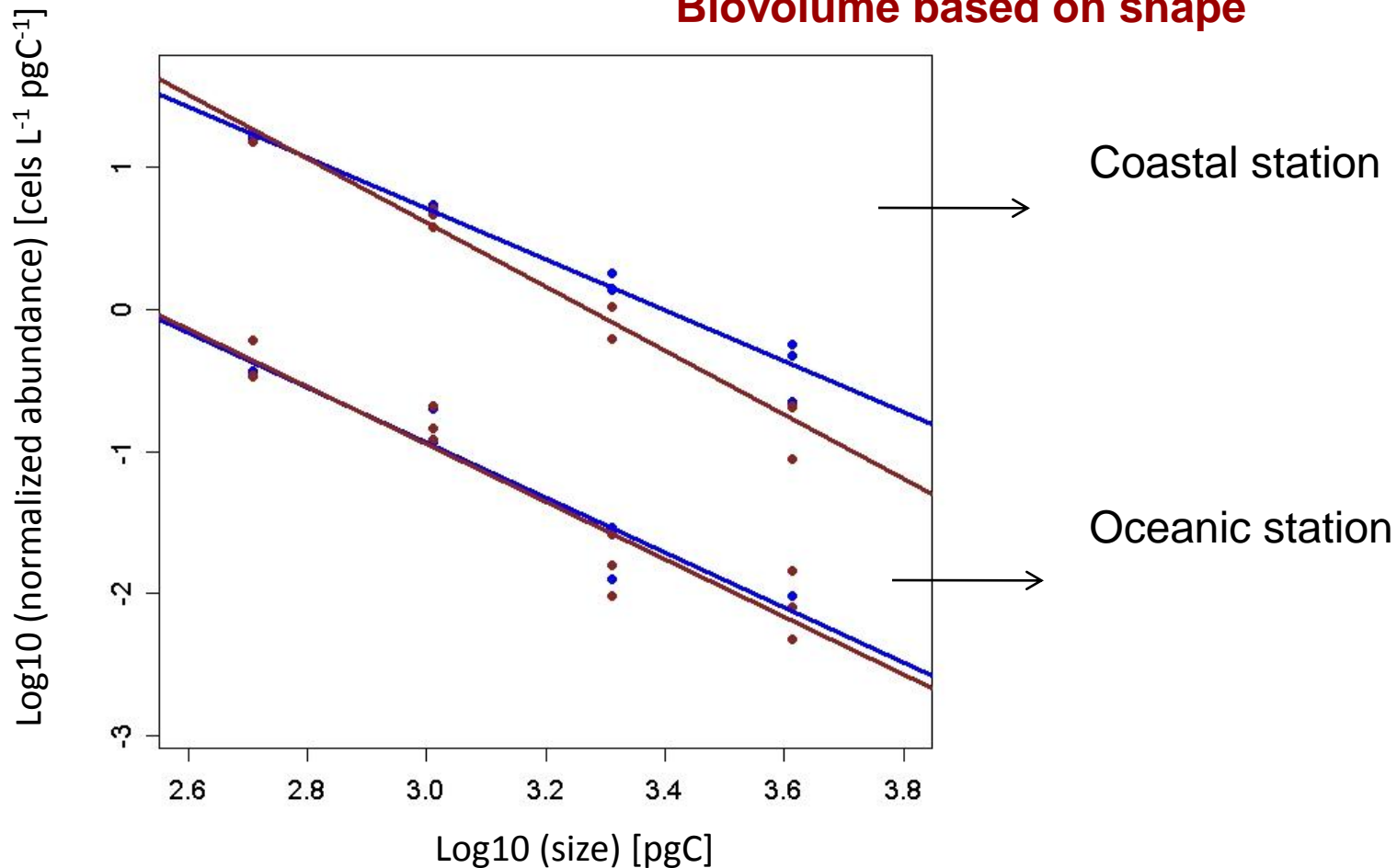
Traditionally biovolume has been measured assigning shape to the cells and calculating the volume accordingly.



# 1. Biovolume calculation

The way we measure the volume can modify the size-spectra slope depending on the morphological composition of the sample.

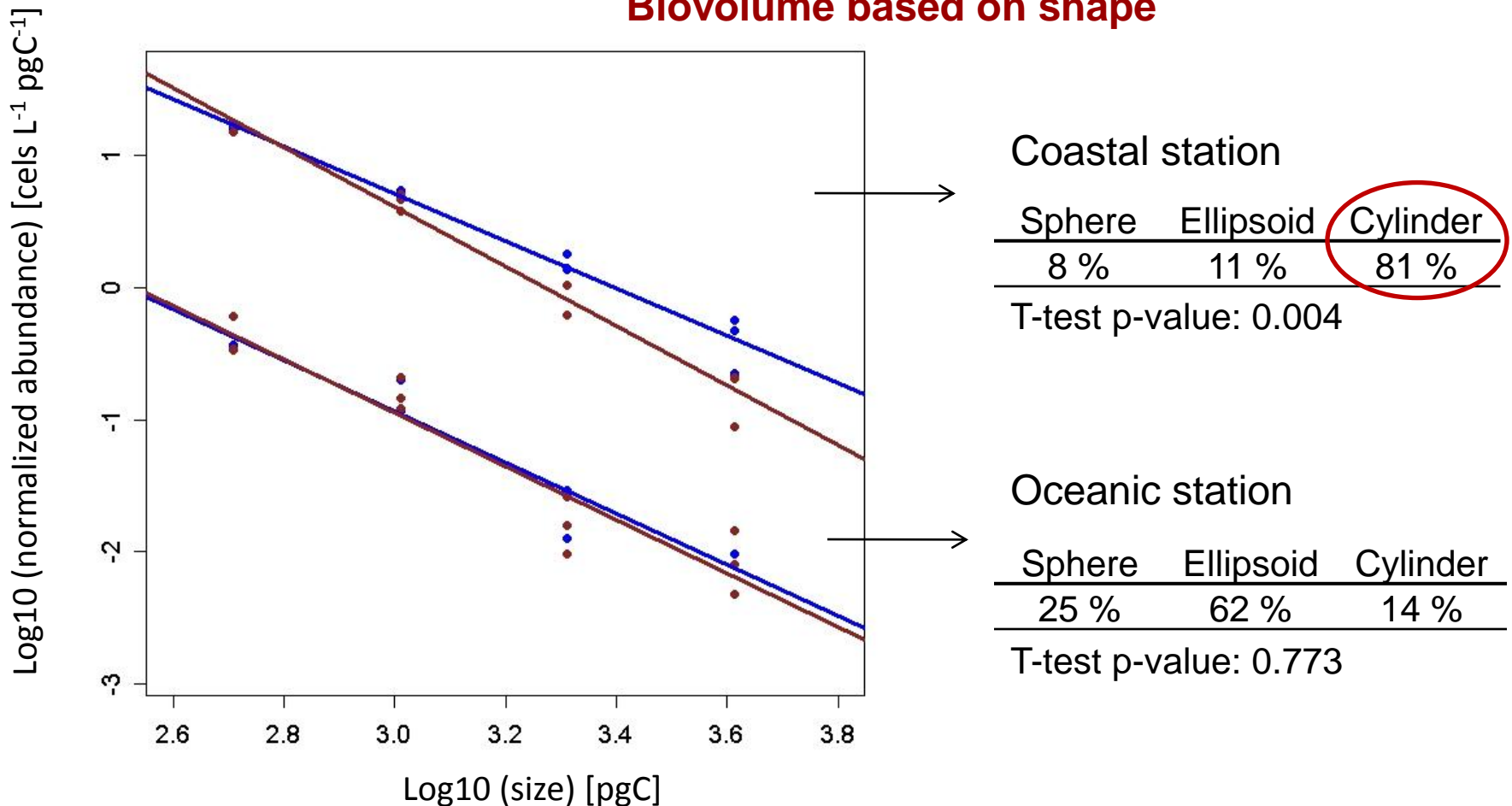
**Biovolume based on projected area**  
**Biovolume based on shape**



# 1. Biovolume calculation

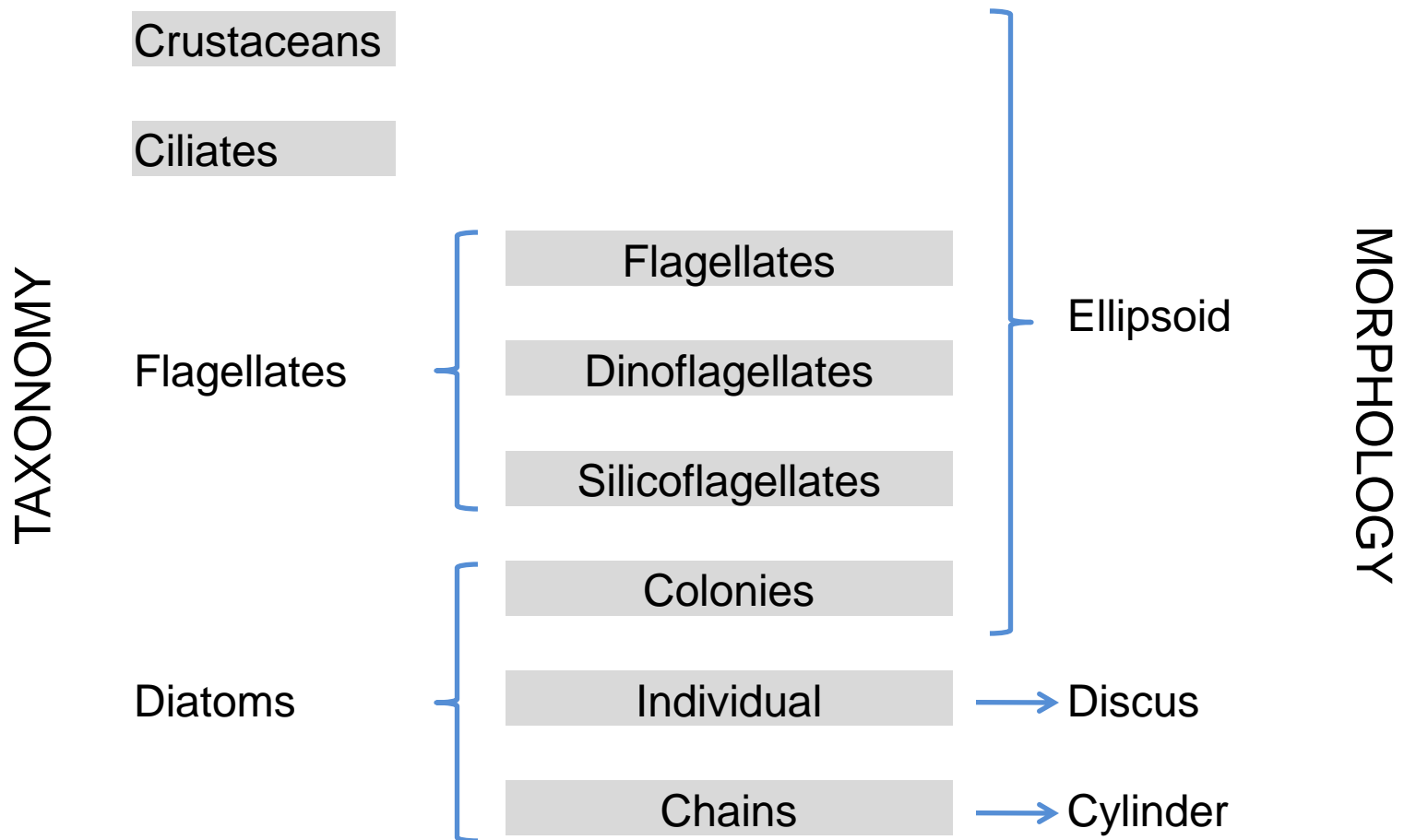
The way we measure the volume can modify the size-spectra slope depending on the morphological composition of the sample.

**Biovolume based on projected area**  
**Biovolume based on shape**



# 1. Biovolume calculation

To know automatically the particle shape we need to classify taxonomically in morphologically homogeneous classes.



# 1. Biovolume calculation

Abundance-oriented Support Vector Machine

Training set

$$S = \{(x_1, y_1, c_1), (x_2, y_2, c_2), \dots, (x_n, y_n, c_n)\}$$

# 1. Biovolume calculation

Abundance-oriented Support Vector Machine

Training set

$$S = \{(x_1, y_1, c_1), (x_2, y_2, c_2) \dots (x_n, y_n, c_n)\}$$

A diagram illustrating a data matrix. On the left, a blue bracket spans five rows of a table, labeled "5500 images". The table has five columns: "x", "Var1", "Var2", "Var3", and "...". The rows are labeled "1", "2", "3", "4", and "...". Below the table, a blue bracket spans the four feature columns ("Var1" to "..."), labeled "170 image features".

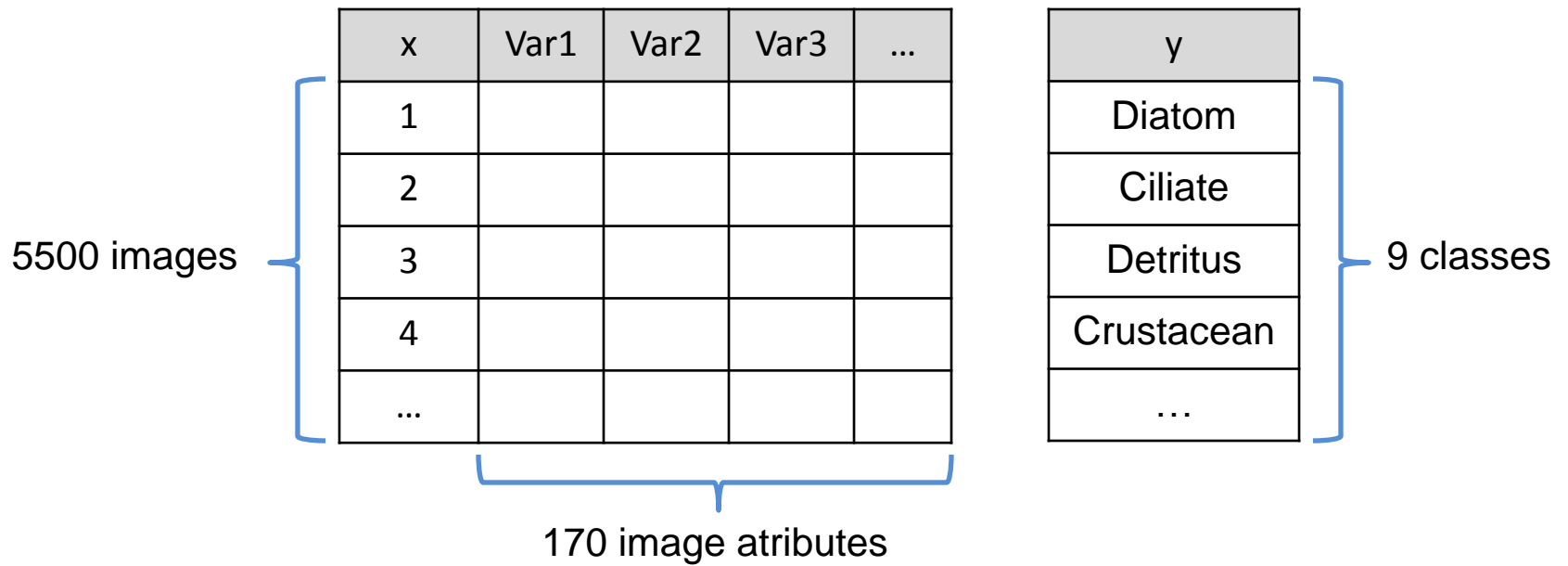
x	Var1	Var2	Var3	...
1				
2				
3				
4				
...				

# 1. Biovolume calculation

Abundance-oriented Support Vector Machine

Training set

$$S = \{(x_1, y_1, c_1), (x_2, y_2, c_2) \dots (x_n, y_n, c_n)\}$$





# 1. Biovolume calculation

Abundance-oriented Support Vector Machine

Training set

$$S = \{(x_1, y_1, c_1), (x_2, y_2, c_2), \dots, (x_n, y_n, c_n)\}$$

Model

$$h : S' \longrightarrow Y'$$

# 1. Biovolume calculation

Abundance-oriented Support Vector Machine

Training set

$$S = \{(x_1, y_1, c_1), (x_2, y_2, c_2) \dots (x_n, y_n, c_n)\}$$

Model

$$h : S' \longrightarrow Y'$$

Loss function

$$\Delta_{\text{LOSS}}(h, S') = \frac{\sum_{x_i \in S'} c_i [h(x_i) \neq y_i]}{\sum_{x_i \in S'} c_i}$$

# 1. Biovolume calculation

Abundance-oriented Support Vector Machine

Training set

$$S = \{(x_1, y_1, c_1), (x_2, y_2, c_2) \dots (x_n, y_n, c_n)\}$$

Model

$$h : S' \longrightarrow Y'$$

Loss function

$$\Delta_{\text{LOSS}}(h, S') = \frac{\sum_{x_i \in S'} c_i [h(x_i) \neq y_i]}{\sum_{x_i \in S'} c_i}$$

An error occurs when the predicted class does not match the actual class.

# 1. Biovolume calculation

Abundance-oriented Support Vector Machine

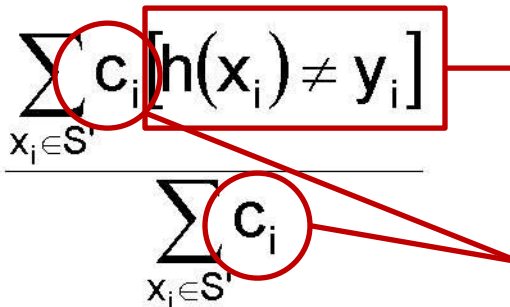
Training set

$$S = \{(x_1, y_1, c_1), (x_2, y_2, c_2) \dots (x_n, y_n, c_n)\}$$

Model

$$h : S' \longrightarrow Y'$$

Loss function

$$\Delta_{\text{LOSS}}(h, S') = \frac{\sum_{x_i \in S'} c_i [h(x_i) \neq y_i]}{\sum_{x_i \in S'} c_i}$$


An error occurs when the predicted class does not match the actual class.

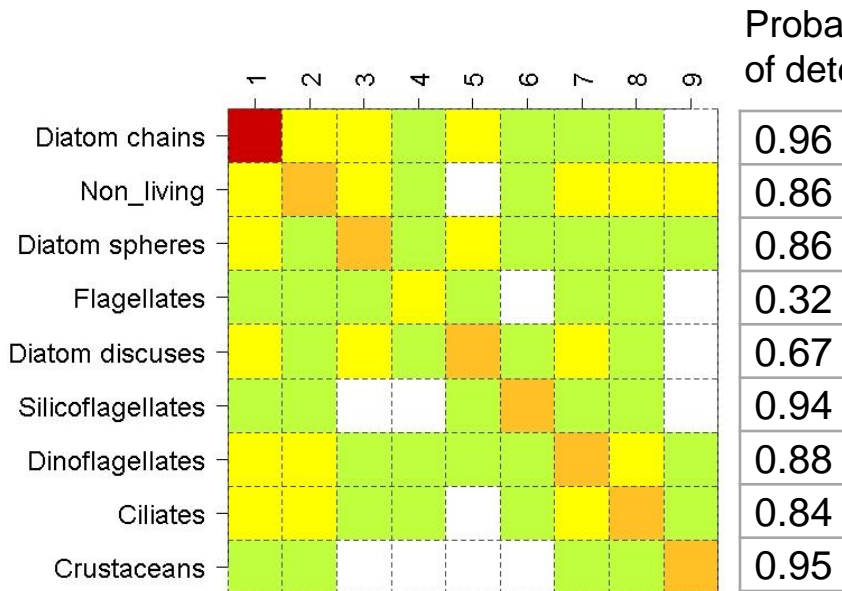
In an abundance-oriented classification the cost of error (c) is 1 for all the examples.

# 1. Biovolume calculation

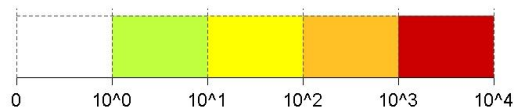
## Abundance-oriented Support Vector Machine

Abundance estimates

Accuracy = 0.89



Number of cells

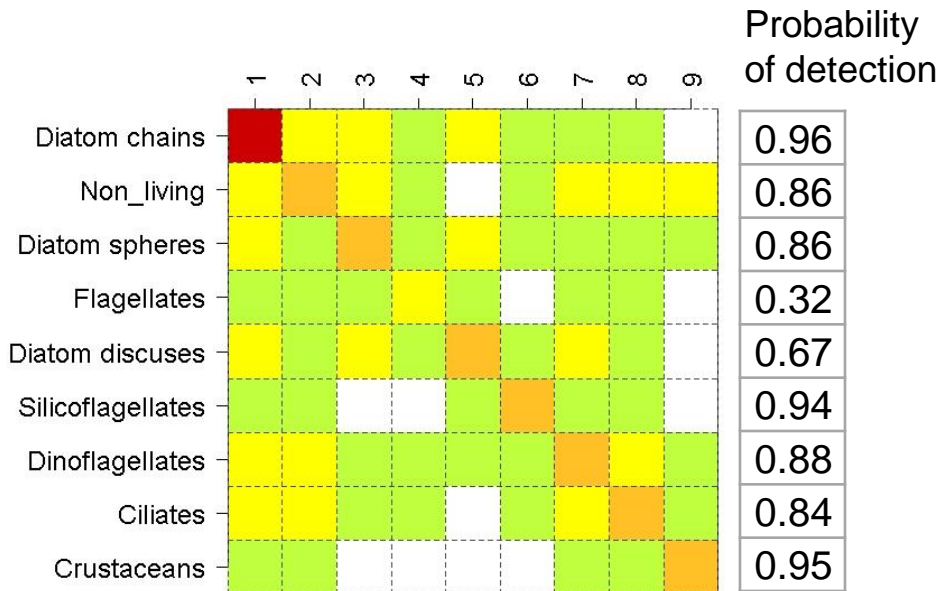


# 1. Biovolume calculation

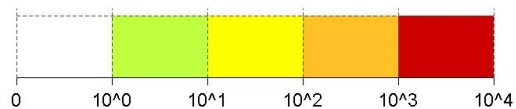
## Abundance-oriented Support Vector Machine

Abundance estimates

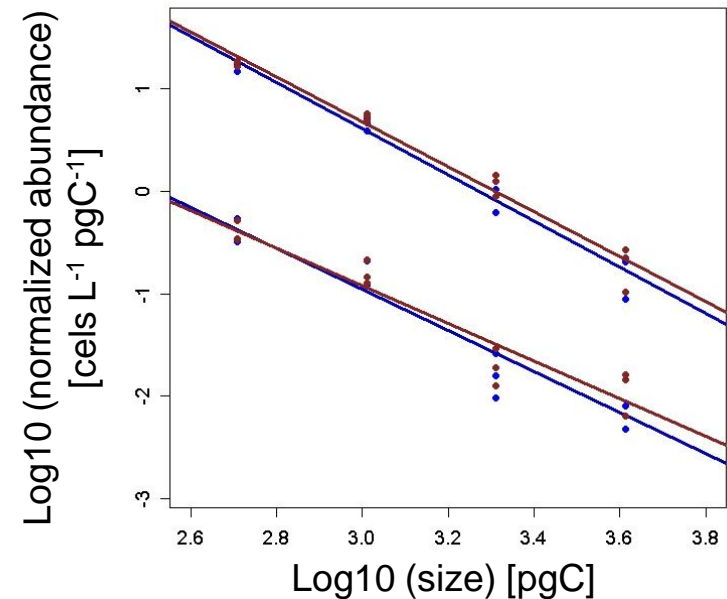
Accuracy = 0.89



Number of cells



Biovolume based on manual shape  
Biovolume based on automatic shape



## 2. Biomass-oriented classification

To improve the biomass estimates the SVM is built considering the error a function of biomass.

Loss function

$$\Delta_{\text{LOSS}}(h, S') = \frac{\sum_{x_i \in S'} c_i [h(x_i) \neq y_i]}{\sum_{x_i \in S'} c_i}$$

## 2. Biomass-oriented classification

To improve the biomass estimates the SVM is built considering the error a function of biomass.

Loss function

$$\Delta_{\text{LOSS}}(h, S') = \frac{\sum_{x_i \in S'} c_i [h(x_i) \neq y_i]}{\sum_{x_i \in S'} c_i}$$

The cost of misclassifying one example ( $c_i$ ) is the value of biomass for this example.



## 2. Biomass-oriented classification

To improve the biomass estimates the SVM is built considering the error a function of biomass.

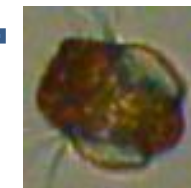
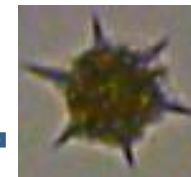
Loss function

$$\Delta_{\text{LOSS}}(h, S') = \frac{\sum_{x_i \in S'} c_i [h(x_i) \neq y_i]}{\sum_{x_i \in S'} c_i}$$

The cost of misclassifying one example ( $c_i$ ) is the value of biomass for this example.



Low cost



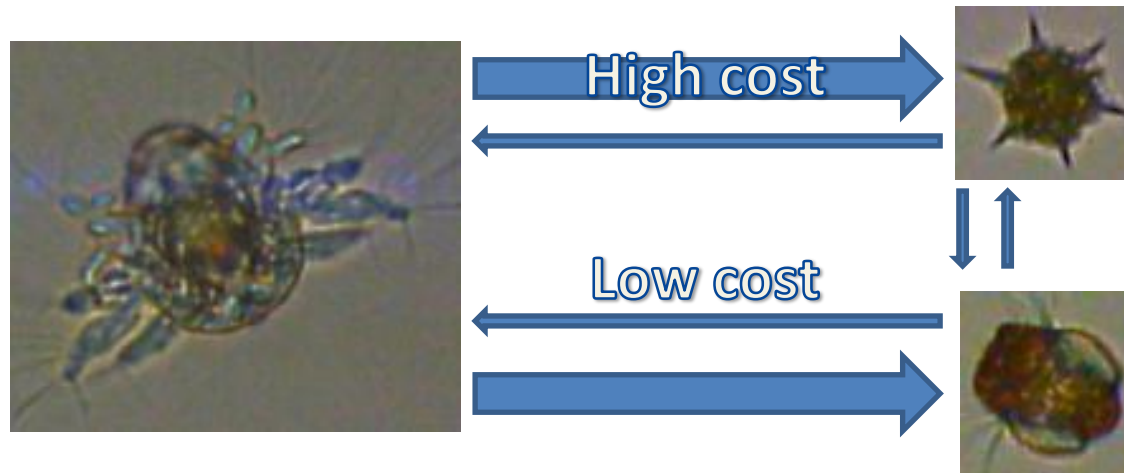
## 2. Biomass-oriented classification

To improve the biomass estimates the SVM is built considering the error a function of biomass.

Loss function

$$\Delta_{\text{LOSS}}(h, S') = \frac{\sum_{x_i \in S'} c_i [h(x_i) \neq y_i]}{\sum_{x_i \in S'} c_i}$$

The cost of misclassifying one example ( $c_i$ ) is the value of biomass for this example.

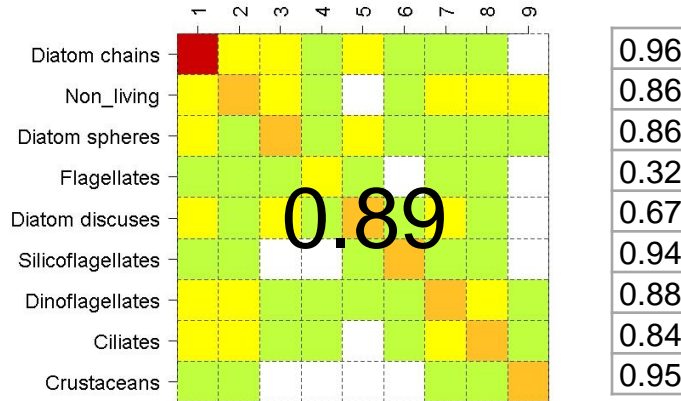


The accuracy of the biomass-oriented SVM on biomass estimations increases a 3%

Abundance estimates

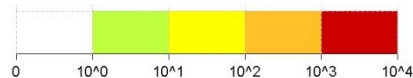
Biomass estimates

Abundance oriented SVM

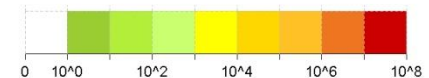


Biomass oriented SVM

Number of cells



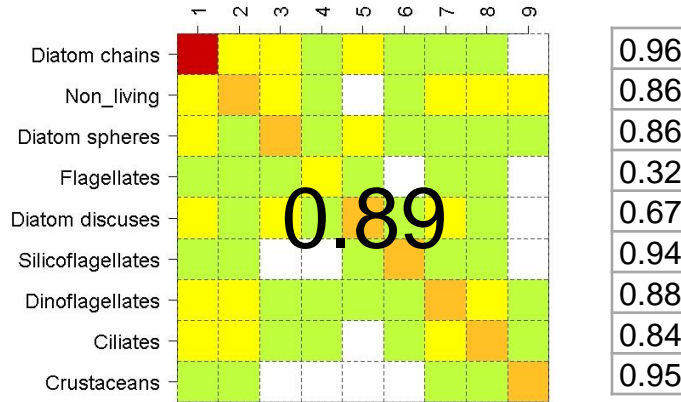
pg Carbon



# The accuracy of the biomass-oriented SVM on biomass estimations increases a 3%

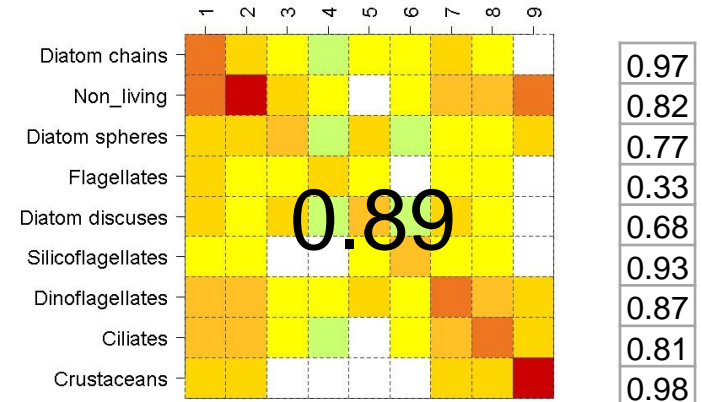
## Abundance estimates

Abundance oriented

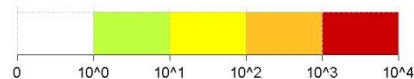


## Biomass estimates

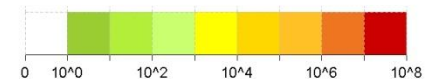
Biomass oriented



### Number of cells



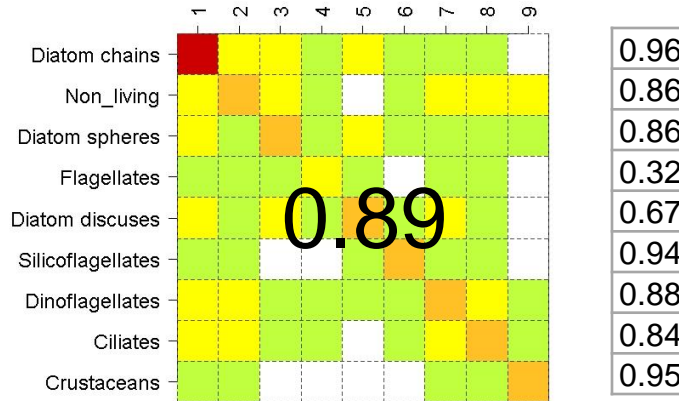
### pg Carbon



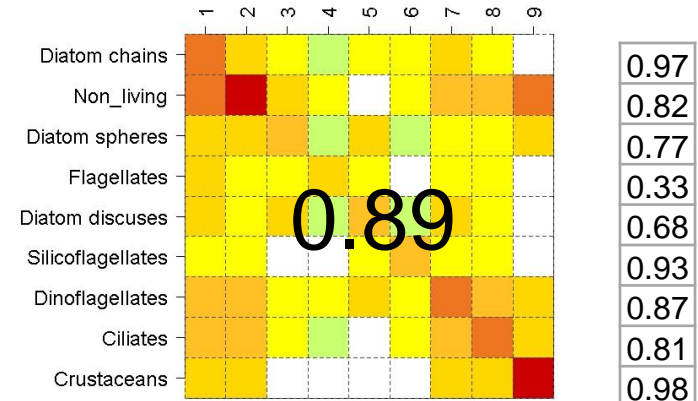
# The accuracy of the biomass-oriented SVM on biomass estimations increases a 3%

## Abundance estimates

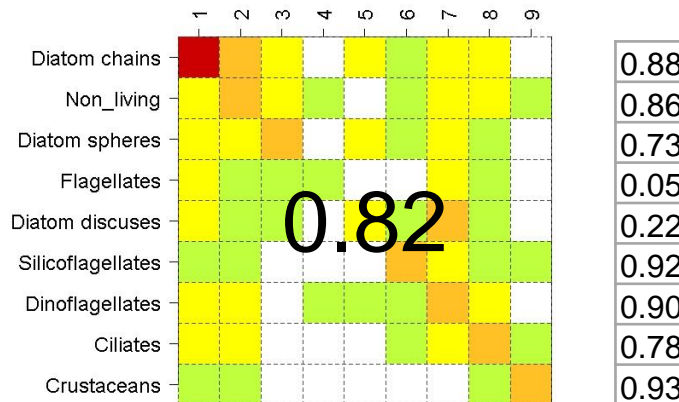
Abundance oriented



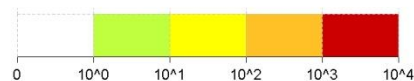
## Biomass estimates



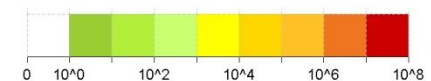
Biomass oriented



### Number of cells



### pg Carbon

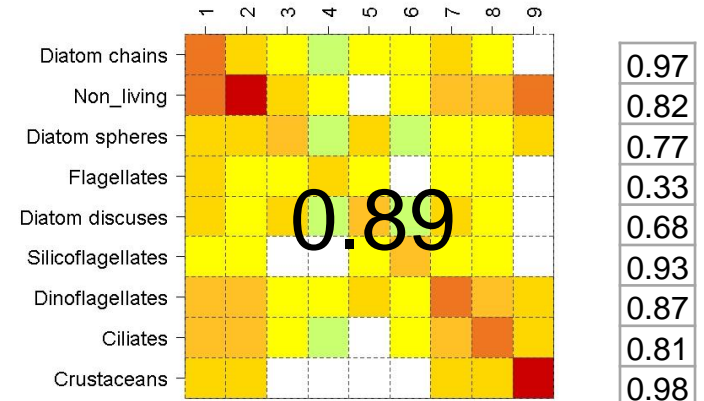
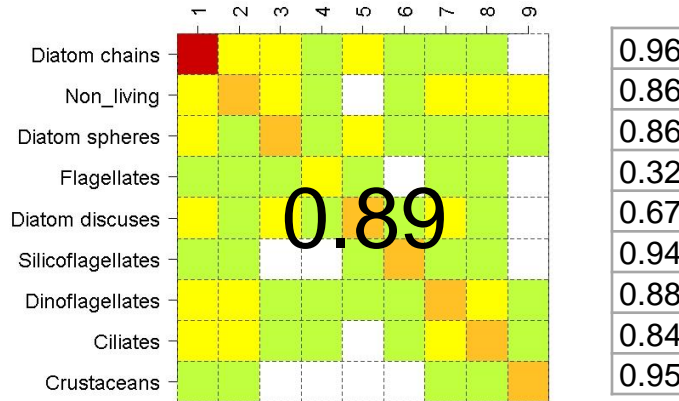


# The accuracy of the biomass-oriented SVM on biomass estimations increases a 3%

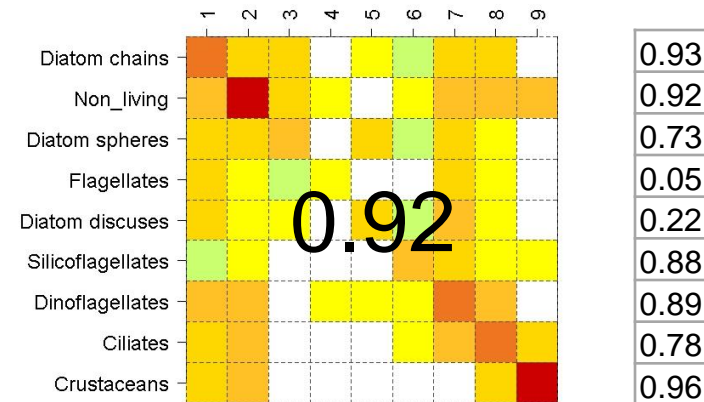
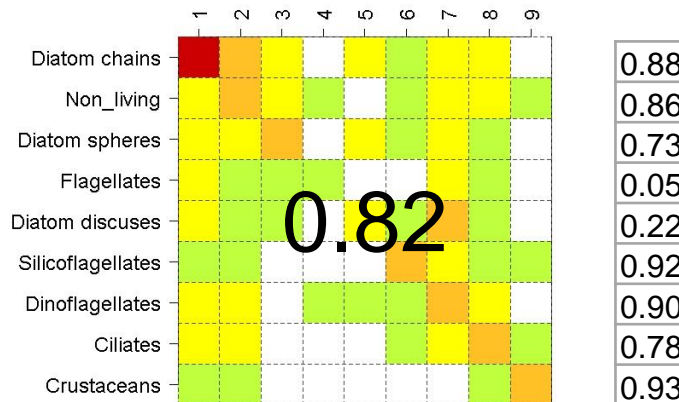
## Abundance estimates

## Biomass estimates

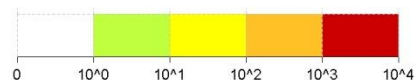
Abundance oriented



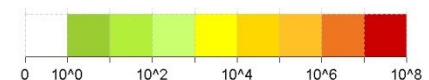
Biomass oriented



### Number of cells



### pg Carbon



# Conclusions

- Size spectra calculated with projected area-based volume or shape-based volume can be different depending on the morphological composition of the sample.
- To improve the biomass estimates the SVM can be designed considering the error a function of biomass.