



The computer does the hard work

(semi)-automatic classification of
zooplankton with **Zoolmage**

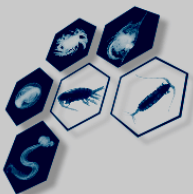
Philippe Grosjean & Denis Kevin

Numerical Ecology of Aquatic Systems, Mons-Hainaut University, Belgium

'OPC to CCD' seeking for a brain

- Hardware is definitely available now to planktonologists as Mark just explained
- Gathering terabytes of plankton images is easy
- Transforming the pixels into biologically/ecologically meaningful data is the next challenge

The most sophisticated oceanographic imaging system remains desperately useless without an equally sophisticated software to process the huge amount of raw data it produces

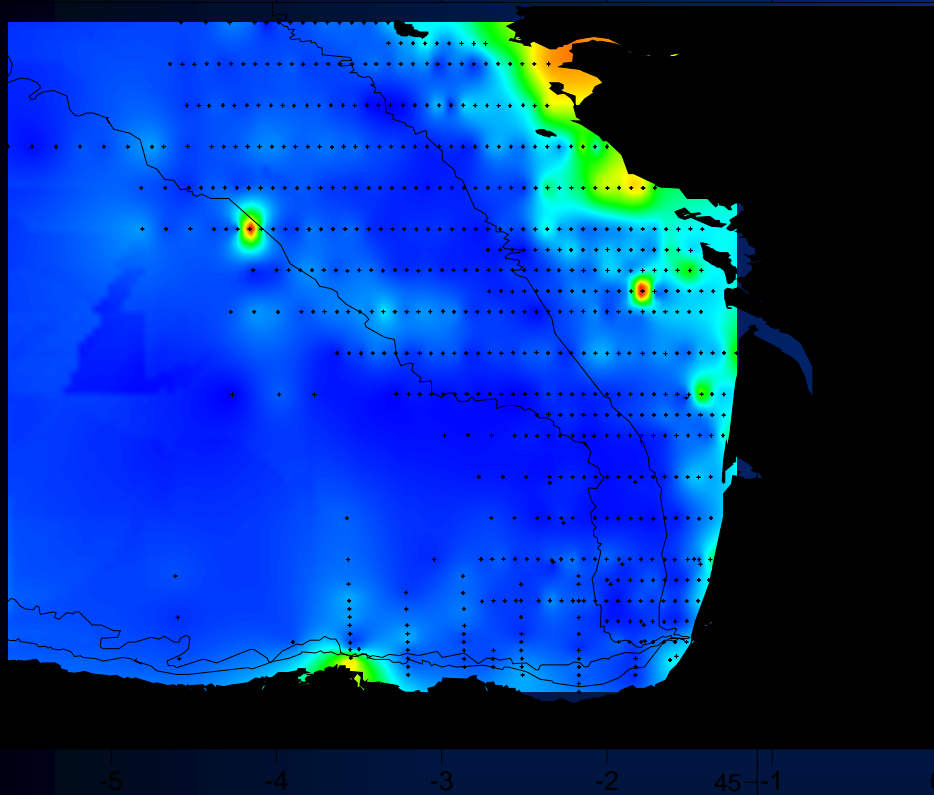


Oceanographer wants/needs more data

- Need for both (3D)-space and time coverage across large areas
- Patchiness of plankton distribution imposes to increase the sampling density
- Colorful maps are often more striking than simple plots; oceanographers love them, but maps are data-hungry beasts!

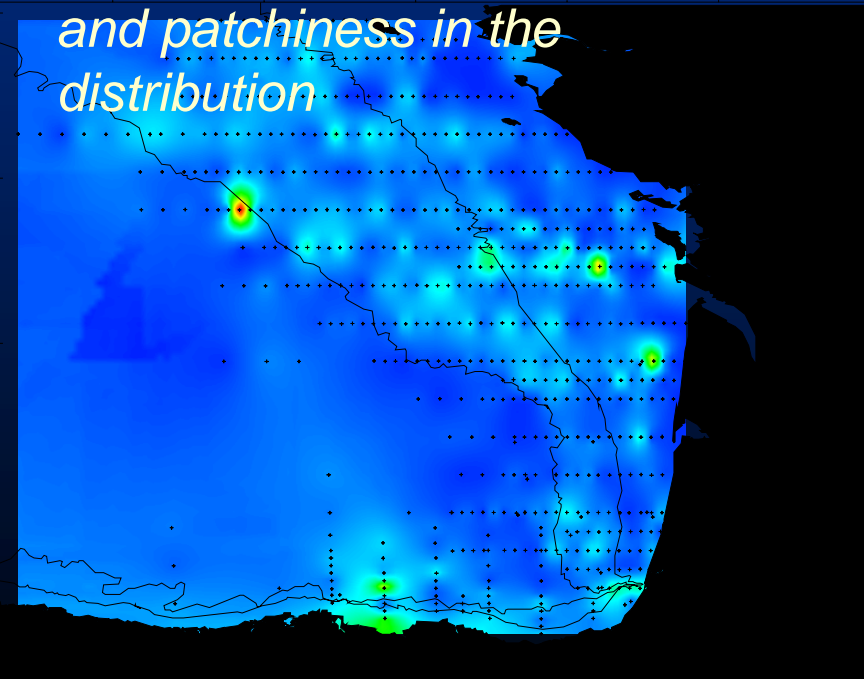


More data: These maps are much more appealing...



Zooplankton abundance in the Bay of Biscay at two different dates

Note the large number of stations sampled (black dots) and patchiness in the distribution

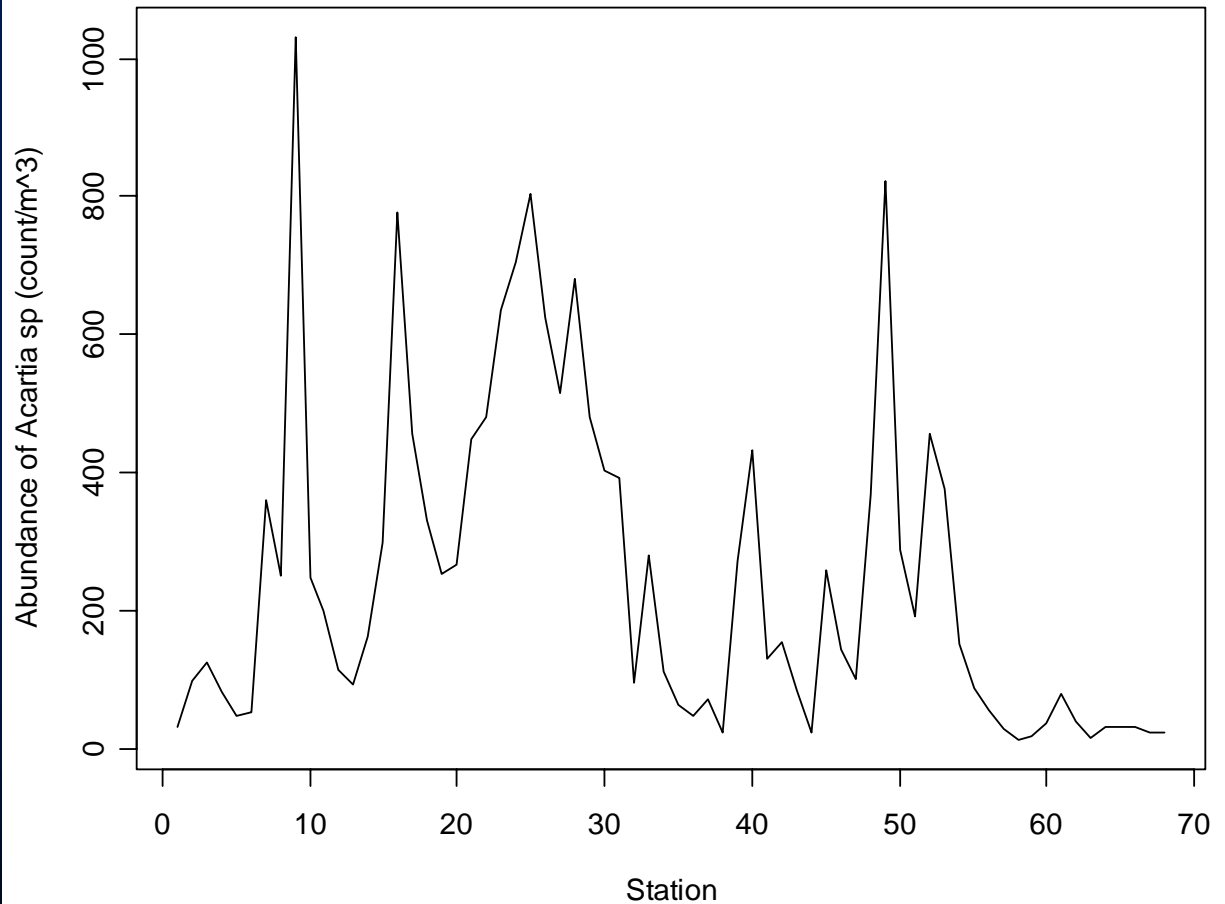


Data and graphs: X. Irigoien et al, AZTI. Analysis of plankton digital images with PVA, a precursor of Zoolmage



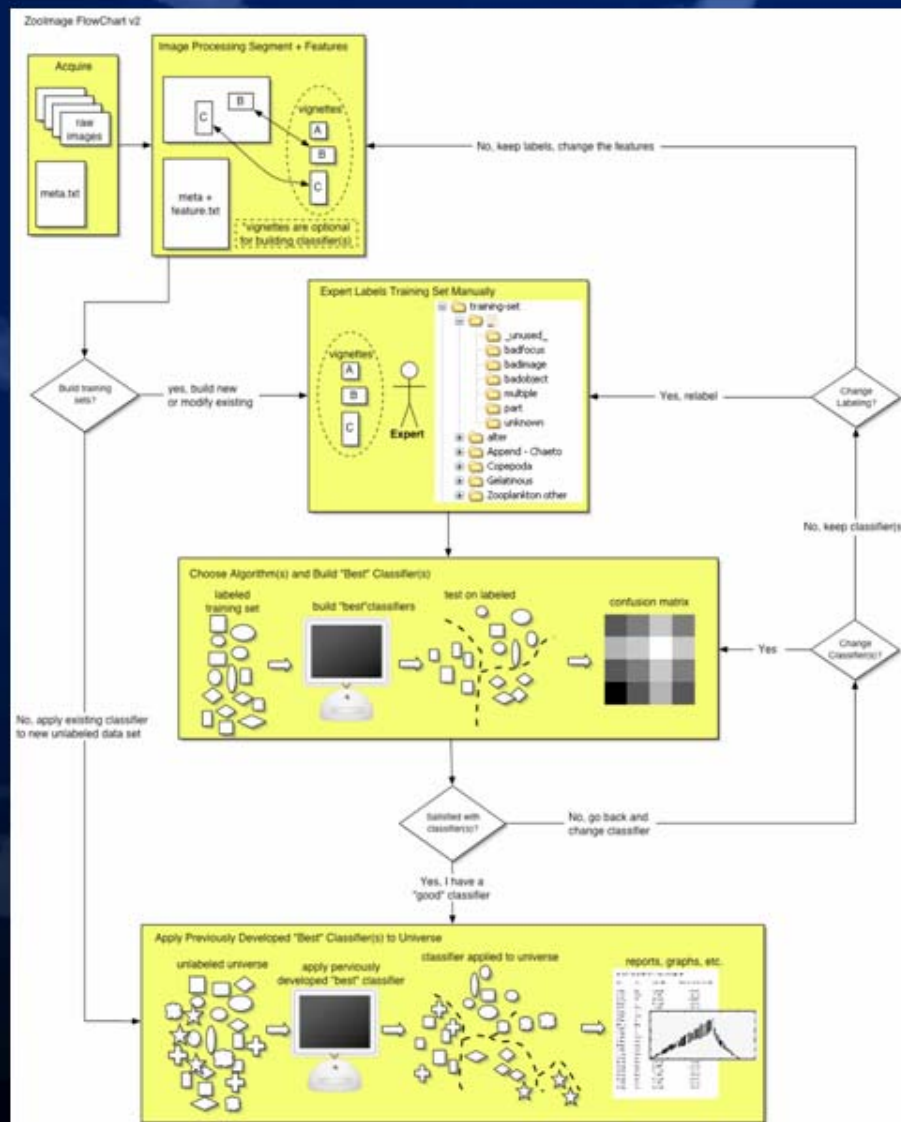
... than this plot

- Abundance of a copepod along a transect
- Space and time are confused
- No 2D/3D resolution



Plankton image analysis is complex

- Image analysis (of zooplankton) is a complex task
- It requires a complex and specialized software
- Example: data process flowchart in ZooImage



(diagram by Ben Tupper)

Plankton image analysis is complex

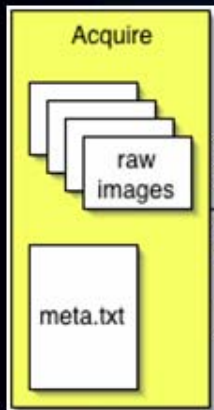
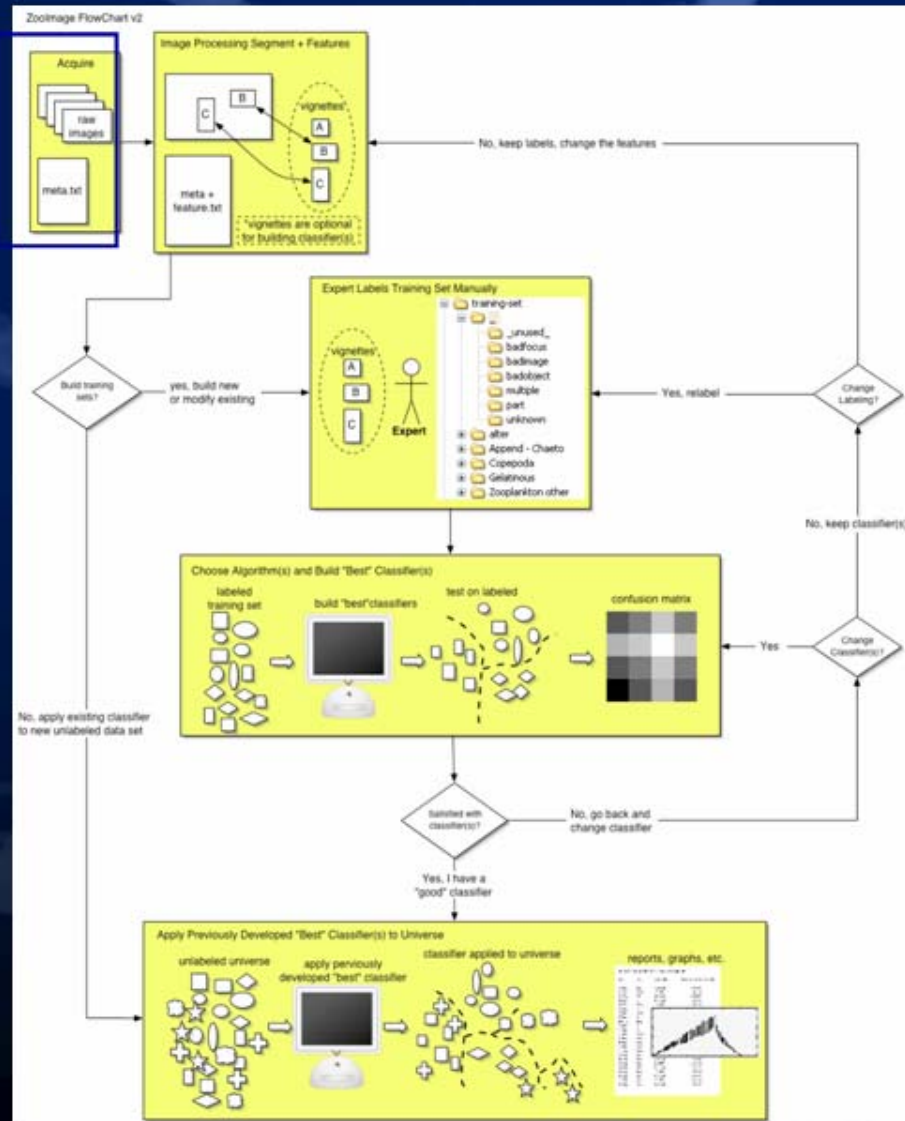


Image analysis (of plankton) is a complex task

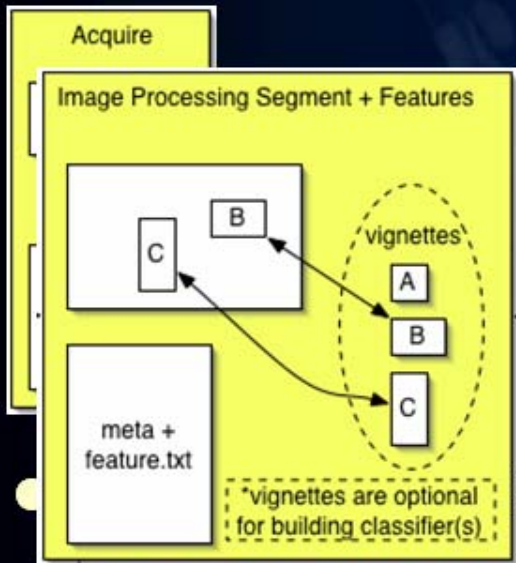
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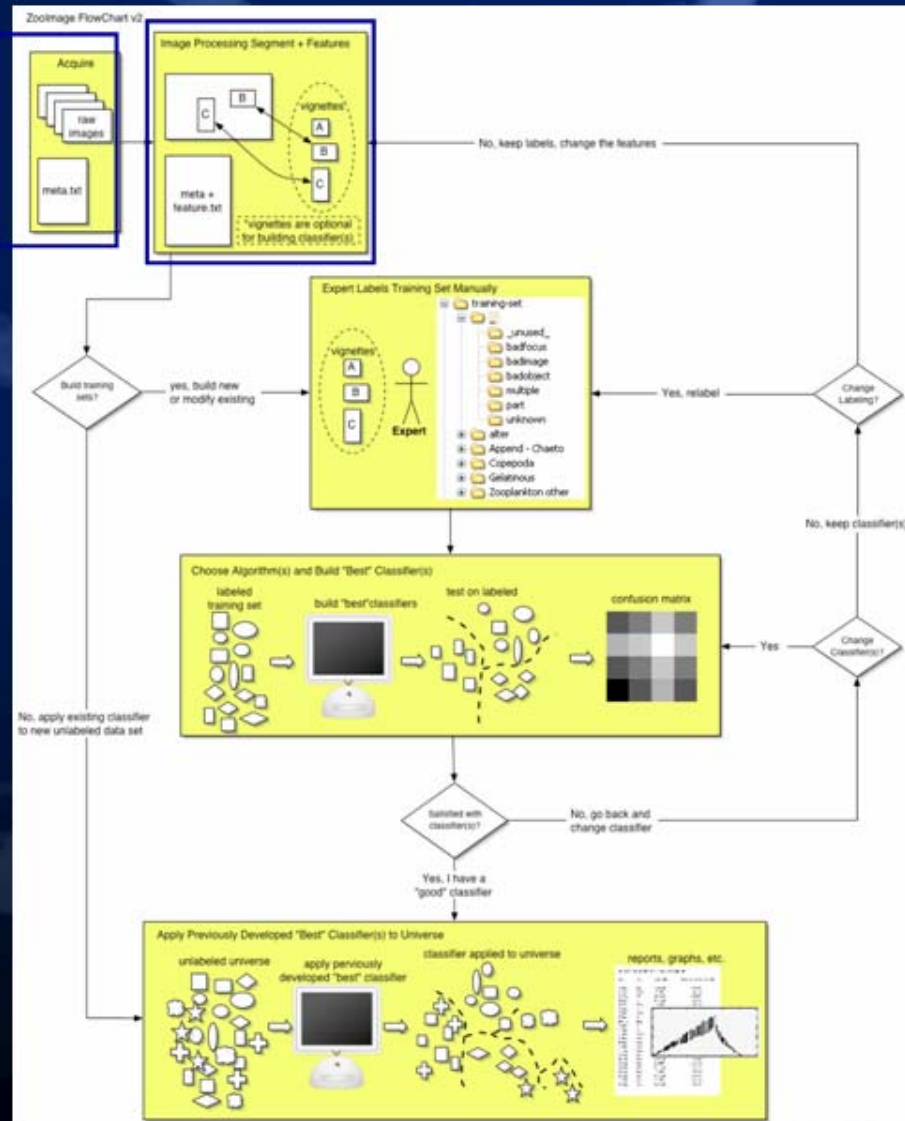
is (of
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software

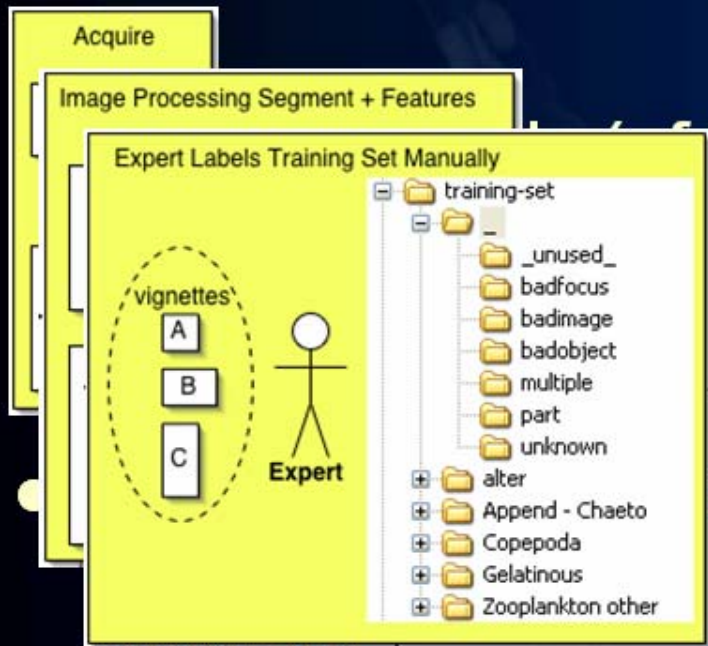
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(diagram by Ben Tupper)

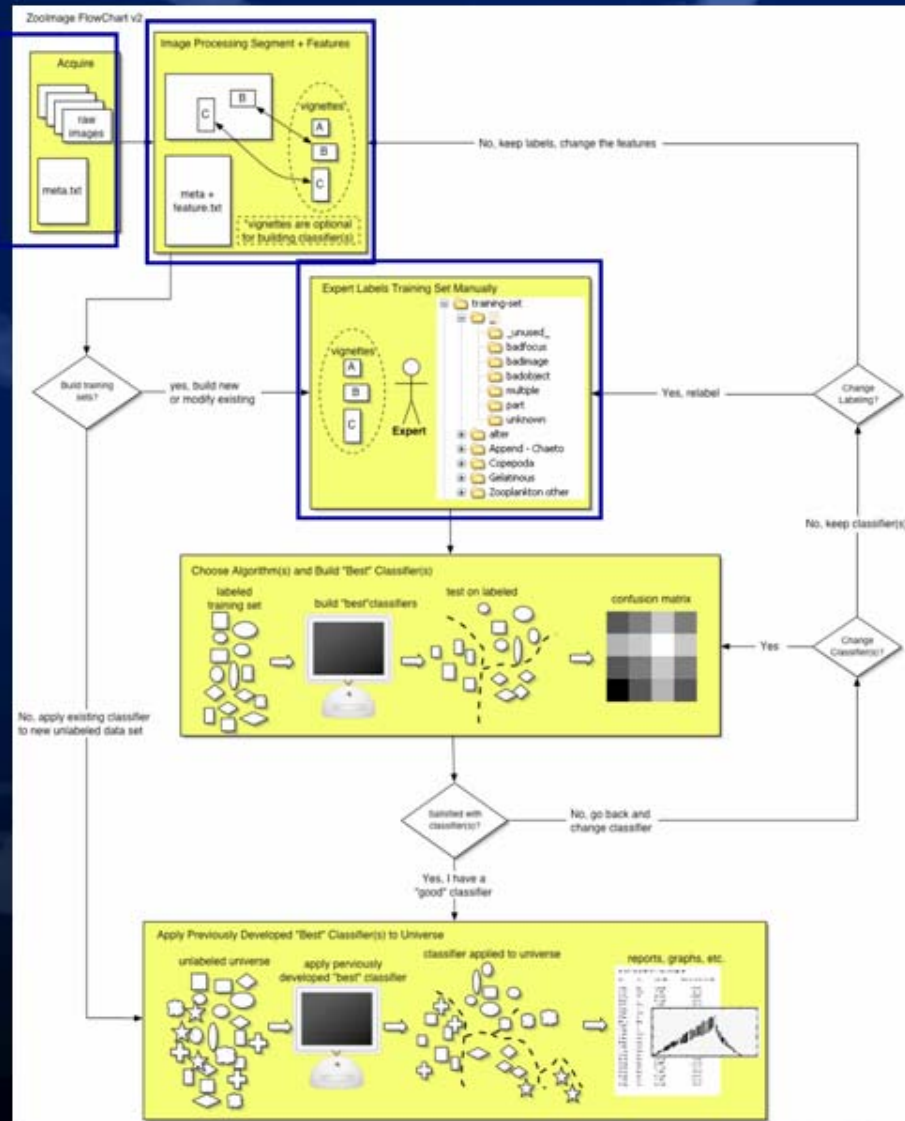


Plankton image analysis is complex



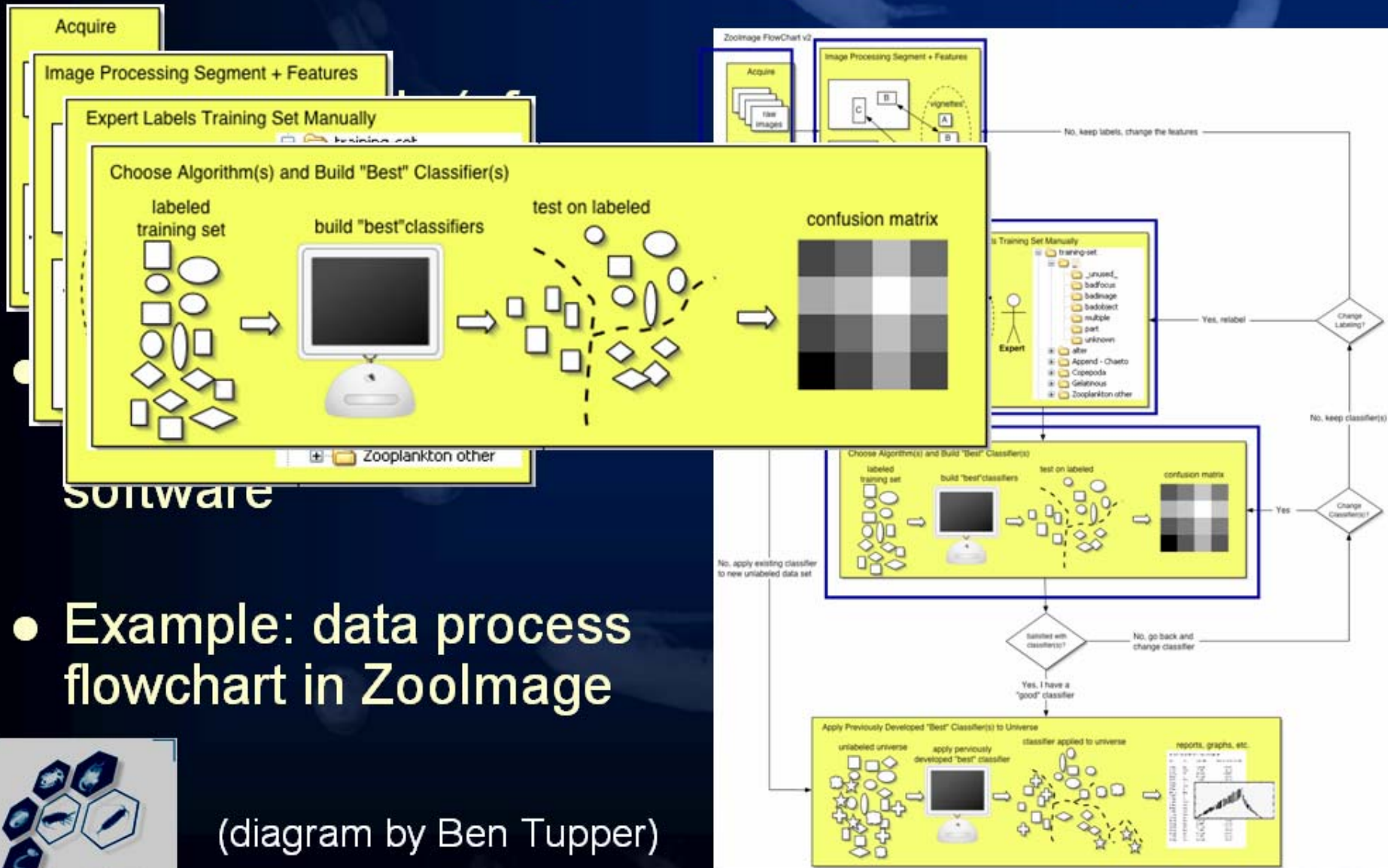
software

- Example: data process flowchart in Zoolmage

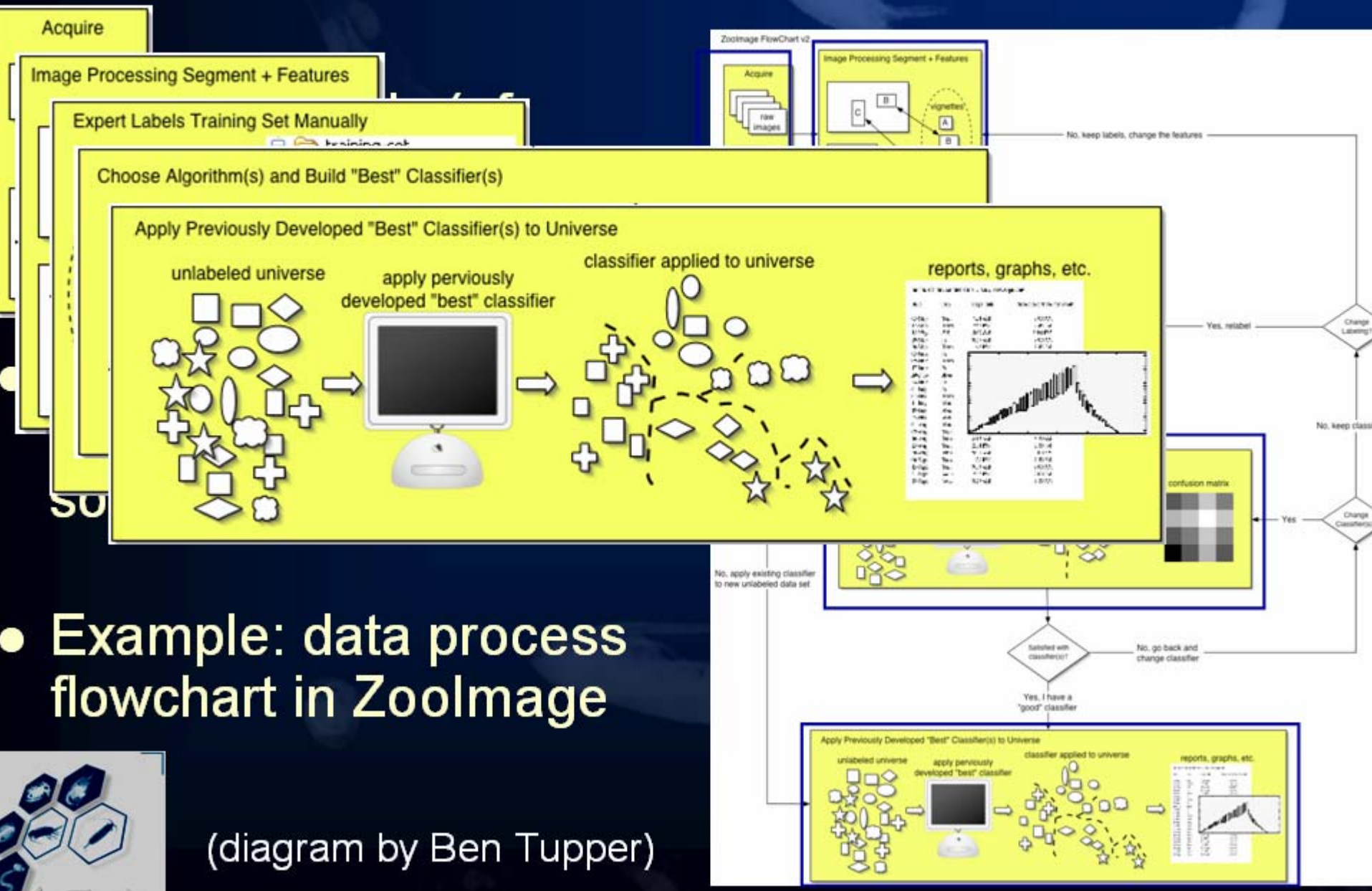


(diagram by Ben Tupper)

Plankton image analysis is complex



Plankton image analysis is complex



- Example: data process flowchart in Zoolmage

(diagram by Ben Tupper)

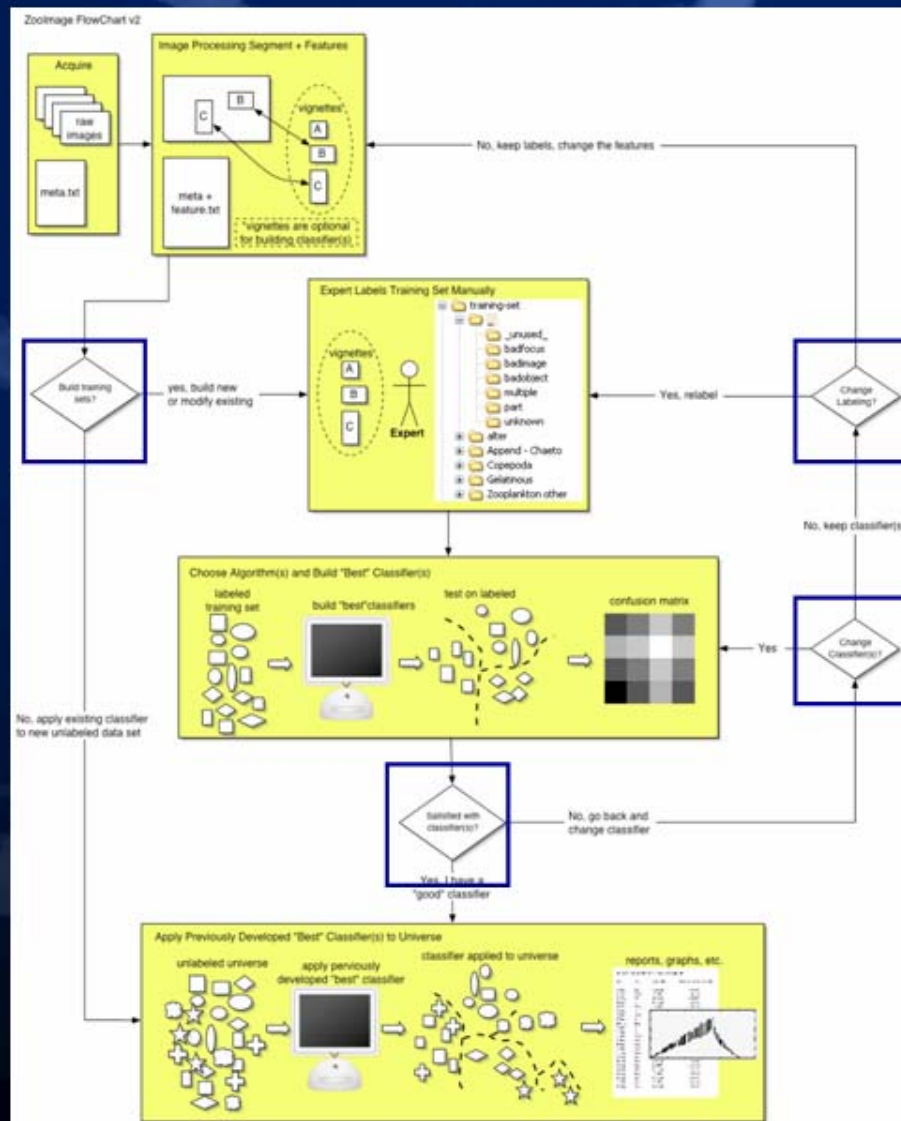


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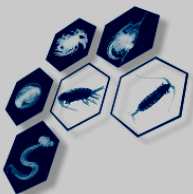


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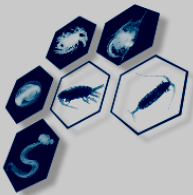
Why software development lies behind hardware development?

- **Academic:** The 'politically correct' way of working does not favor software tools development (scripts \Rightarrow data analysis \Rightarrow results \Rightarrow publication(s) \Rightarrow 'don't-waste-you-time-and-think-at-your-next-publication').
- **Business:** The hardware sells better than the software. Complex software such as for plankton image analysis costs too much to develop, for a too small market to be profitable



How to do then? (theory)

- Collaborate on a common 'Open Source' project (avoid reinventing the wheel continuously)
- Provide a flexible and general framework
 - Single-use scripts of 'academics' become easily plugins shared with the community
 - Commercial solutions of 'businessmen' are leveraged by a free software to analyze the data...
« hey! Good news: the brain exists already, and it is free. Let's just implement the bridge between our



How to do then? (practice)

- Write and donate to the community a starting point for the Open Source software. Ex: **Visual Plankton**, **ZooProcess** (see corresponding posters), **Zoolmage**
- Convince developers and users (Zoolmage workshop, San Sebastian, November 2005)
- Convince managers it is worth financing such kind of project: Benfield et al, 2007, « white paper » to be published in Journal of Oceanography
- Organize international collaboration: SCOR Working Group 130. First meeting just after the symposium



The ZooImage software and framework

<http://www.sciviews.org/zooimage>

The screenshot displays the R Console window with the following text:

```
Type rfNews() to see new features/changes
A ZIClass object predicting for 5 classes
[1] "Chaetognatha" "Copepoda"
[5] "Salpida"

Algorithm used: randomForest
Mismatch in classification: 0%
k-fold cross validation error estimation (k = 10):
13.69%

Error per class:
Error (%)
Copepoda          5.00
Crustacea other   15.28
Chaetognatha     15.79
Salpida          26.32
marine snow      26.47

classes          predicted
01 Chaetognatha  32  2  3  0  1
02 Copepoda      0 95  4  1  0
03 Crustacea other 0  9 61  2  0
04 marine snow   1  1  3 25  4
05 Salpida       2  0  0  3 14
```

The ZooImage1 assistant window is open, showing a toolbar with icons for Analyze, Objects, Apps, Functions, Utilities, Options, and Help. The status bar indicates the path: Ready - C:/ZooPhytoImage Examples/ScanG16-train&data.

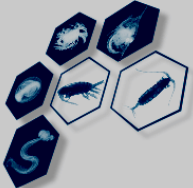
Four image thumbnails are displayed in a grid, each with a 500 µm scale bar and a filename below it:

- Top-left: `0-20.H1+A1_111.jpg`
- Top-right: `MTLG.2004-10-20.H1+A1_137.jpg`
- Bottom-left: `0-20.H1+A1_17.jpg`
- Bottom-right: `MTLG.2004-10-20.H1+A1_187.jpg`

Zoolmage history and current state

- **2004-2005:** first routines at UMH and PVA at AZTI
- **November 2005:** First public release of Zoolmage at the GLOBEC SPACC Zoolmage workshop (San Sebastian, Spain), for developers
- **November 2006:** version 1.0-0, features freeze, beta version
- **current:** version 1.2-1, usable by experienced data analysts, stability, 'friendliness' and end user's documentation to be perfected/completed for universal use.
- Windows platform today, Linux and Mac OS ports in the future.

... see contributions (6) in session 9 for actual use



Zoolmage is a collaborative work

- **Xabier Irigoien et al**, AZTI: PVA, workshop Zoolmage, San Sebastian, november 2005 (also with **Angel Lopez-Urrutia**)
- **Mike Sieracki & Ben Tupper**, Bigelow Lab: FlowCAM plugin
- **Nick Mortimer**, CSIRO: PlanktonJ (see corresponding poster)
- **Jens Rasmussen**: forum (<http://zooimage.overchord.net>)

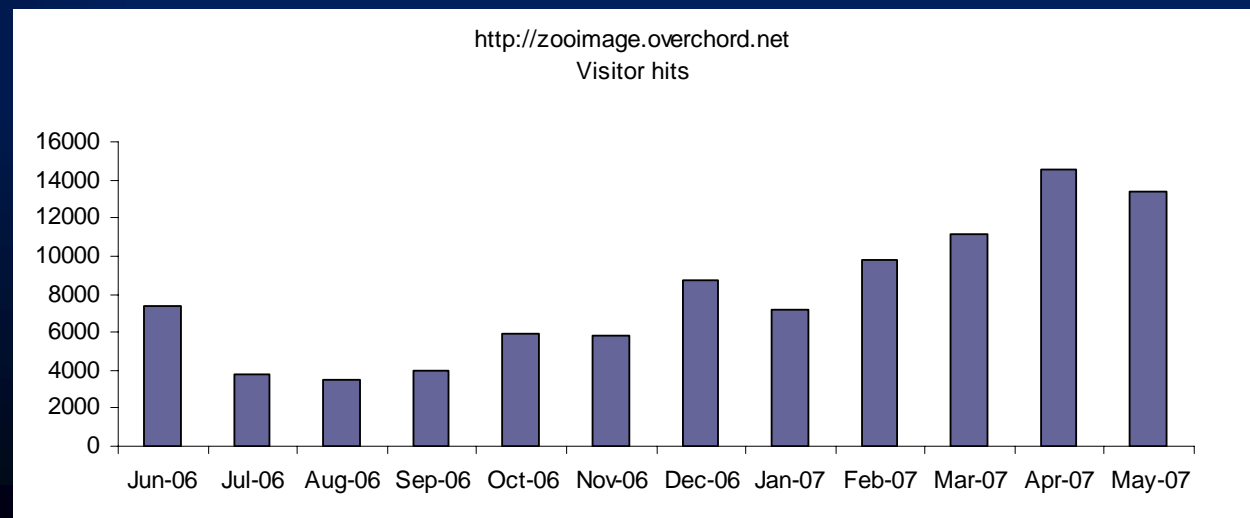
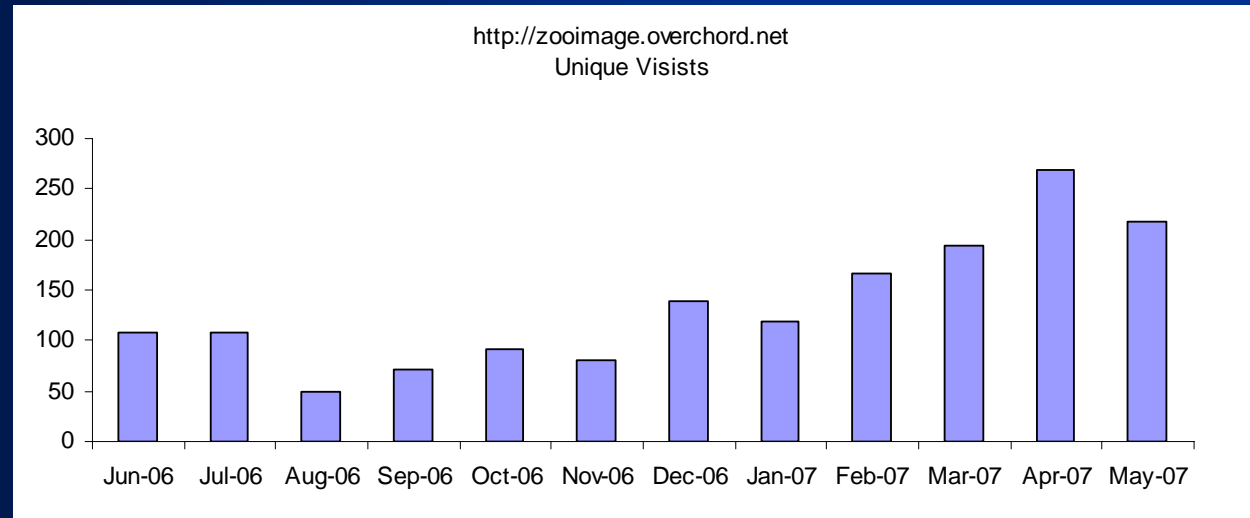


... more in the future !?

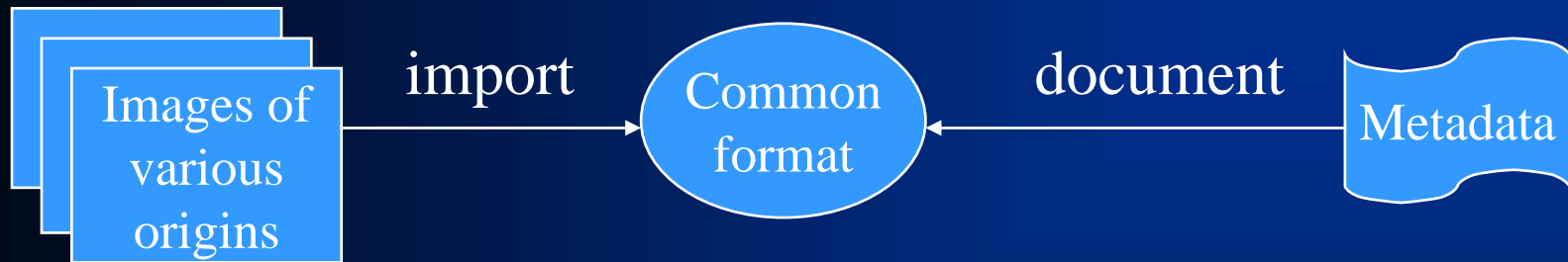
Plankton Image analysis forum: exchange between developers & users

<http://zooimage.overchord.net>

- Started in November 2005 and has grown steadily
- General topics and application specific areas for support and discussion
- Activity monitoring shows increasing interest among our community



ZooImage framework (I)



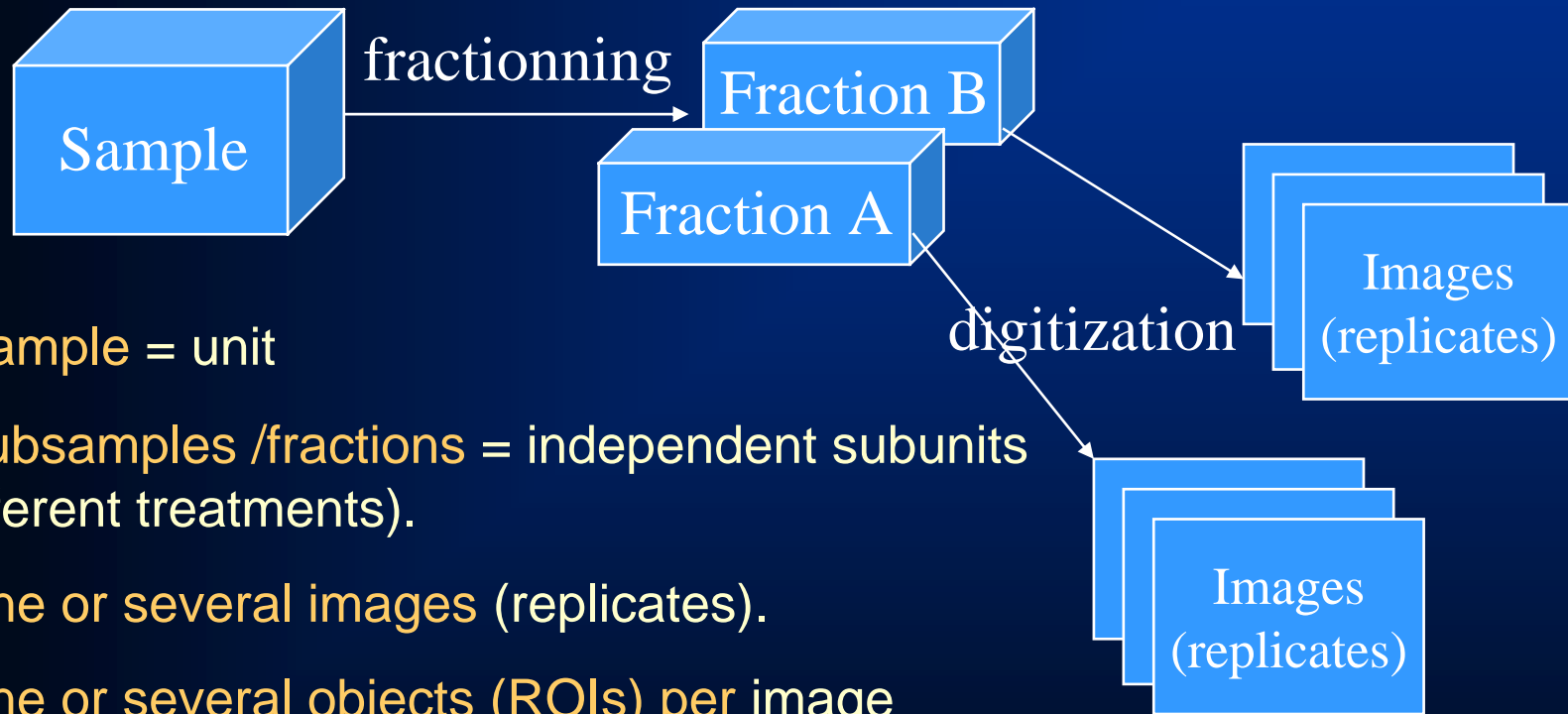
- **Standard naming conventions** for image files: `SCS[.xxxx-xx-xx].SS+F[nn]` eases exchange of data.
- **Standard metadata fields** ease automation of tasks.

The screenshot shows a window titled "BIO.2000-05-05.p72+A.zim - Sc1" with a menu bar (File, Edit, Search, View, Tools, Options, Language, Help). The main content area displays the following metadata:

```
ZI1
- [Image]
  Author=Naiara_Serrano
  Hardware=HP_Scanjet_8200
  Software=HP_driver_version_2.0
  ImageType=reflect_24bits_color_600dpi
- [Fraction]
  Code=A
  Min=-1
  Max=-1
- [Subsample]
  SubPart=0.024
  SubMethod=volumetry
  CellPart=1.00
  Replicates=1
  VolIni=10.56
  VolPrec=
```



Flexibility: image *versus* sample

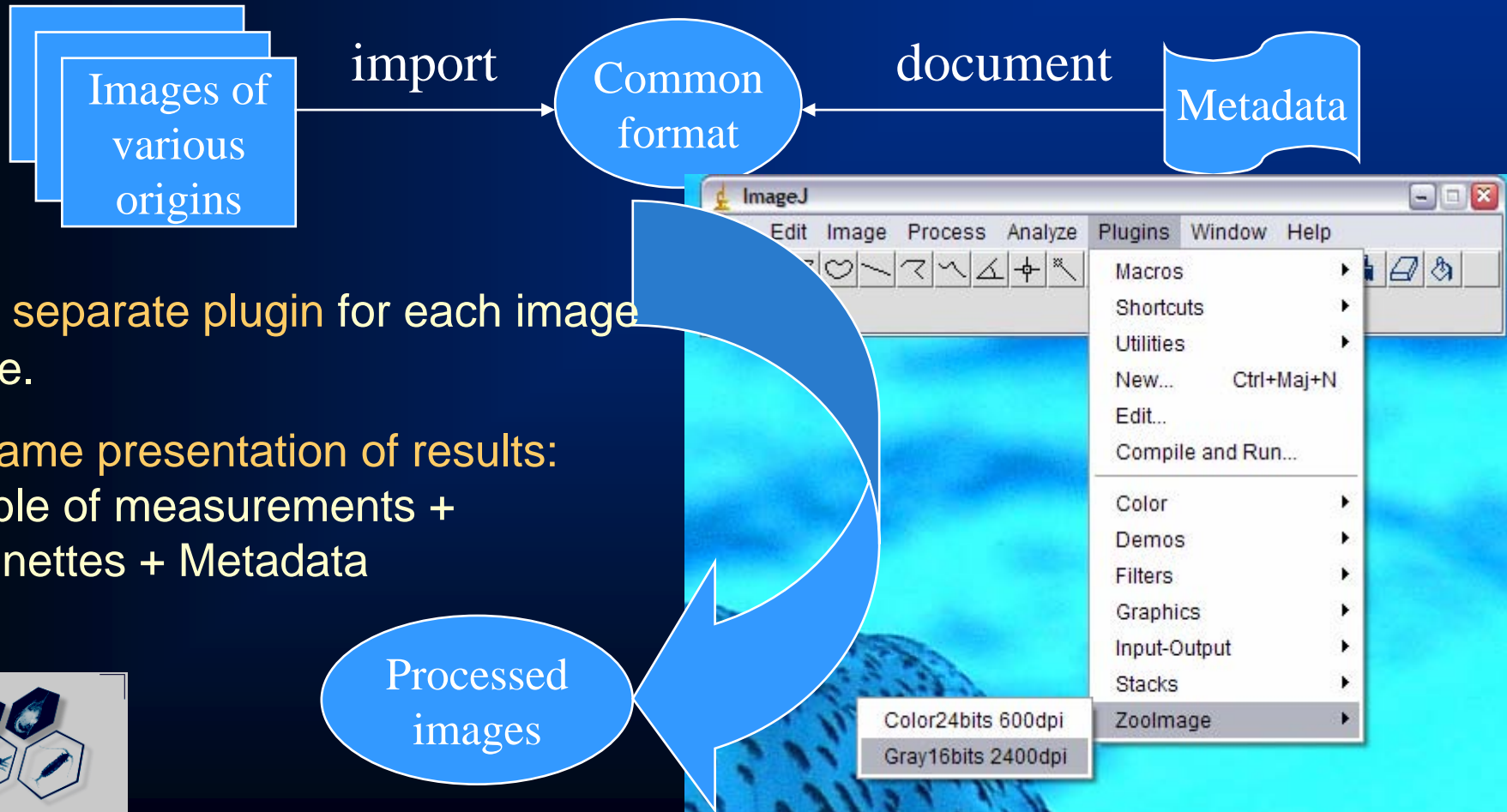


- **Sample** = unit
- **Subsamples /fractions** = independent subunits (different treatments).
- **One or several images** (replicates).
- **One or several objects (ROIs)** per image

=> *Most schemes are taken into account*



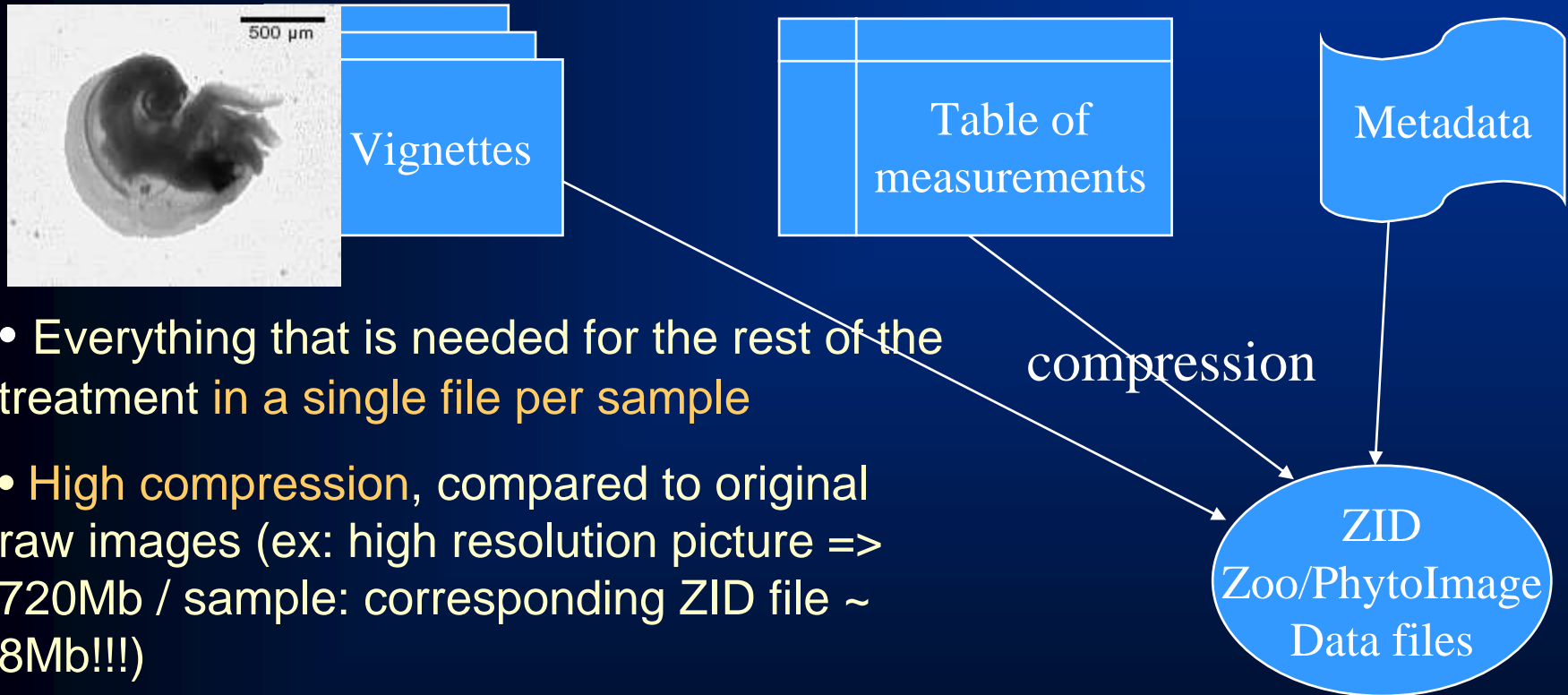
Separate plugins for image processing



- A separate plugin for each image type.
- Same presentation of results: Table of measurements + Vignettes + Metadata



ZID files: common format & compression



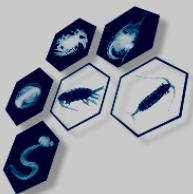
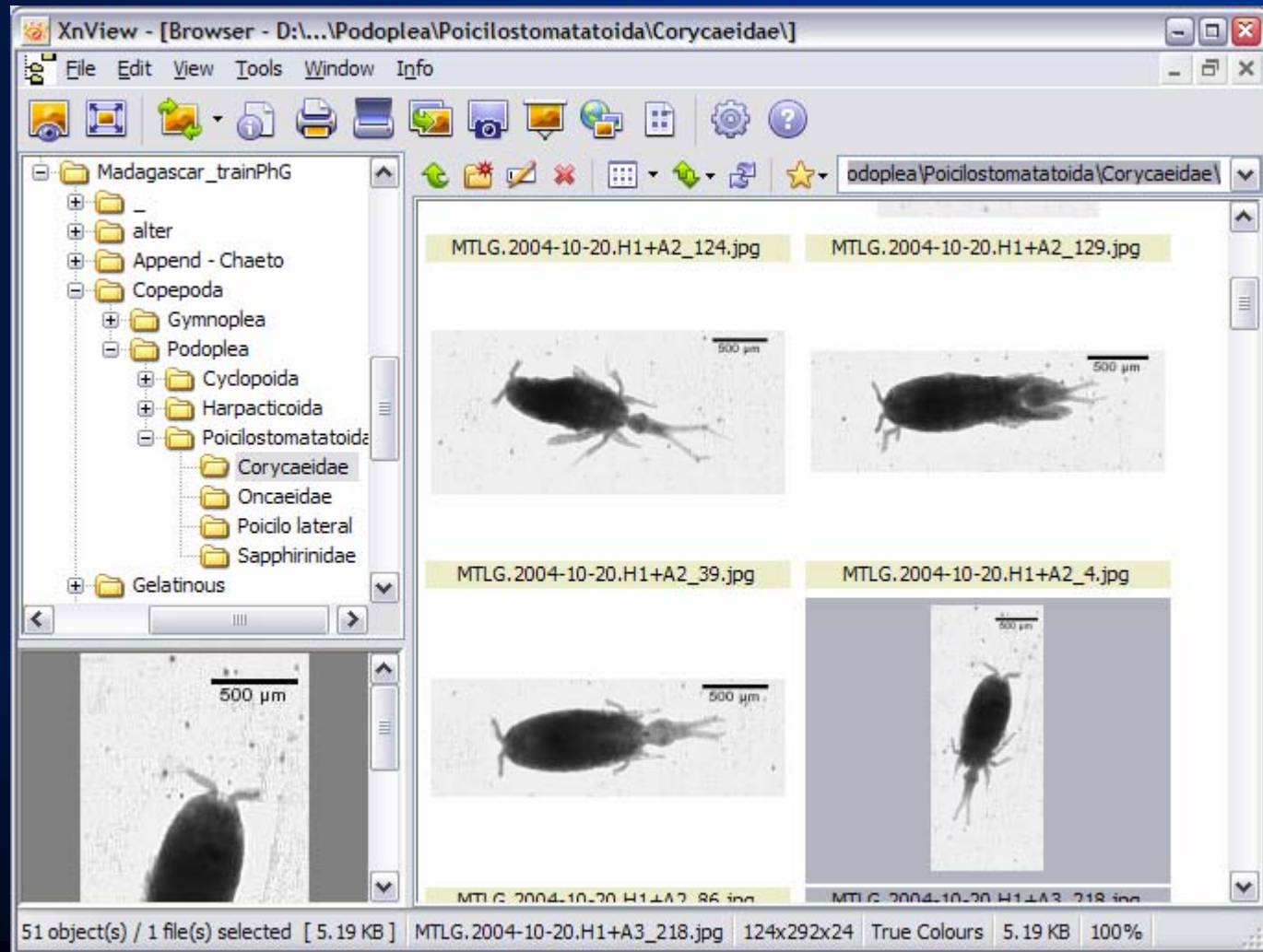
- Everything that is needed for the rest of the treatment in a single file per sample
- High compression, compared to original raw images (ex: high resolution picture => 720Mb / sample: corresponding ZID file ~ 8Mb!!!)

=> disk space problems for very large series / images are solved.

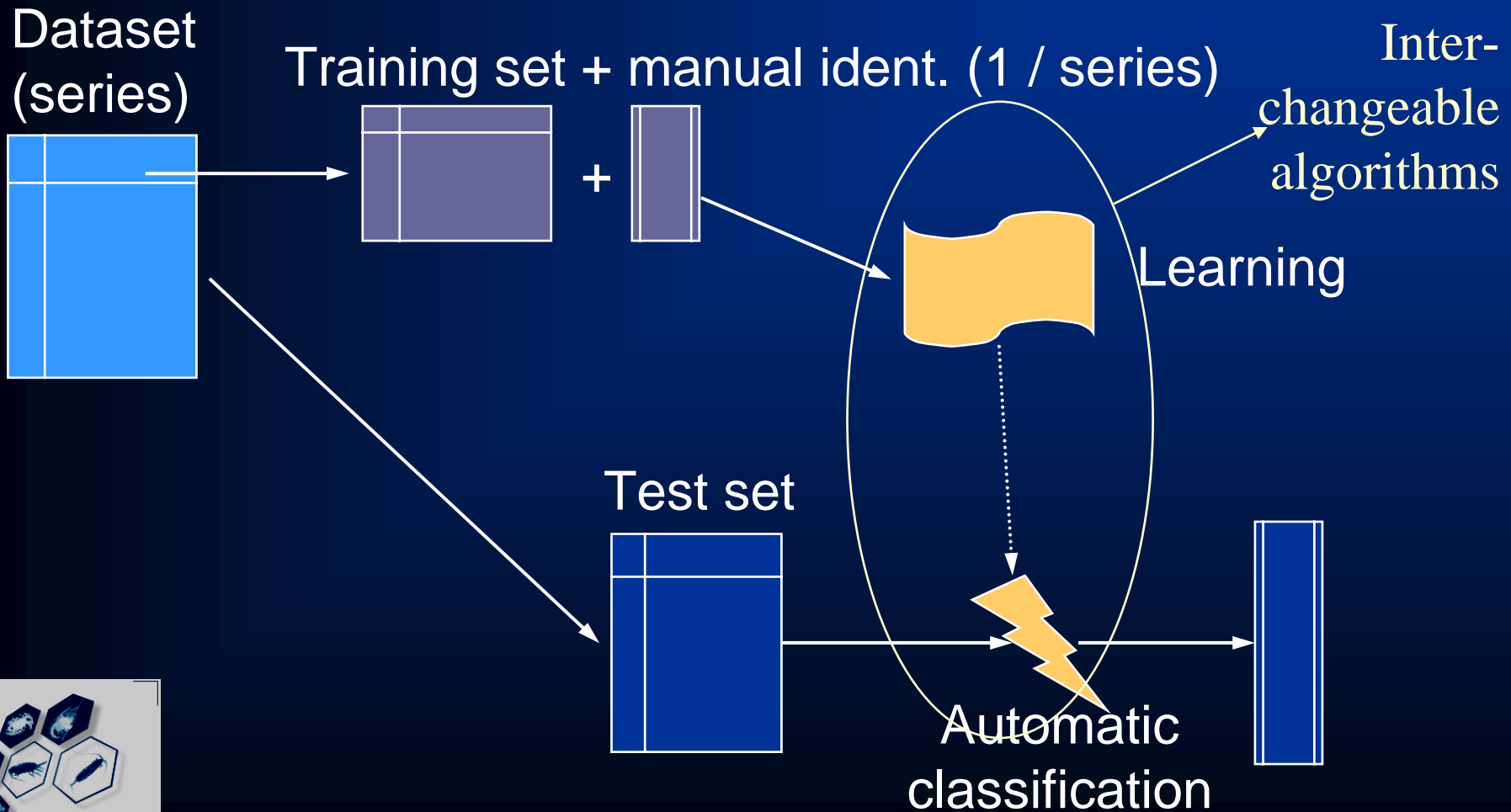


Hierarchy grouping & manual training sets

- Any groups you want.
- Hierarchy reflect relationship – various possible levels of details.
- Taken into account automatically by the software.



Common framework for classifiers



Computing of pertinent measurements

Zoolmage computes (mixing of fractions, averaging over replicates and conversion per cubic meter of seawater are done automatically):

- **Abundances per taxa** (absolute, relative, log-scale),
- **Biomasses, carbon content, etc.;** total or per taxa (you must provide a conversion table),
- **Size spectra; total or per taxa.** Calculation of the slope of an exponential decreasing model. The number and width of classes are totally free (even irregularly spaced classes can be computed).



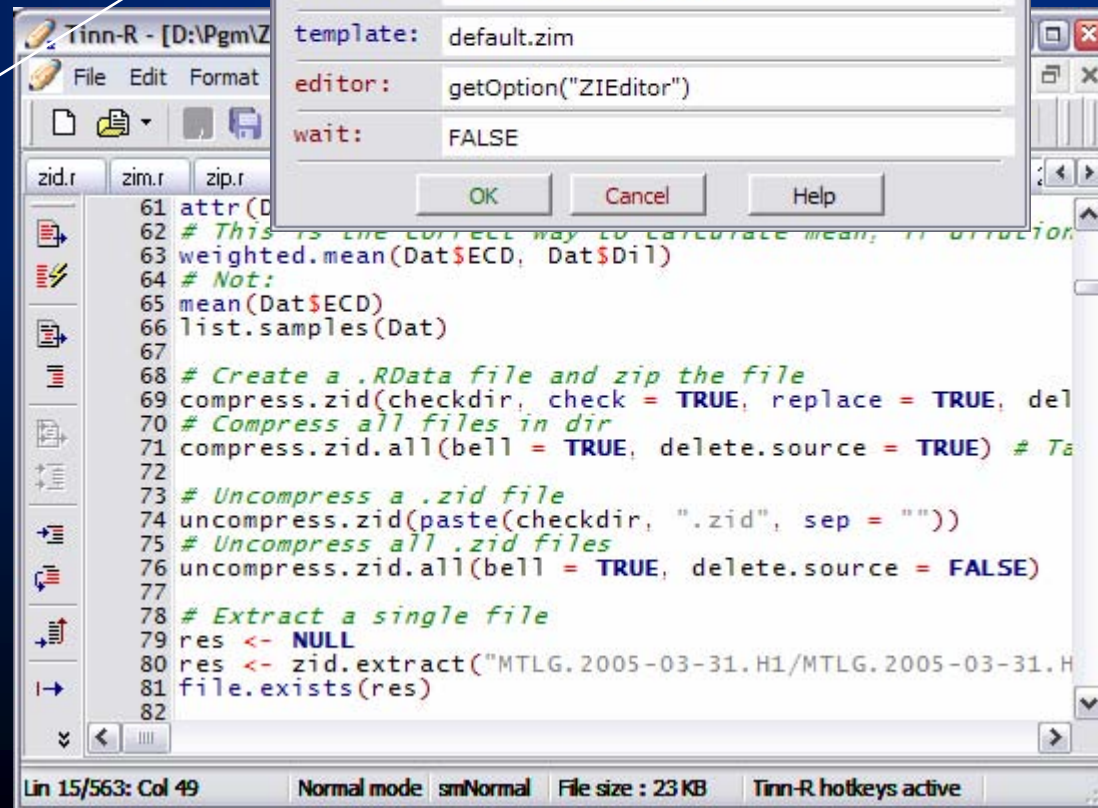
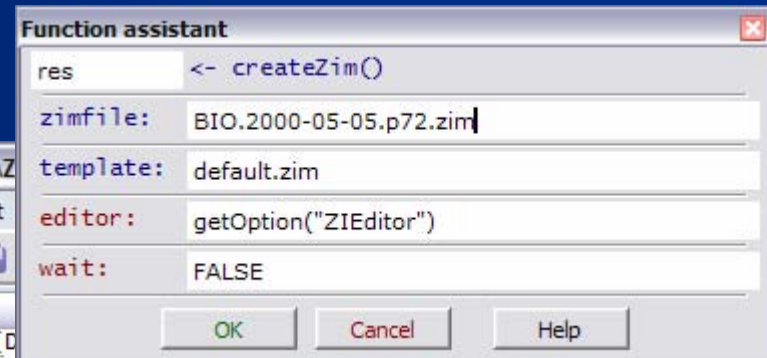
Accessibility

- Three levels, three user interfaces:

1. Full point&click assistant (complete beginner),

2. Dialog boxes prompting for command options (intermediate user),

3. Toolbox of functions for pure programming (developers)



Current performances & future

- 20-30 taxa with 75-80% global accuracy on an average training set
- ZoolImage analyses almost any kind of image, except Zooscan and VPR (for the moment)
- Developement highly dependent on contributions and actual use, but better algorithms, more graphs, more friendly GUI and a lot more documentation are planned

