

# Are recent advances in automated benthic macroinvertebrate taxa identification a viable option to manual keying?

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# Why use automated taxa identification?

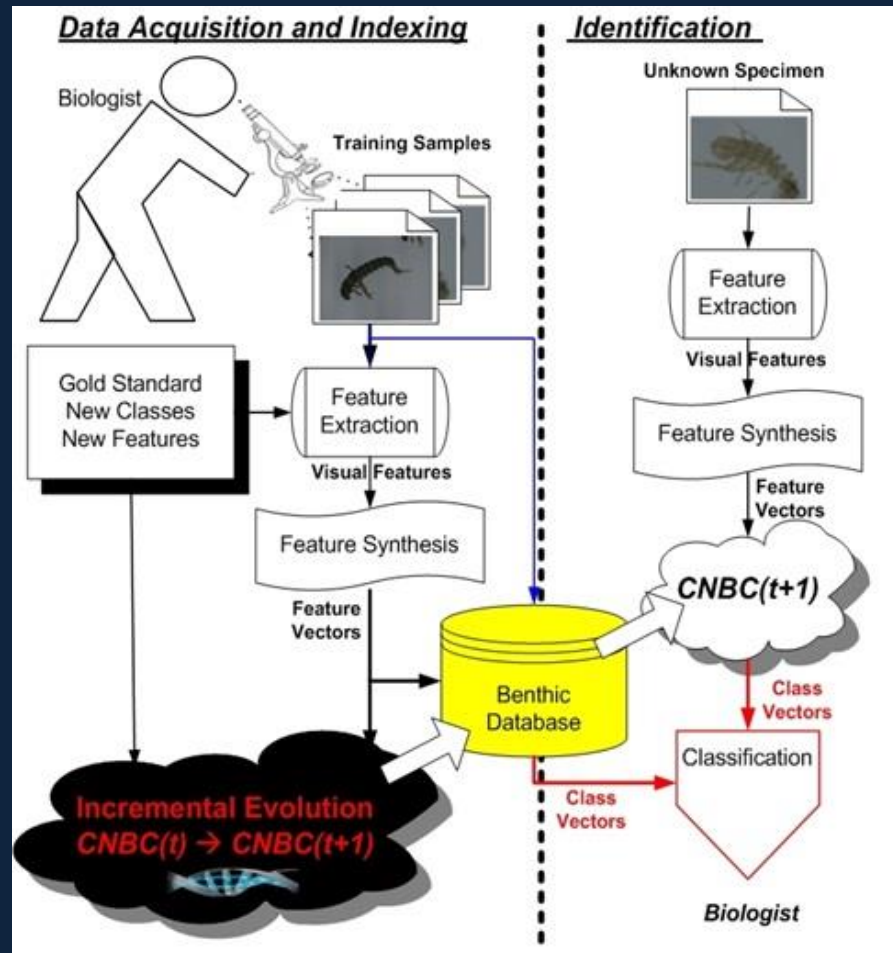
- growing demand for biological water quality assessments
- mismatch between resources and demands
- identification accounts for 1/3 of the cost of each macroinvertebrate sample (in Finland)

Possible solution:

Cut identification cost with computer vision

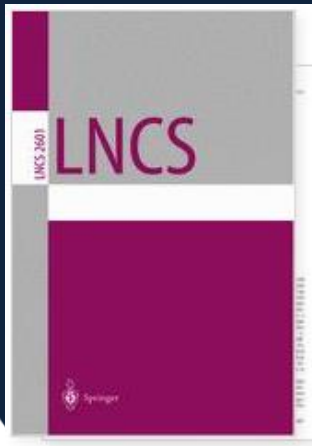
- cheap
- Fast, allows higher sample volumes

# How automated taxa identification works



# First trials: Prototype 1

8 taxa set, flatbed scanner, 1592 single posture images



Results:  
80% correct and  
400-10000 times  
faster than a  
human expert  
(Tirronen et al.  
2009)



Results:  
97% correct  
(Kiranyaz et al.  
2011)

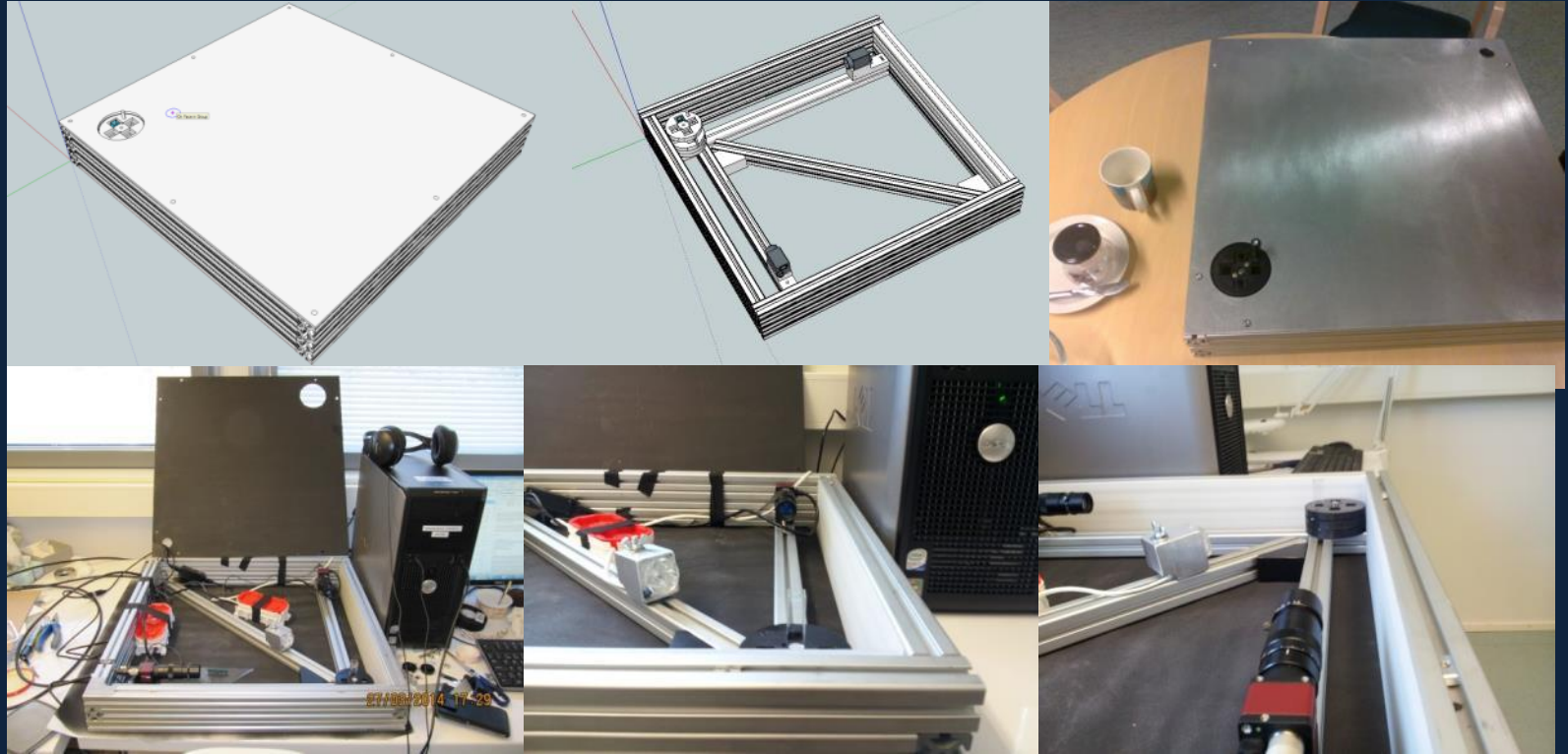
# Additional studies

(8->) 35 species, 6814 single posture images, flatbed scanner

- Results:
- New classifier
- Random Bayes Array (RBA)
- 81% correct
- RBA did not use its full potential (naive priors)
- Ärje et al. 2013, Environmetrics
- Prototype1: too work intensive =>
- New prototype development started in 2013
- Prototype 2: an extension of the picking process
- New feature:
- Two posture imaging => two independent identification results / specimen = better identification



# Prototype 2: two posture design



# Prototype 2

Most complex data set to date

– consists of 42 species, 6670 images

- Two postures from each individual
- Half of the data used for training the algorithm, half for testing

# Prototype 2: Actual footage

## Left camera

Baetis muticus



Baetis rhodani



Baetis rhodani 2



Limnius volckmari



Simuliidae



Oulimnius  
tuberculatus



## Right camera

Baetis muticus



Baetis rhodani



Baetis rhodani 2



Limnius volckmari



Simuliidae



Oulimnius  
tuberculatus





# How the RBA algorithm reaches a decision

Limnius volckmari



Limnius volckmari



Baetis rhodani	Baetis muticus	Limnius volckmari	Simuliidae	Oulimnius tub.	Final posterior
<ul style="list-style-type: none"><li>• 0.07</li></ul>	<ul style="list-style-type: none"><li>• 0.05</li></ul>	<ul style="list-style-type: none"><li>• 0.88</li></ul>	<ul style="list-style-type: none"><li>• 0</li></ul>	<ul style="list-style-type: none"><li>• 0</li></ul>	<ul style="list-style-type: none"><li>• 0.8</li></ul>
<ul style="list-style-type: none"><li>• 0.10</li></ul>	<ul style="list-style-type: none"><li>• 0.08</li></ul>	<ul style="list-style-type: none"><li>• 0.72</li></ul>	<ul style="list-style-type: none"><li>• 0</li></ul>	<ul style="list-style-type: none"><li>• 0</li></ul>	

# Results :

## Overall Classification errors (CE)

	Right camera	Left camera	Both cameras
Mean(CE)	0.27	0.29	<b>0.22</b>
Sd(CE)	0.0015	0.0016	0.0012

**Two postures clearly improve identification:  
From 71% -> 78% correct**



# Tricky pictures



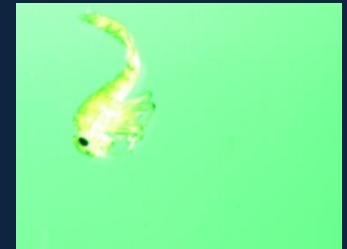
*Asellus aquaticus*



*Baetis digitatus*



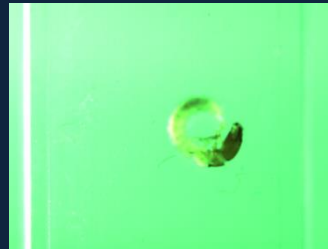
*Baetis niger*



*Baetis rhodani*



*Ceratopogonidae*



*Chimarra marginata*



*Dicranota*



*Elmis aenea*



*Elodes*



*Gammarus lacustris*



*Habrophlebia*



*Leuctra nigra*

# Computer vision- a viable alternative to manual keying?

- Prototype 2 produced 78% correct with suboptimal pictures
- No priors – suboptimal performance
- Two postures improved the identification
- Sharper pictures (DOF, lighting) and more complex algorithms will increase the accuracy further

# Benefits:

- Cheap (prototype 2 costs < 10000€)
- Functions with non expert operators
- Predictable error structure
- Additional metrics for free (size spectra / biomass)
- Prototype 3 under development, ready in spring of 2016 (Finnish Academy funding)
- First test of human vs. machine planned in 2016 (during human proficiency testing)
- Can be used solo or to augment DNA techniques
- Fully operational in under 4 years

# Thank you!

