# Re-engineering DNA Surveillance

Tobias Ehrenberger
tobias.ehrenberger@students.fh-hagenberg.at

Department of Medical- and Bioinformatics
Upper Austria University of Applied Sciences
Softwarepark 11, 4232 Hagenberg, Austria

Version 1·00·—2 – 26. Mai 2010 – Tobias Ehrenberger

# Outline

1. About DNA Surveillance

2. Motivation and Aims

3. Tasks

4. Architecture

5. The New User Interfaces

6. Conclusion

# About DNA Surveillance

## What is DNA Surveillance?

- A species identification tool
- using phylogenetic methods
- available on the internet.

# About DNA Surveillance

## What is DNA Surveillance?

- A species identification tool
- using phylogenetic methods
- available on the internet.

## How does it work?

Input:  Unknown Sequence + Reference Alignment

Output:  Phylogenetic Tree

# About DNA Surveillance

## What is DNA Surveillance?

- A species identification tool
- using phylogenetic methods
- available on the internet.

## How does it work?

Input:    Unknown Sequence + Reference Alignment

Output:    Phylogenetic Tree

## Statistical Support

- Bootstrapping

# Motivation and Aims

## Why Re-engineering?

# Motivation and Aims

## Why Re-engineering?

- No sources available.
- Current system can not be maintained.

# Motivation and Aims

## Why Re-engineering?
- No sources available.
- Current system can not be maintained.

## Aims
- Maintainability
- Usability
- Flexibility
- Modularity

# Motivation and Aims

## Why Re-engineering?

- No sources available.
- Current system can not be maintained.

## Aims

- Maintainability
- Usability
- Flexibility
- Modularity

# Motivation and Aims

## Why Re-engineering?

- No sources available.
- Current system can not be maintained.

## Aims

- Maintainability
- Usability
- Flexibility
- Modularity

# Motivation and Aims

## Why Re-engineering?

- No sources available.
- Current system can not be maintained.

## Aims

- Maintainability
- Usability
- Flexibility
- Modularity

# Motivation and Aims

## Why Re-engineering?

- No sources available.
- Current system can not be maintained.

## Aims

- Maintainability
- Usability
- Flexibility
- Modularity

# Tasks

## Modules

- Database Schema
- WebApp for Reference Alignment Setup
- Option for auto-generating DNA Surveillance Instances
- WebApp for Users
- Phylogenetics Server

# Tasks

## Modules

- Database Schema
- WebApp for Reference Alignment Setup
- Option for auto-generating DNA Surveillance Instances
- WebApp for Users
- Phylogenetics Server

## Preceding Work

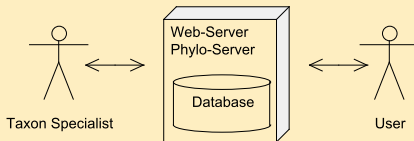Re-engineering started by Waltraud Sichart in 2009

# Tasks

## Modules

- ~~Database Schema~~
- ~~WebApp for Reference Alignment Setup~~
- Option for auto-generating DNA Surveillance Instances
- WebApp for Users
- Phylogenetics Server

## Preceding Work

Re-engineering started by Waltraud Sichart in 2009
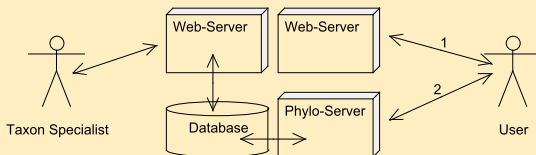
# Architecture

## Current DNA Surveillance
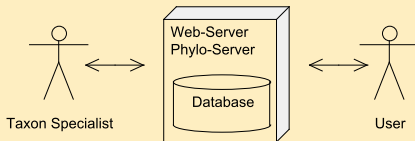
# Architecture

## Current DNA Surveillance



## New version

# The New User Interface

## WebApp for Reference Alignment Setup

# The New User Interface

## User Input Environment

**Enter a Sequence:**

**OR choose a file for processing a bunch of sequences:**
[_____] [Browse...] [Reset]

**Please select a reference alignment:**
● COI Barcode region

**Bootstrap replicates:** [No bootstrapping ∨]  **with threshold**  [50% ∨]
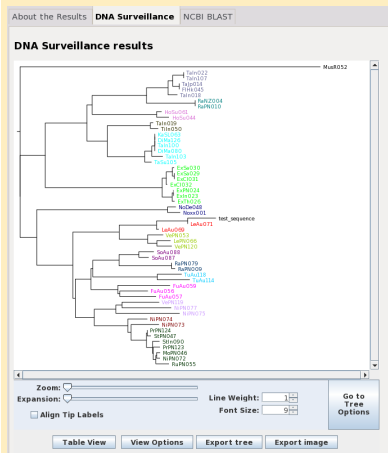[Submit]

Required:

- Reference Alignment
- Unknown Sequence
- or File of Sequences

Optional:

- Bootstrap Analysis

# The New User Interface

## Output:



Results:
- Phylogenetic Tree
- Distance Matrix
- BS-Results

In addition:
- BLAST-Result

# Conclusion

## In a nutshell. . .

New DNA Surveillance

- consists of modules
- provides extended functionality and
- is maintainable

# Conclusion

## In a nutshell. . .

New DNA Surveillance

- consists of modules
- provides extended functionality and
- is maintainable

## Open Tasks

- More Tests (+ Bugfixing)
- Final Release
- . . .

# That's it!

Thank you for your attention!

# That's it!

Questions?