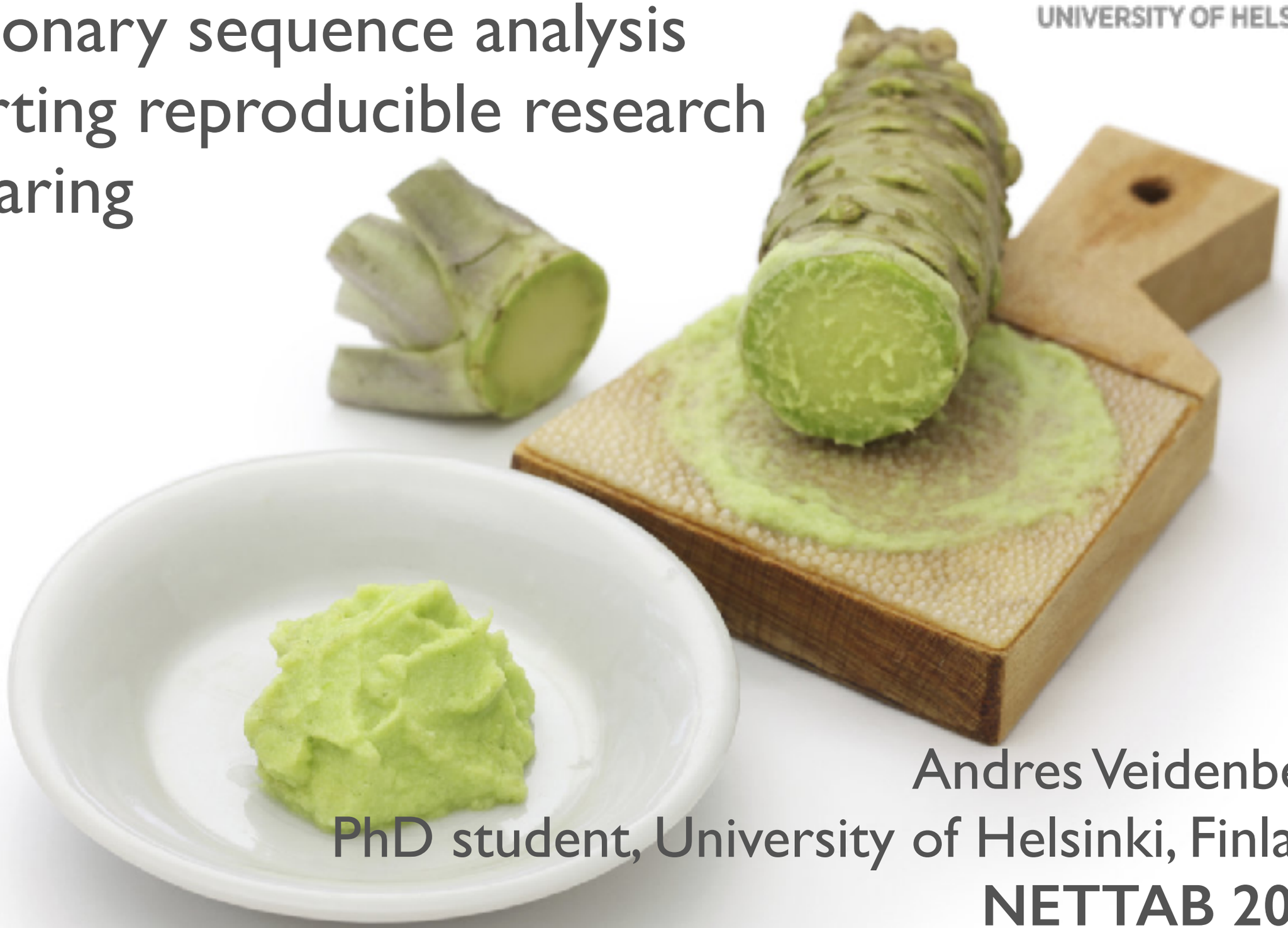
# was@bi

## a web-based platform for evolutionary sequence analysis supporting reproducible research and sharing

UNIVERSITY OF HELSINKI



Andres Veidenberg
PhD student, University of Helsinki, Finland

**NETTAB 2016**

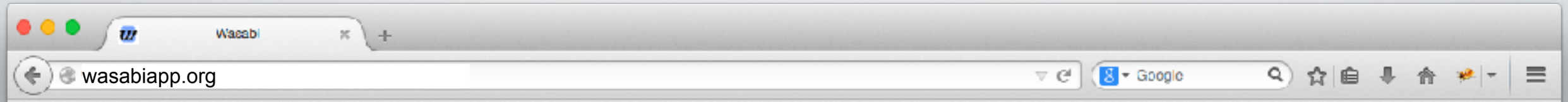
# *was@bi*, and:

1) Data provenance

2) Visualization and publishing

3) Plugin system

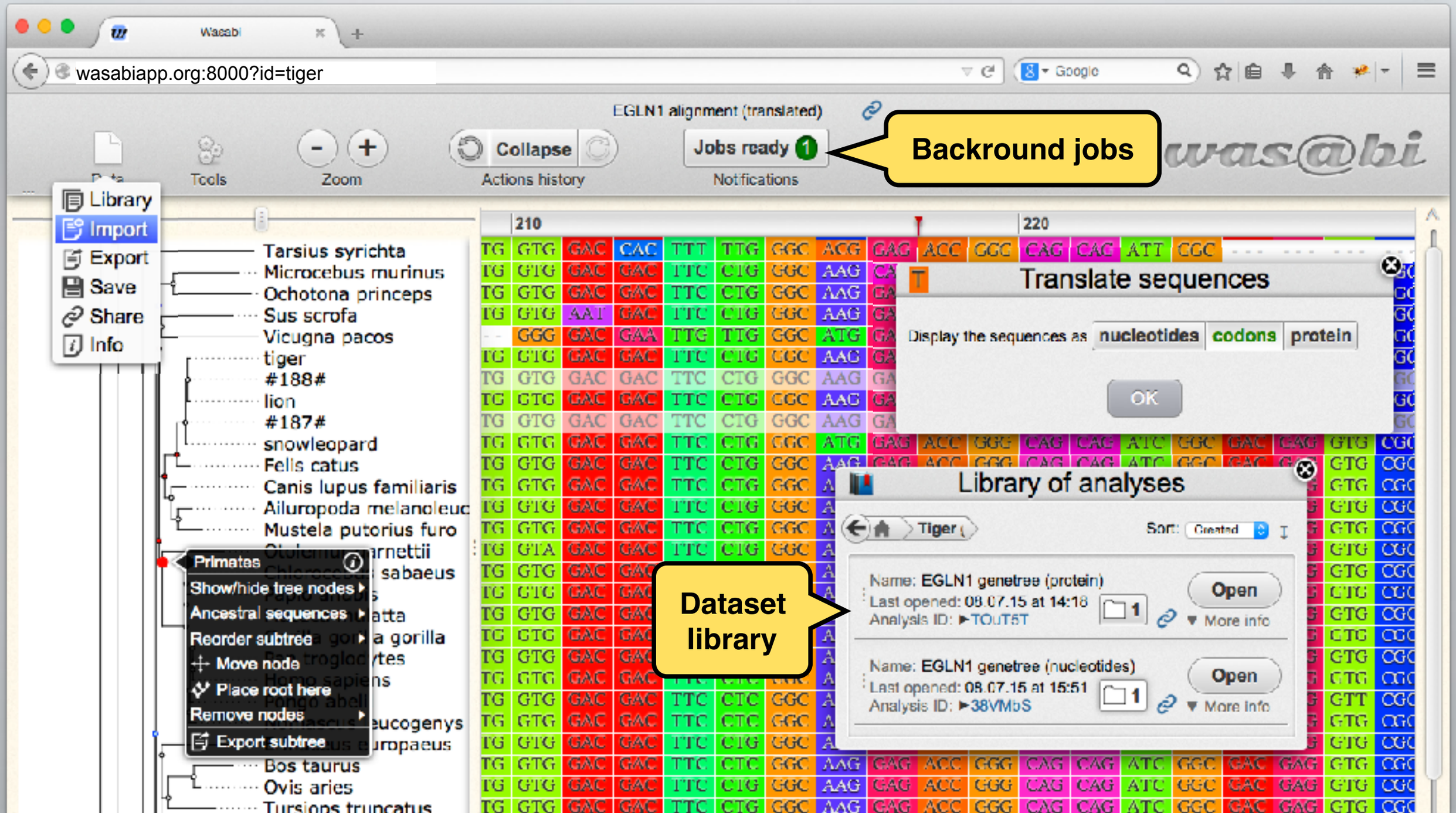
Details and nice video: **http://wasabiapp.org**



# was@bi

Portable HTML5 web app + python server module

http://wasabiapp.org:8000



Wasabi

wasabiapp.org:8000?id=tiger

EGLN1 alignment (translated)

Data | Tools | Zoom | Collapse | Actions history | Jobs ready 1 | Notifications

Bac

Library
Import
Export
Save
Share
Info

Tarsius syrichta
Microcebus murinus
Ochotona princeps
Sus scrofa
Vicugna pacos
tiger
#188#
lion
#187#
snowleopard
Felis catus
Canis lupus familiaris
Ailuropoda melanoleuc
Mustela putorius furo
arnettii
sabaeus
atta
a gorilla
ytes
ns

Primates
Show/hide tree nodes
Ancestral sequences
Reorder subtree
Move node
Place root here

210

Display

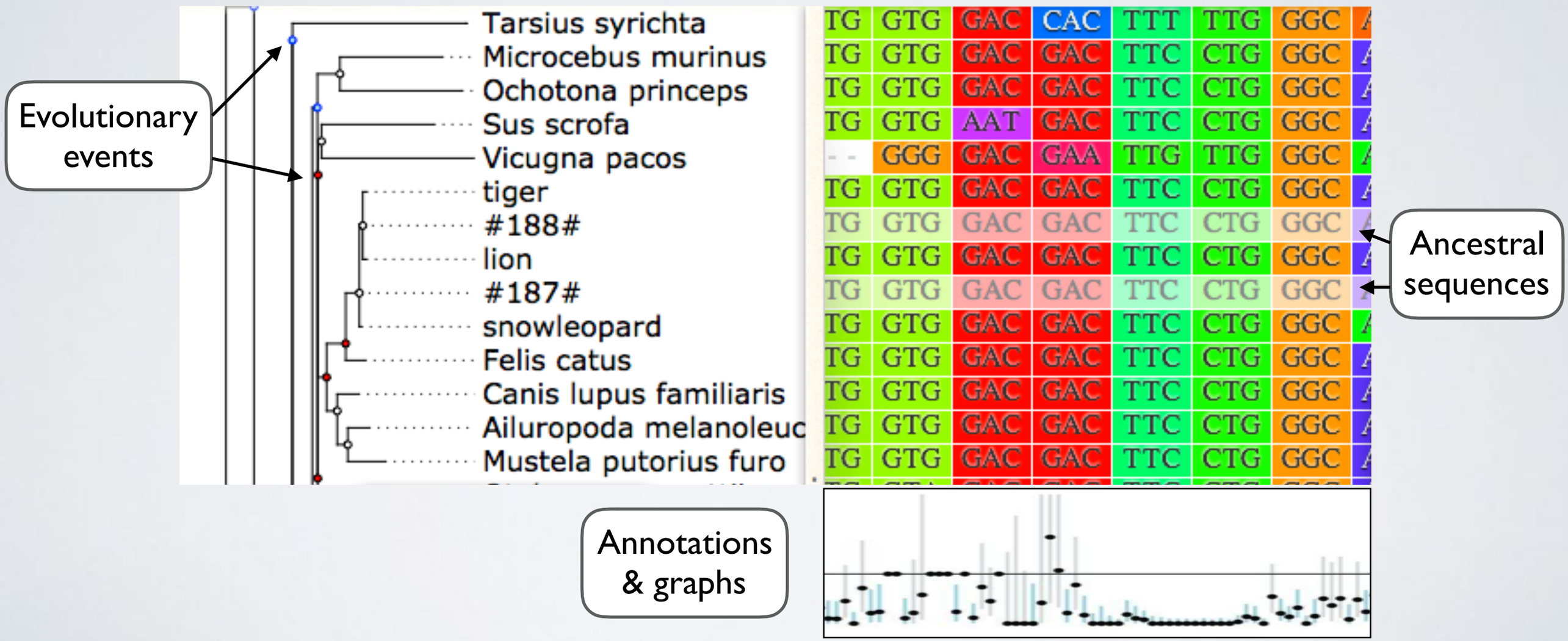
Dataset library

Tiger

Name: EGLN
Last opened
Analysis ID:

Name: EGLN
Last opened
Analysis ID:

# Tree + sequence alignment



# DATA PROVENANCE

Wasabi

wasabiapp.org:8000/PuNpqd

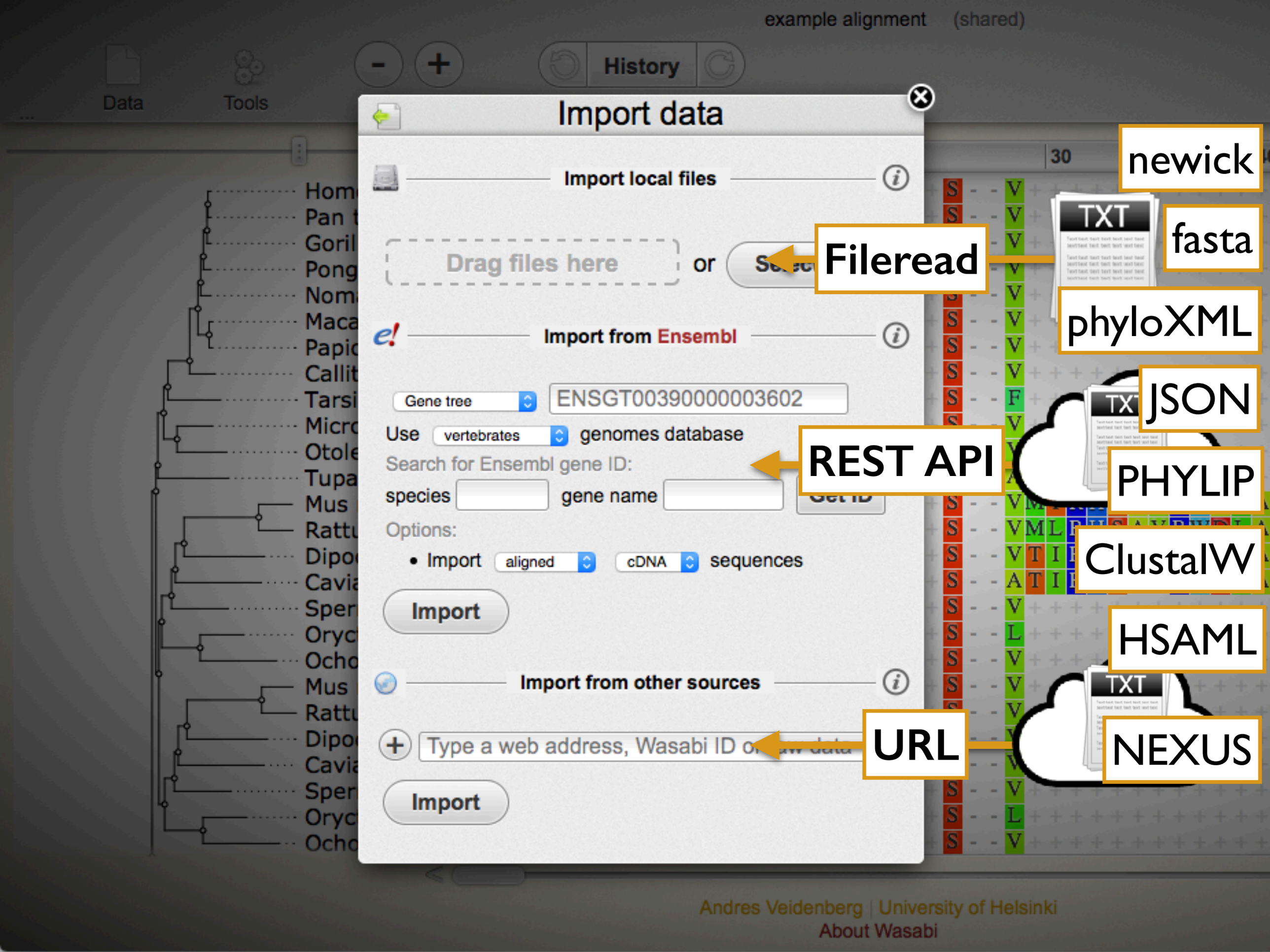
example alignment (shared)

History

Actions history

20 30 40 50

Tarsius sy
Microcebu
Otolemur
Tupaia be
Mus musc
Rattus no
Dipodomy
Cavia por
Spermoph
Oryctolag
Ochotona
Mus musc
Rattus no
Dipodomy
Cavia por
Spermoph
Oryctolag
Ochotona
Homo sap
Pan troglo
Gorilla go
Pongo abe


example alignment (shared)
Data
Tools
History
Import data
Import local files
Drag files here
or
Fileread
Import from Ensembl
Gene tree
ENSGT00390000003602
Use vertebrates genomes database
Search for Ensembl gene ID:
REST API
species
gene name
Get ID
Options:
Import aligned cDNA sequences
Import
Import from other sources
Type a web address, Wasabi ID or raw data
URL
Import
newick
fasta
phyloXML
JSON
PHYLIP
ClustalW
HSAML
NEXUS
TXT

EGLN1 genetree (end result: protein)

Data | Tools | Zoom | History | Actions history

240 250 260 270

Xenopus t
Latimeria
Loxodonta
Procavia c
Sus scrofa
Bos tauru
Ovis aries
Tursiops t
Equus cab
Canis lupu
Ailuropod
Mustela p
Felis catu
Myotis luc
Pteropus
Ictidomys
Mus musc
Rattus no
Cavia por
Oryctolag
Ochotona
Otolemur
Tarsius sy
Callithrix
Macaca m
Papio anu

EGLN1 genetree (end result: protein) (shared)

Data Tools Zoom History Actions history

240 250 260 270

Xenopus t
Latimeria
Loxodonta
Procavia c
Sus scrofa
Bos tauru
Ovis aries
Tursiops t
Equus cab
Canis lupu
Ailuropod
Mustela p
Carnivora
Click or drag
Felis catus
Myotis luc
Pteropus
Ictidomys
Mus musc
Rattus no
Cavia por
Oryctolag
Ochotona
Otolemur
Tarsius sy
Callithrix
Macaca m
Papio anu

EGLN1 genetree (end result: protein) (unsaved)

Data | Tools | Zoom | Actions history: Remove | Notifications: Update alignment

240 250 260 270

Xenopus t
Latimeria
Loxodonta
Procavia c
Sus scrofa
Bos tauru
Ovis aries
Tursiops t
Equus cab
Myotis luc
Pteropus
Ictidomys
Mus musc
Rattus no
Cavia por
Oryctolag
Ochotona
Otolemur
Tarsius sy
Callithrix
Macaca m
Papio anu
Chloroceb
Nomascus
Gorilla go
Pan troglo

EGLN1 genetree (end result: protein)

Data | Tools | Zoom | History | Actions history

240 250 260 270

Xenopus t
Latimeria
Loxodonta
Procavia c
Sus scrofa
Bos tauru
Ovis aries
Tursiops t
Equus cab
Canis lupu
Ailuropod
Mustela p
Felis catus
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Ictidomys
Mus musc
Rattus no
Cavia por
Oryctolag
Ochotona
Otolemur
Tarsius sy
Callithrix
Macaca m
Papio anu

EGLN1 genetree (end result: DNA)

Data | Tools | Zoom | History | Actions history

# Library of analyses

Wasal > Tiger

Sort: Created

Name: Wasabi use cases
Created: 07.08.15 at 12:09
Collection ID: ▶usecases
Open

Name: Tiger genome
Created: 23.06.15 at 15:03
Collection ID: ▶tiger
Open

Name: EGLN1 genetree (end result: protei
Created: 15.06.15 at 11:48
Analysis ID: ▶TOuT5T
Open

Name: EGLN1 genetree (end result: DNA
Created: 08.07.15 at 14:32
Analysis ID: ▶38VMbS
Imported

280

Callithrix
Otolemur
Tupaia be
Oryctolag
Ochotona
Cavia por
Ictidomys
Rattus no

Gaps collapsed; codons

Data | Tools | Zoom | History | Actions history

Library of analyses

EGLN > PAGA > Tree p > Reloc

Sort: Created

Name: Wasabi use cases
Created: 07.08.15 at 12:09
Collection ID: ▶usecases
Imported

Name: Tiger genome
Created: 23.06.15 at 15:03
Collection ID: ▶tiger
Open

Name: EGLN1 genetree (end result: DNA)
Created: 08.07.15 at 14:32
Analysis ID: ▶38VMbS
Open

Name: PAGAN placement of big cats
Created: 08.07.15 at 15:53
Analysis ID: ▶oTtVtl
Open

Name: Tree pruning
Created: 08.07.15 at 16:10
Analysis ID: ▶u6MkXH
Open

Name: Relocated subtree of the big cats
Created: 14.08.15 at 17:55
Analysis ID: ▶NRWwhe
Open

Name: Gaps collapsed; codons
Created: 17.08.15 at 11:38
Analysis ID: ▶Xbfz7l
Restore

Gaps collapsed; codons

Data | Tools | Zoom | History | Actions history

Library of analyses

EGLN > PAGA > Tree p > Reloc

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Name: Wasabi use cases
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Analysis ID: ▶NRWwhe
Open

Name: Gaps collapsed; codons
Created: 17.08.15 at 11:38
Analysis ID: ▶Xbfz7l
Restore

Shared data from Wasabi — Inbox

**wasabiwebapp@gmail.com** Inbox - helsinki eile 23:53

Shared data from Wasabi

To: Andres Veidenberg

---

To view the dataset that was shared with you, go to http://wasabiapp.org:8000?id=tiger

---

Wasabi is a web application for phylogenetic sequence analysis.
You can learn more about Wasabi from http://wasabiapp.org

This message was sent to the e-mail address registered in Wasabi app.

You can edit your Wasabi account at http://wasabiapp.org:8000/G0CEXI

# PUBLISHING

# Wasabi: An Integrated Platform for Evolutionary Sequence Analysis and Data Visualization

Andres Veidenberg,[1] Alan Medlar,[1] and Ari Löytynoja*,[1]
[1]Institute of Biotechnology, University of Helsinki, Helsinki, Finland
***Corresponding author:** E-mail: ari.loytynoja@helsinki.fi.
**Associate editor**: Naoki Takebayashi

## Abstract

**Wasabi is an open source, web-based environment for evolutionary sequence analysis. Wasabi visualizes sequence data together with a phylogenetic tree within a modern, user-friendly interface: The interface hides extraneous options, supports context sensitive menus, drag-and-drop editing, and displays additional information, such as ancestral sequences, associated with specific tree nodes. The Wasabi environment supports reproducibility by automatically storing intermediate analysis steps and includes built-in functions to share data between users and publish analysis results. For computational analysis Wasabi supports PRANK and PAGAN for phylogeny-aware alignment and alignment extension, Along with drag-and-drop import of local files, Wasabi can access remote es and EPO alignments directly from Ensembl. To demonstrate a gs from recent comparative genomics studies, including a ly: These case studies can be browsed within Wasabi at web browser and does not require any installation. One s licensed under the AGPLv3.**

**ical workflow using Wasabi, w**
**reanalysis of the *EGLN1* gene from th**
**http://wasabiapp.org:8000?id=usecases.**
**can start using it at http://wasabiapp.**

**e research, data visualization.**

**ds: evolutionary sequ**

## Introduction

In evolutionary sequence analysis, phylogenetic trees and sequence alignments are intrinsically linked: Sequence alignments define character homologies upon which phylogenetic inference is based and trees are integral in correcting for hierarchical dependencies among sequence data. In multiple sequence alignment, this connection was noticed early (Sankoff 1975) and was central in the first progressive alignment algorithm (Hogeweg and Hesper 1984). Although popular alignment programs use a tree to guide the alignment procedure, they consider the tree a nuisance parameter. The

Wasabi is inspired by our earlier tool, webPRANK (Löytynoja and Goldman 2010), a web interface to the PRANK alignment program. webPRANK was limited to the analysis of only small data sets and to a single analysis method. Wasabi, however, was developed using modern web technologies to scale to much larger data sets, while maintaining responsiveness. Wasabi additionally contains features for integrating heterogeneous data sets, file management and an intuitive, modern web interface (see fig. 1 for overview) for navigating and selecting appropriate analysis options. Additionally, due to the increasing complexity of

wasabiapp.org

Gaps collapsed; codons (shared)

Data Tools Zoom History Actions history

Mus musculus
Tarsius syrichta
Microcebus mur
Ochotona prince
Sus scrofa
Vicugna pacos
tiger
lion
snowleopard
Felis catus
Canis lupus fam
Ailuropoda mela
Mustela putoriu
Otolemur garne
Chlorocebus sab
Papio anubis
Macaca mulatta
Gorilla gorilla go
Pan troglodytes
Homo sapiens
Pongo abelii
Nomascus leuco
Erinaceus europ
Bos taurus
Ovis aries

30 40

## Library of analyses

EGLN > PAGA > Tree p > Reloc

Sort: Created

Name: Tiger genome
Created: 23.06.15 at 15:03
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Analysis ID: ▶NRWwhe
Open

Name: Gaps collapsed; codons
Created: 17.08.15 at 11:38
Analysis ID: ▶Xbfz7I
Restore

About Wasabi

Journal | Communications

JOURNAL COMMUNICATIONS | ARTICLE OPEN

# Hypoxia-related genes are soft targets in adaptation to new environments

**John Doe[1] and Mary Major[2]**

[1]University of Cambridge, Harvard, USA; [2]Trinity College, London, UK

*Journal Communications* **1**, Article number: 1234 | doi:01.1001/jcomms1234

Received 02 December 2015 | Accepted 13 May 2016 | Published 02 June 2016



## Abstract

Lorem ipsum dolor sit amet, consectetur adipiscing elit. Aliquam pellentesque venenatis consectetur. Donec pharetra blandit dignissim. Phasellus felis augue, blandit id egestas quis, iaculis in erat. Morbi tristique ornare tellus, et sodales dolor semper in. Praesent iaculis, odio id sagittis luctus, ante erat pharetra lacus, eget accumsan ligula libero quis est. Duis varius eros in nulla rhoncus, at cursus dui porta. Suspendisse mauris lorem, dapibus id rhoncus et, molestie vel lacus. Sed et elit eget enim bibendum tempus id sit amet arcu. Sed a ultricies nisl. Integer ipsum massa, commodo vitae placerat sit amet, varius consequat ipsum. Suspendisse non mauris a sem placerat vulputate at in lorem. Donec purus

Aliquam sit amet lacus aliquam, pharetra lorem at, finibus lectus. Sed in ipsum ac mi auctor volutpat. Nunc consequat tellus et metus vulputate, quis feugiat dui molestie. Nam molestie nisl sem. Nam scelerisque odio vel justo egestas maximus. Donec dolor libero, efficitur in semper sed, malesuada nec quam. Phasellus viverra leo eu nunc convallis laoreet. Aliquam finibus orci quis augue suscipit, ac laoreet neque mattis. Cum sociis natoque penatibus et magnis dis parturient montes, nascetur ridiculus mus. Quisque et varius lectus, in tempus arcu. Ut sollicitudin, libero a facilisis rutrum, metus nulla ultricies risus, lacinia convallis ipsum risus at nisl. Fusce elementum varius risus, vitae imperdiet turpis lacinia ut.

**Figure 1: Reanalysis of EGLN1 genetree in Wasabi.**


Cho et al. (2013; see original study) detected a snow leopard-specific mutation in EGLN1 that is likely to be associated with adaptation to high altitude. We replicated the analysis with Wasabi and saw that the suggested position is not perfectly conserved across species and an identical Met39>Lys39 substitution has happened in alpaca, another species living in high altitudes. Browse the dataset in Wasabi pop-up.

Cras tincidunt dignissim sem a elementum. Sed at hendrerit est. Vivamus mattis tincidunt erat, a blandit justo. Nulla facilisi. Ut sem nisl, ultrices vestibulum aliquet ac, bibendum nec elit. Etiam iaculis, turpis at gravida gravida, neque enim pretium mi, et dictum libero purus nec ante. Nullam sagittis velit sit amet tellus gravida, vel facilisis dolor euismod. Sed tristique pharetra lobortis. Phasellus interdum scelerisque quam volutpat pharetra.

In hendrerit nisi ipsum, nec iaculis dolor bibendum ac. Integer eget nibh vel massa tristique interdum id quis magna.

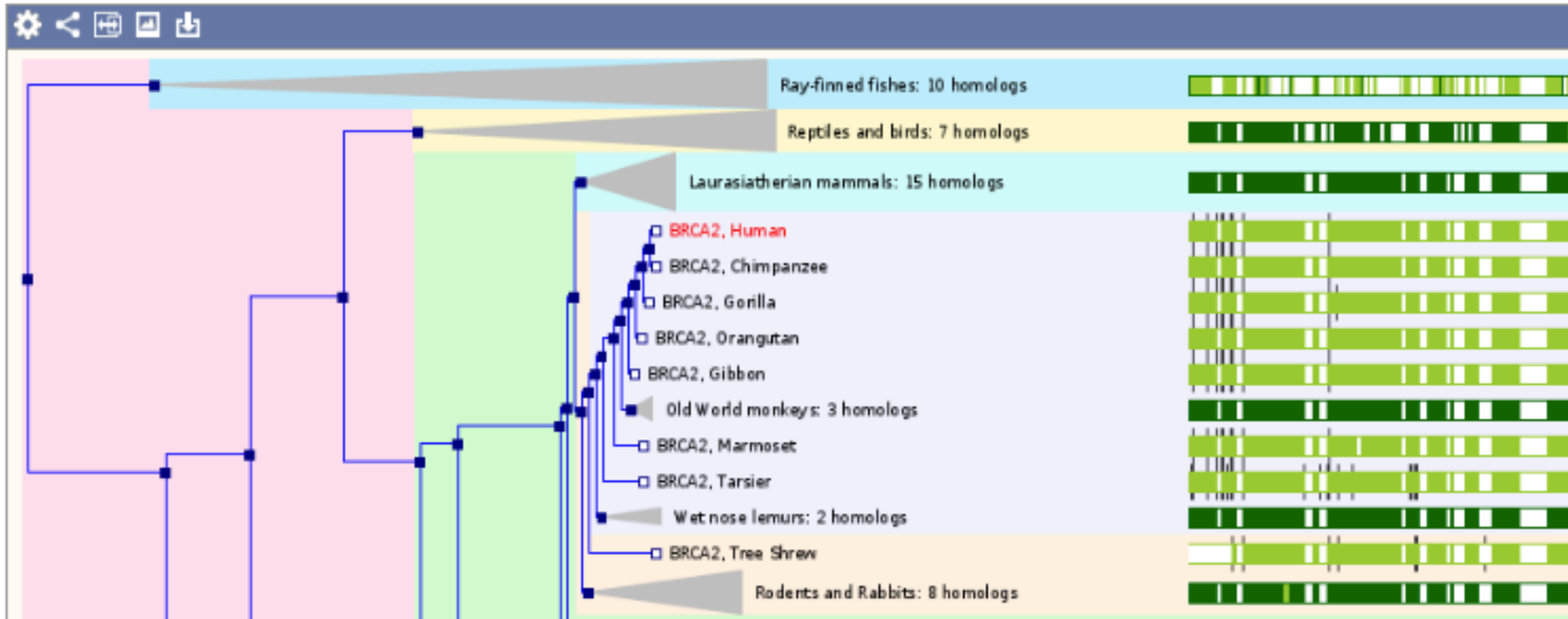
# Gene: BRCA2 ENSG00000139618

| | |
|---|---|
| **Description** | BRCA2, DNA repair associated [Source:HGNC Symbol;Acc:HGNC:1101] |
| **Synonyms** | XRCC11, FACD, FAD1, PNCA2, FAD, BRCC2, FANCD1, GLM3, BROVCA2, FANCD |
| **Location** | Chromosome 13: 32,315,474-32,400,266 forward strand.<br>GRCh38:CM000675.2 |
| **About this gene** | This gene has 7 transcripts (splice variants), 64 orthologues, is a member of 1 Ensembl protein family and is as |
| **Transcripts** | Show transcript table |

## Gene tree

### GeneTree ENSGT00390000003602

| | |
|---|---|
| **Number of genes** | 65 |
| **Number of speciation nodes** | 62 |
| **Number of duplication** | 2 |
| **Number of ambiguous** | 0 |
| **Number of gene split events** | 0 |



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|---|---|
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| **Synonyms** | XRCC11, FACD, FAD1, PNCA2, FAD, BRCC2, FANCD1, GLM3, BROVCA2, FANCD |
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| **Transcripts** | Show transcript table |

## Gene tree

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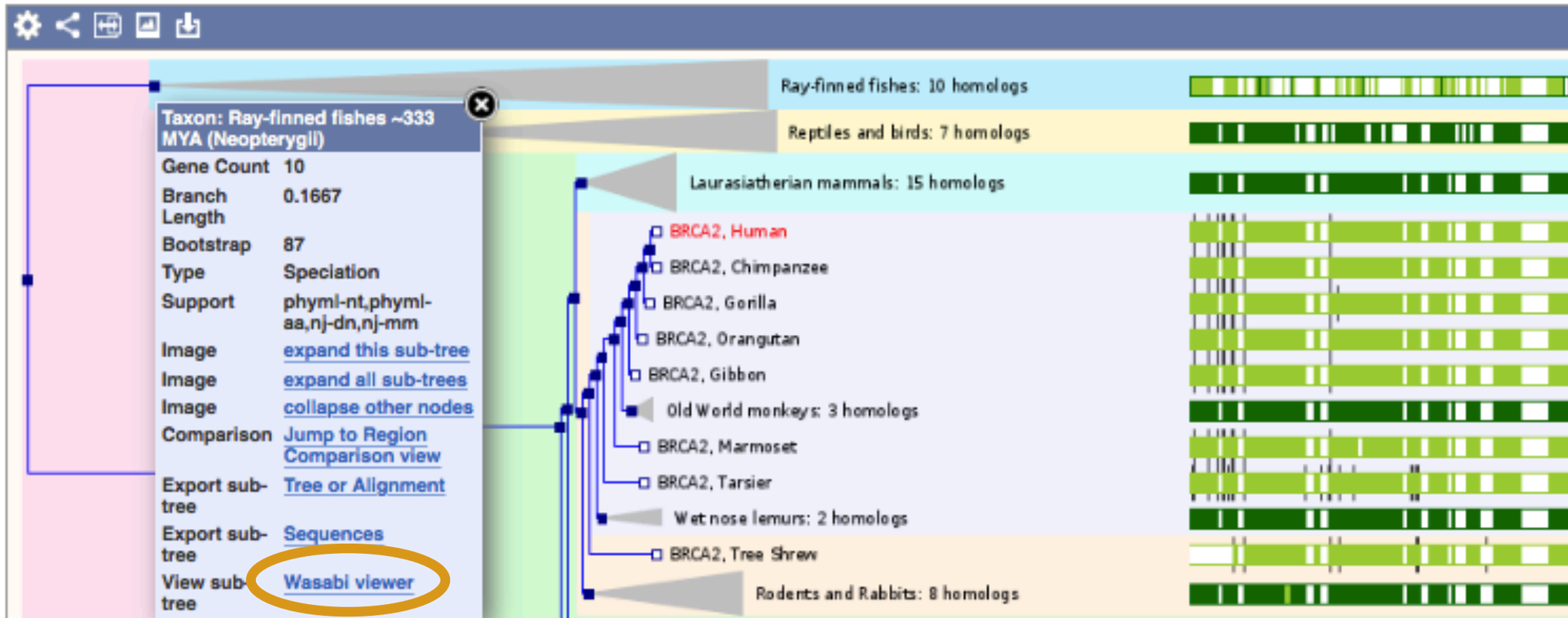

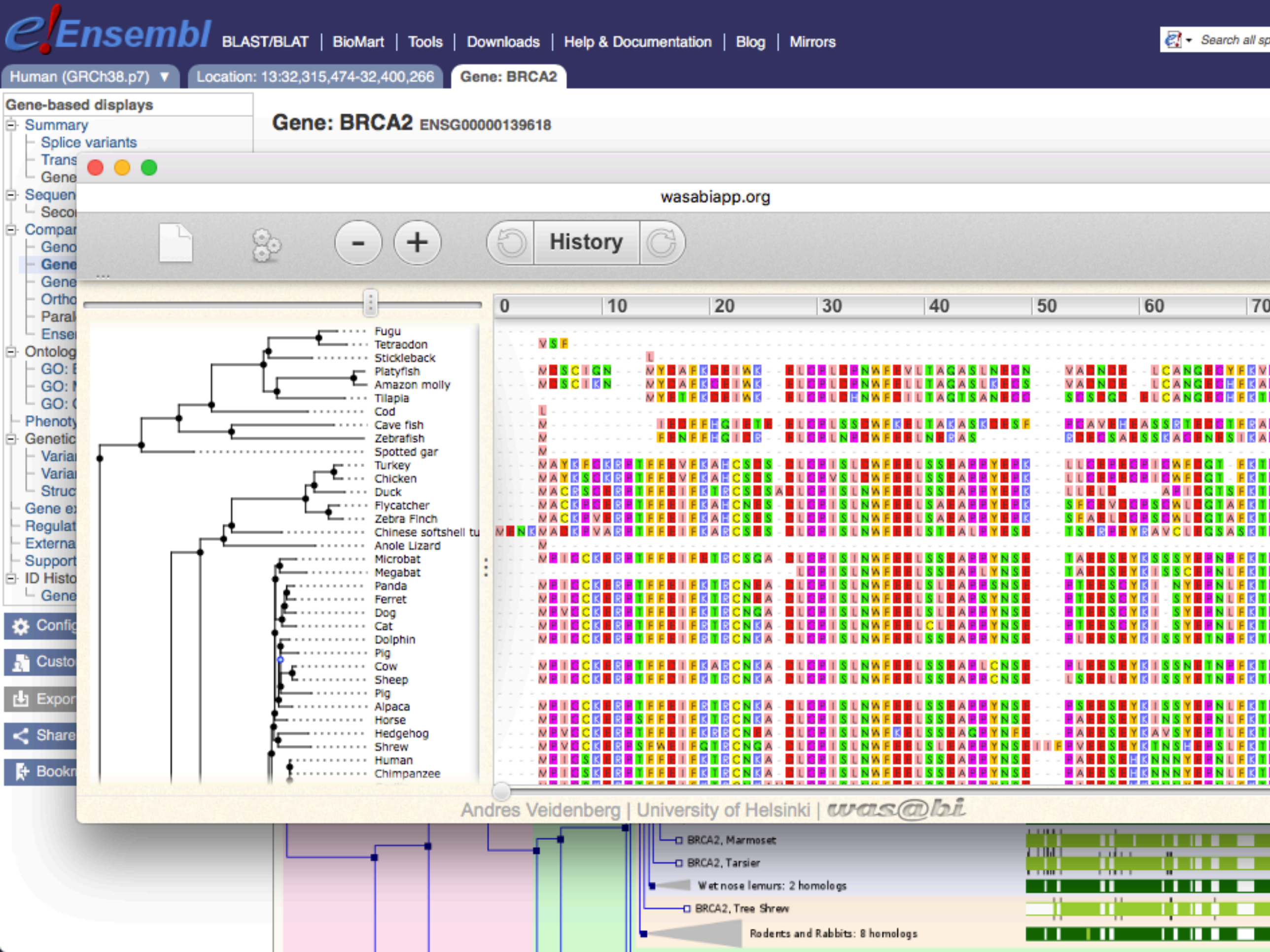
Ensembl
BLAST/BLAT | BioMart | Tools | Downloads | Help & Documentation | Blog | Mirrors
Human (GRCh38.p7)
Location: 13:32,315,474-32,400,266
Gene: BRCA2
Gene-based displays
Summary
Splice variants
Gene: BRCA2 ENSG00000139618
wasabiapp.org
History
Fugu
Tetraodon
Stickleback
Platyfish
Amazon molly
Tilapia
Cod
Cave fish
Zebrafish
Spotted gar
Turkey
Chicken
Duck
Flycatcher
Zebra Finch
Chinese softshell tu
Anole Lizard
Microbat
Megabat
Panda
Ferret
Dog
Cat
Dolphin
Pig
Cow
Sheep
Pig
Alpaca
Horse
Hedgehog
Shrew
Human
Chimpanzee
Andres Veidenberg | University of Helsinki | was@bi
BRCA2, Marmoset
BRCA2, Tarsier
Wet nose lemurs: 2 homologs
BRCA2, Tree Shrew
Rodents and Rabbits: 8 homologs

# PLUGINS

```
biotek1018:~ veidenbe$ /Users/veidenbe/Desktop/wasabi/Wasabi/binaries/pagan/pagan --help

PAGAN v.0.54 (5 February, 2014). (C) 2010-2014 by Ari Löytynoja <ari.loytynoja@gmail.com>.
 This program is provided "as-is", with NO WARRANTY whatsoever; this is a development version
 and may contain bugs.

Minimal progressive alignment options:
  --seqfile arg          sequence infile (FASTA)
  --treefile arg         tree file

Generic options:
  --outfile arg
  --outformat arg
  --raxml-tree
  --translate
  --mt-translate
  --output-ancestors
  --config-file arg
  --config-log-file a
  --no-terminal-edges
  --silent
  --noise arg
  --log-output-file a
```

Executable

```
{"title": "Alignment modes", "name": "mode", "type": "select", "extendable": "configuratio
  {"title": "alignment", "desc": "Make a phylogenetic alignment"},
  {"title": "extension", "desc": "Extend current alignment with data from query file"},
  {"title": "pileup", "desc": "Compile a a pileup of sequence reads in query file"},
  {"title": "ancestors", "desc": "Infer ancestral sequences for current alignment"}
]},
{"group": "Alignment options", "options": [
  {"enable": {"mode": "alignment"}, "options": [
    {"type": "file", "source": "imported sequence", "format": "fasta", "option": "seqfile"
    {"title": "Compute guidetree", "type": "bool", "name": "compute tree", "default": {"tr
    {"enable": "tree", "type": "file", "source": "imported tree", "format": "extended newi
    {"enable": "compute tree", "type": "file", "source": "filedrop", "format": "extended n
    {"enable": {"datatype": "dna"}, "type": "select", "title": "Translate", "desc": "Trans
      {"title": "no translation"},
      {"title": "to codons", "option": "codons"},
      {"title": "to protein", "option": "translate"}
    ]}
  ]},
  {"section": "Alignment extension", "enable": {"mode": "extension"}, "desc": "Extend curr
    {"type": "file", "source": "imported_sequence", "format": "fasta", "option": "ref-seqf
    {"type": "file", "source": "imported_tree", "format": "newick_extended", "option": "re
    {"type": "file", "source": "filedrop", "option": "queryfile", "required": "Drop a sequ
    {"select": "Placement targets", "options": [
      {"title": "terminal nodes", "option": "terminal-nodes", "default": true},
      {"title": "internal nodes", "option": "internal-nodes"},
      {"title": "all nodes", "option": "all-nodes"}
```

JSON

# Wasabi plugin description

# Common Workflow Language

```
"program": "pagan",
"name": "PAGAN aligner",
"outfile": "out.xml",
"prefix": "--",
"options": [
  {
   "output": "out",
   "option": "outfile"
  },
  {
   "group": "Edit options", "options": [
    {
     "file": "filedrop fileselect",
     "option": "queryfile",
     "desc": "Extend alignment with query sequer
    },
    {
     "enable": "queryfile == DNA",
     "bool": "Translate to protein",
     "desc": "Translate reference sequence
     "option": "translate"
    },
    {
     "float": "gaps",
     "option": "gap-extension",
     "desc": "gap extension probability",
     "default": 0.5
    },
    {
     "select": "Align as",
     "enable": "sequence == DNA",
```

```
cwlVersion: v1.0
class: CommandLineTool
baseCommand: pagan
requirements:
  - class: InlineJavascriptRequirement

inputs:
  query_file:
    type: File
    inputBinding:
      prefix: --queryfile
      label: "Extend alignment with query sequences
  translate_seq:
    type: boolean
    default: true
    inputBinding:
      prefix: --translate
      label: "Translate reference sequence to prote
  gaps:
    type: float
    inputBinding:
      prefix: --gap-extension
      default: 0.5

outputs:
  outfile:
    type: File

arguments:
  - prefix: --codons
    valueFrom: $(inputs.queryfile.format=="DNA")
```

executable

parameters:

type

prefix

label

defaults

references

expressions

dependent/exclusive

```
biotek1018:~ veidenbe$ /Users/veidenbe/Desktop/wasabi/Wasabi/binaries/pagan/pagan --help

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  --noise arg
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Executable

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  {"title": "ancestors", "desc": "Infer ancestral sequences for current alignment"}
]},
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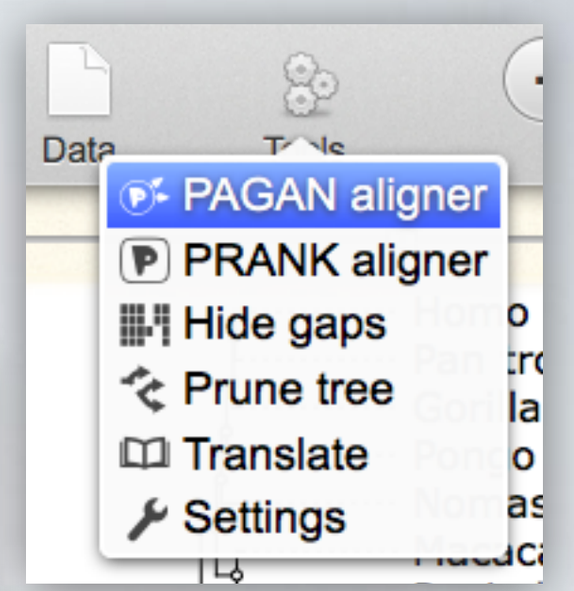
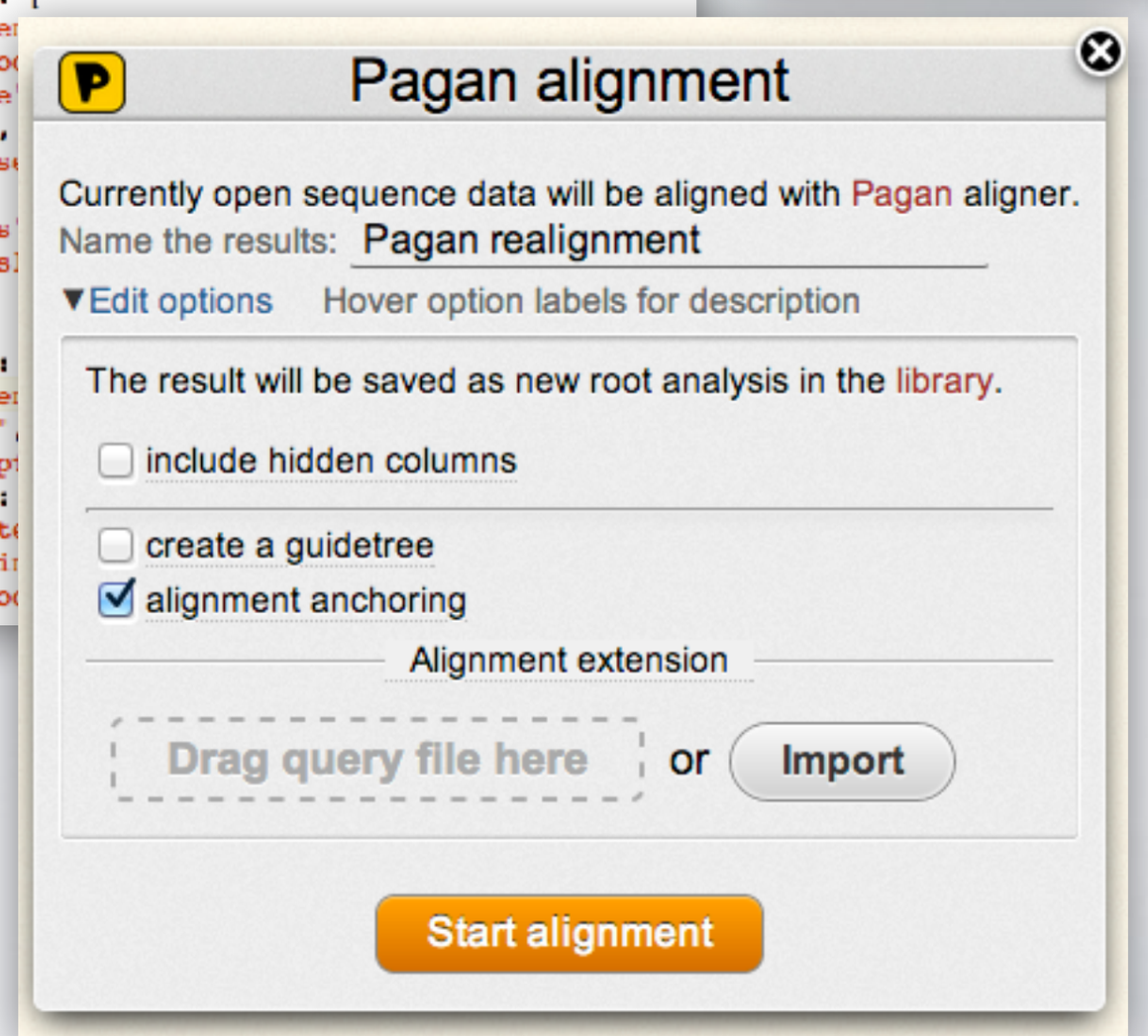
JSON




Wasabi interface

Wasabi

wasabiapp.org:3000/?id=tiger

Gaps collapsed; codons (shared)

Data | Tools | Zoom | History | Actions history | Jobs running 1 | Notifications

was@bi

## Status overview

**Status of background tasks**

Name: realignment
Status: Running
Job type: Realignment
Created: 26.10.16 at 11:20
Job ID: eEWTrR
Feedback: Aligning:

Kill

## Library of analyses

Wasal > Tiger > EGLN

Sort: Created

Name: Wasabi use cases
Created: 07.08.15 at 11:09
Collection ID: ▶usecases
Imported

Name: Tiger genome
Created: 23.06.15 at 14:03
Collection ID: ▶tiger
Open

Name: EGLN1 genetree (end result: DNA)
Created: 08.07.15 at 13:32
Analysis ID: ▶38VMbS
Open

Name: PAGAN placement of big cats
Created: 08.07.15 at 14:53
Analysis ID: ▶cTtVtl
Open

Mus musc
Tarsius sy
Chloroceb
Papio anu
Macaca m
Gorilla go
Pan troglo
Homo sap
Pongo abe
Nomascus
Erinaceus
Bos tauru
Ovis aries
Tursiops t

Andres Veidenberg | University of Helsinki
About Wasabi

Ari

# THANKS!

Alan

## http://wasabiapp.org

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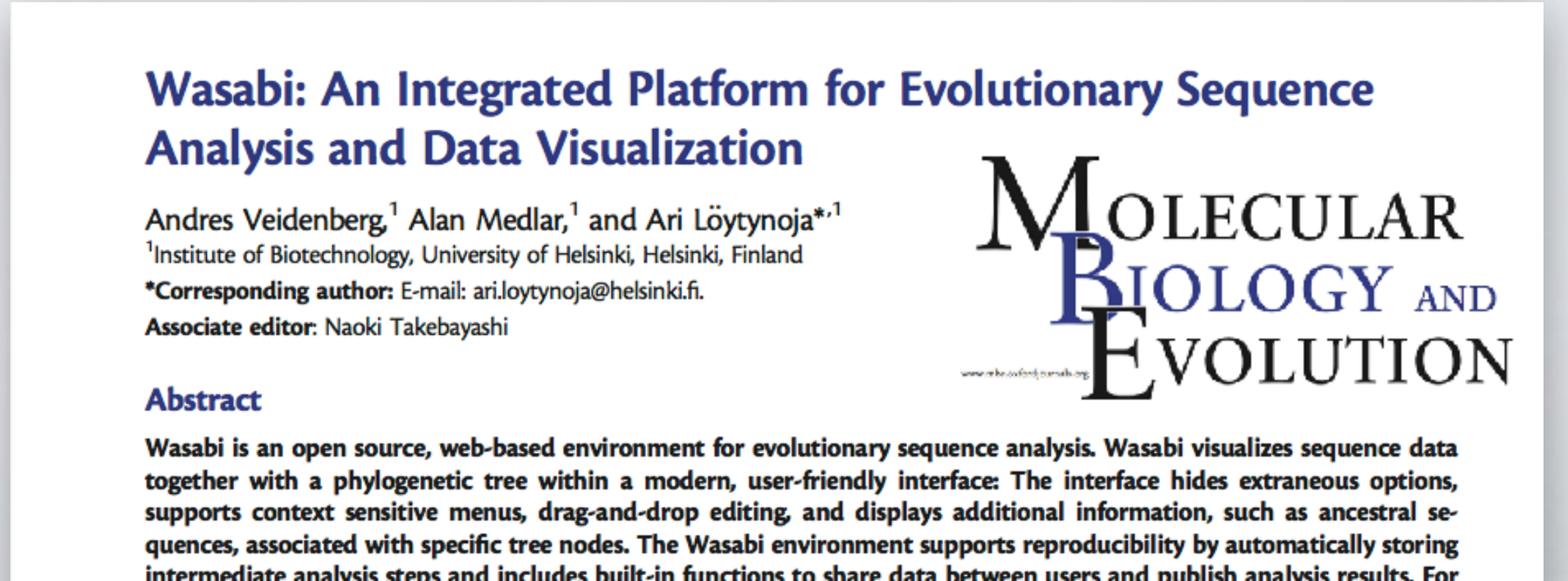
MARIE CURIE ACTIONS

UNIVERSITY OF HELSINKI



Wasabi: An Integrated Platform for Evolutionary Sequence Analysis and Data Visualization

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Associate editor: Naoki Takebayashi

MOLECULAR BIOLOGY AND EVOLUTION

Abstract

Wasabi is an open source, web-based environment for evolutionary sequence analysis. Wasabi visualizes sequence data together with a phylogenetic tree within a modern, user-friendly interface: The interface hides extraneous options, supports context sensitive menus, drag-and-drop editing, and displays additional information, such as ancestral sequences, associated with specific tree nodes. The Wasabi environment supports reproducibility by automatically storing intermediate analysis steps and includes built-in functions to share data between users and publish analysis results. For