



Entelechon's Bioinformatics Collaboration Software

A photograph of laboratory glassware, including a beaker and a flask, on a metal stand. The background is slightly blurred, showing other lab equipment.

Collaboration is crucial

- More and more distributed projects
- Lab collaboration across countries
- With huge data sets, data sharing becomes a bottleneck



Existing tech doesn't cut it

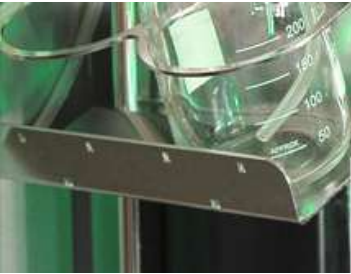
Generic desktop sharing and webcasting solutions don't work for biological data:

- Don't scale well for huge data sets
- Data is „locked in“ on a desktop computer

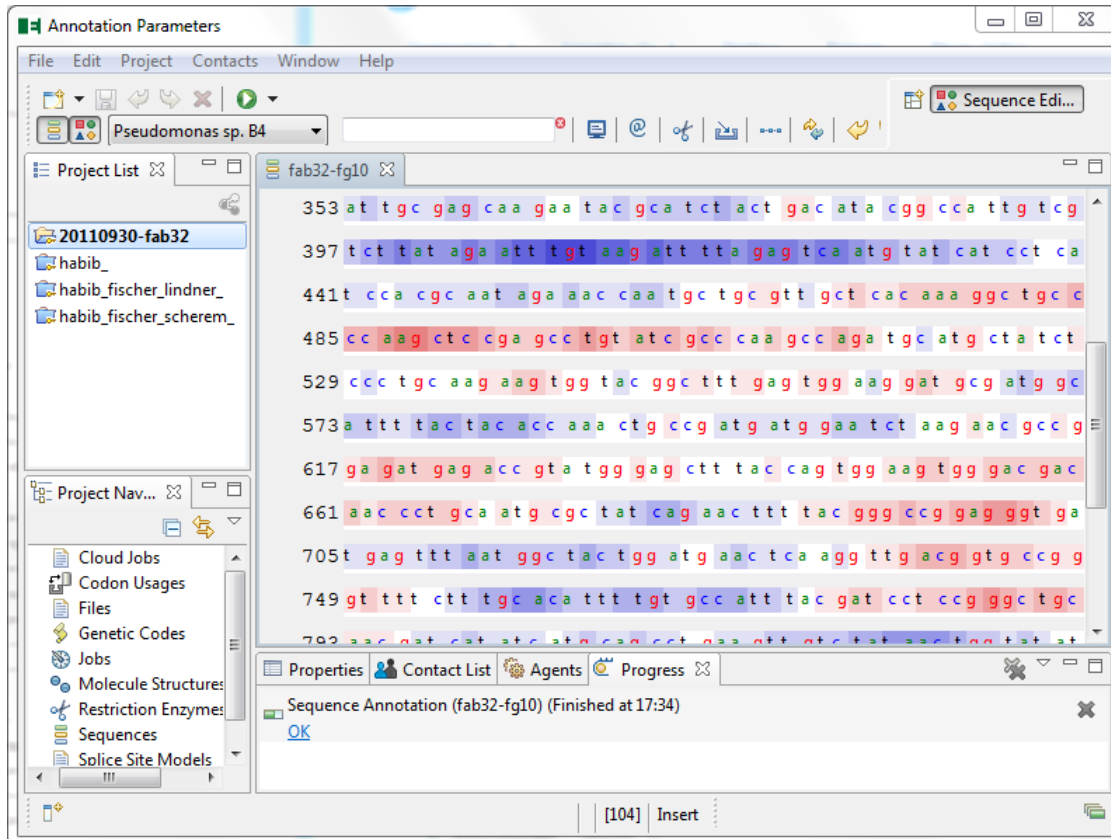
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Entelechon's solution

- Client/Server system
- Specifically for biology
- User interfaces represent biological data
- System „knows“ biology



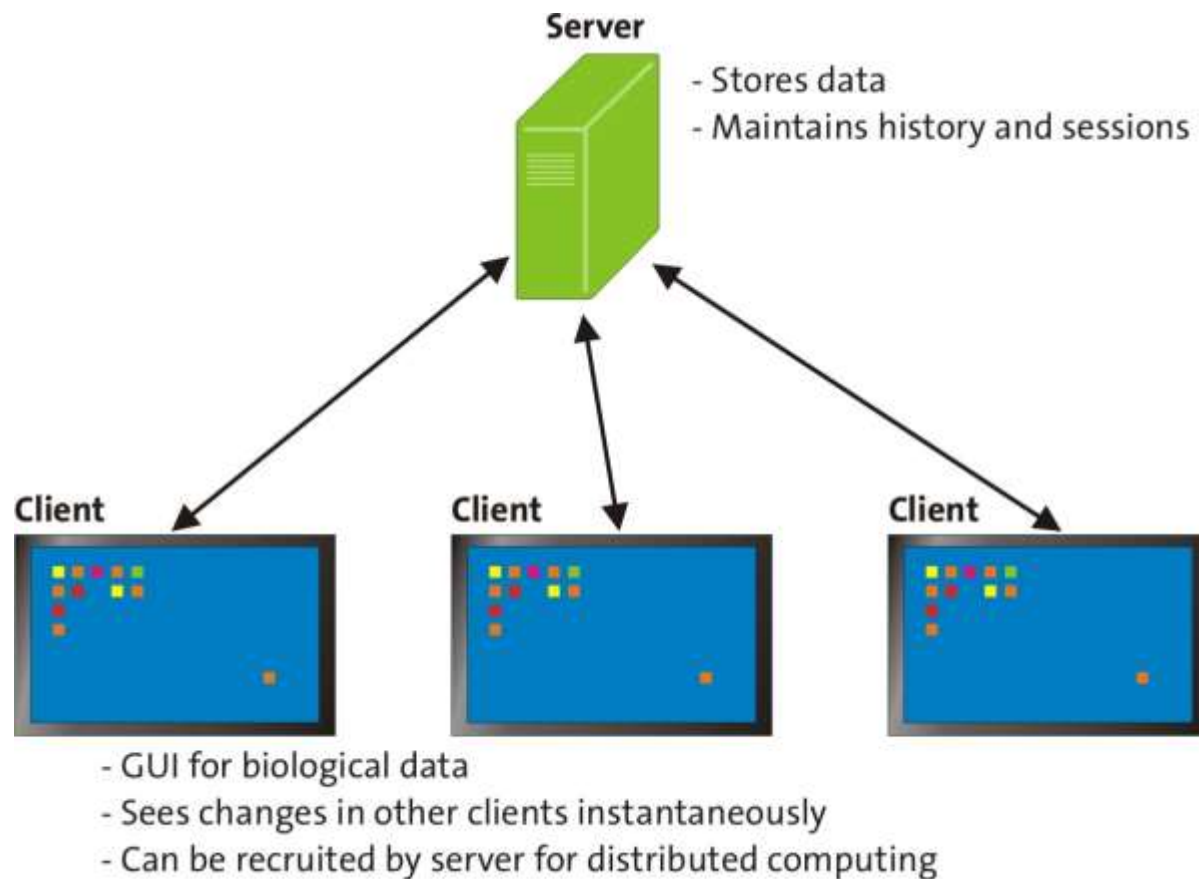
The user interface



The screenshot displays the 'Annotation Parameters' window of the Intelechon software. The main area shows a DNA sequence for 'fab32-fg10' from 'Pseudomonas sp. B4'. The sequence is color-coded by codons and includes line numbers 353, 397, 441, 485, 529, 573, 617, 661, 705, and 749. The interface includes a menu bar (File, Edit, Project, Contacts, Window, Help), a toolbar with icons for file operations and editing, and a 'Project List' on the left showing a tree structure with folders like '20110930-fab32' and sub-items 'habib_', 'habib_fischer_lindner_', and 'habib_fischer_scherem_'. A 'Project Nav...' panel at the bottom left lists various analysis tools such as 'Cloud Jobs', 'Codon Usages', 'Files', 'Genetic Codes', 'Jobs', 'Molecule Structures', 'Restriction Enzymes', 'Sequences', and 'Splice Site Models'. A 'Properties' panel at the bottom right shows 'Sequence Annotation (fab32-fg10) (Finished at 17:34)' with an 'OK' button. The status bar at the bottom indicates '[104] Insert'.



The architecture



A photograph of laboratory glassware, including a beaker and a flask, on a metal stand. The background is slightly blurred, showing more lab equipment.

Interactivity

- Users see each other's actions instantaneously as they type and click
- Data can be edited collaboratively and interactively
- Visual feedback on who did what
- All data manipulations are versioned in a history and can be undone

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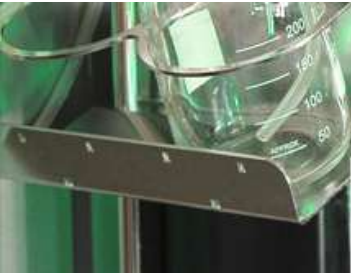
Persistence

- The server session runs continuously
- Connect and disconnect as you need
- See changes since last connection
- No need to „save“ data:
 - Data will be stored on the server continuously
 - Mistakes can be corrected by going back in the history

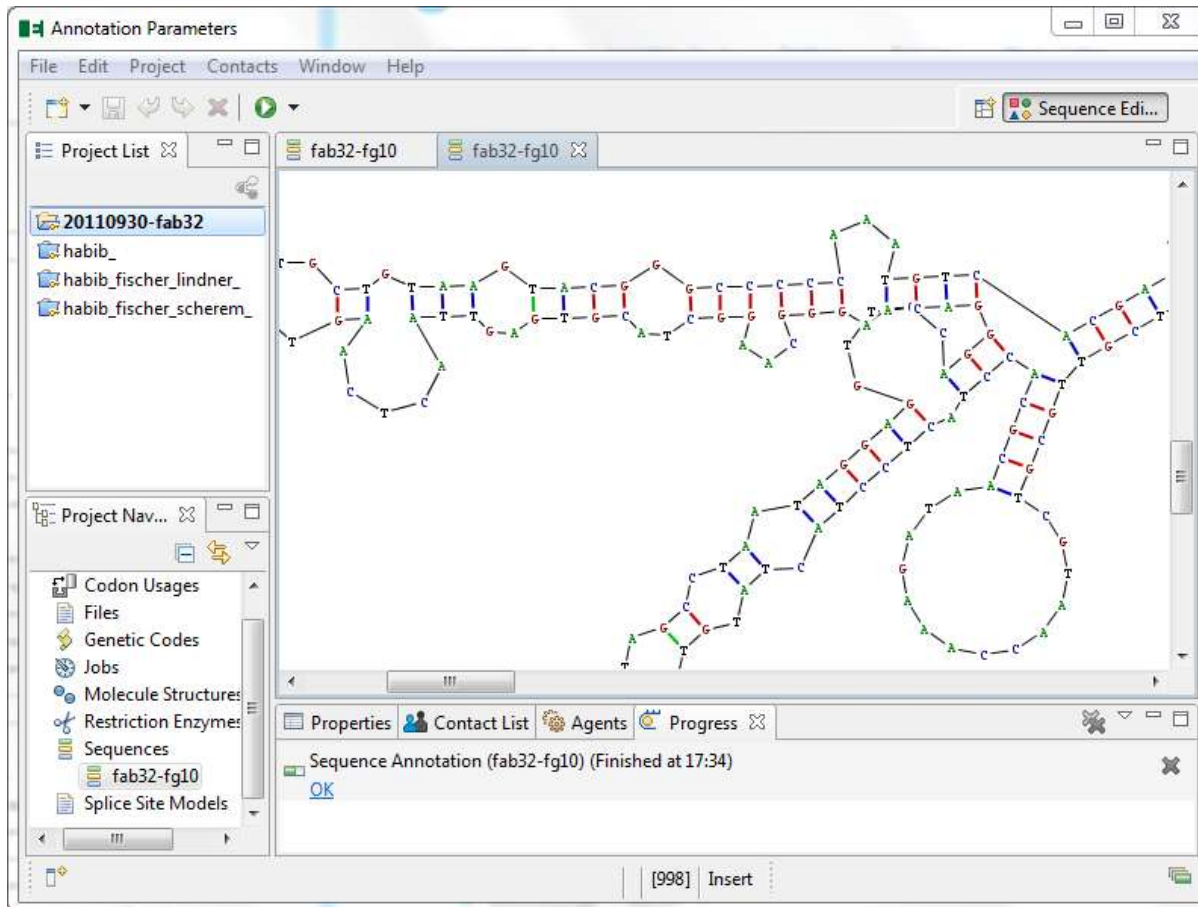
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Secure storage of huge data sets

- Server stores all data
- Small pieces of data are downloaded to clients on demand
- Seamless navigation through large data sets (imaging, chromatography, sequences)



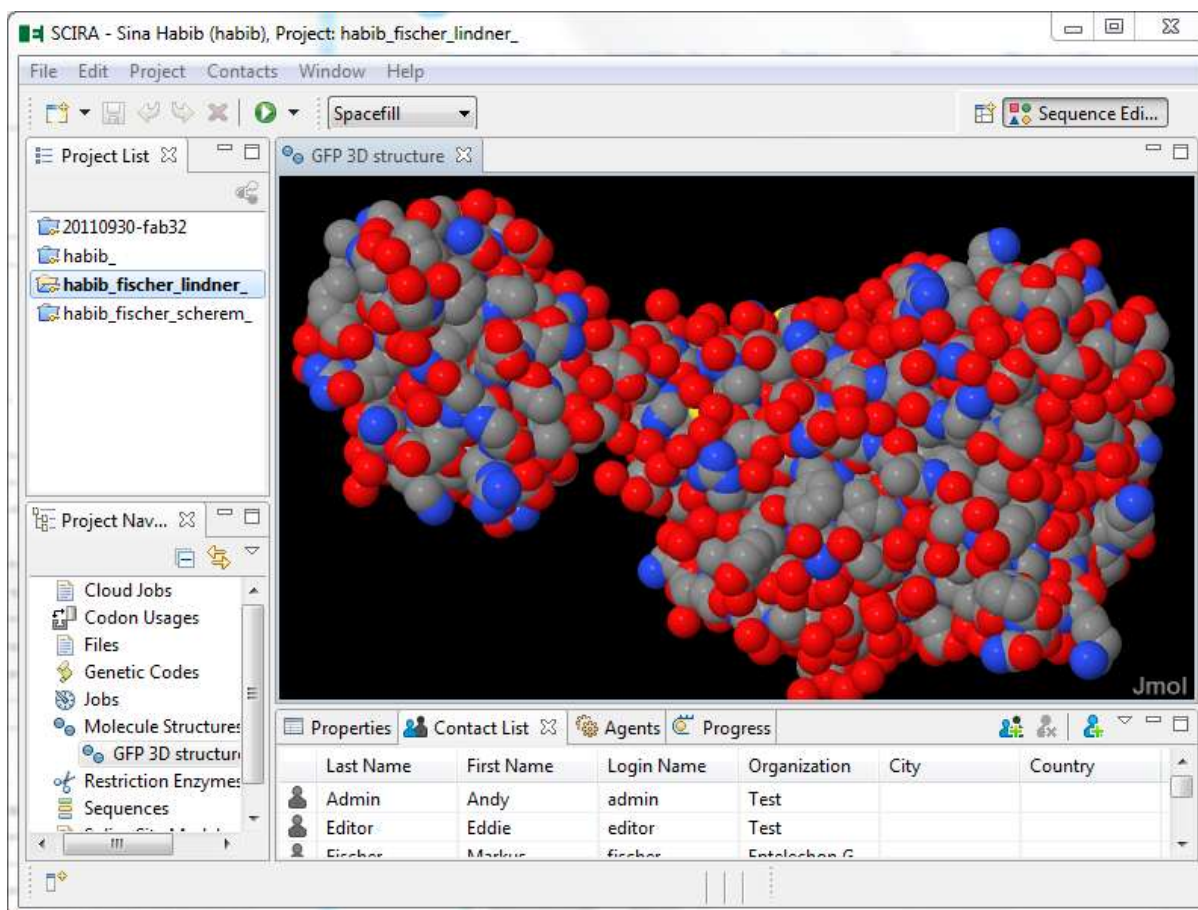
The user interface



The screenshot displays the 'Annotation Parameters' software window. The main area shows a DNA sequence visualization with nucleotides (A, T, C, G) connected by lines, forming a complex structure. The interface includes a menu bar (File, Edit, Project, Contacts, Window, Help), a toolbar, and a 'Project List' on the left. The 'Project List' shows a tree structure with '20110930-fab32' selected, containing sub-items 'habib_', 'habib_fischer_lindner_', and 'habib_fischer_scherem_'. Below the 'Project List' is a 'Project Nav...' panel with a tree view containing 'Codon Usages', 'Files', 'Genetic Codes', 'Jobs', 'Molecule Structures', 'Restriction Enzymes', 'Sequences', and 'Splice Site Models'. The 'Sequences' folder is expanded, showing 'fab32-fg10'. At the bottom, a 'Properties' panel shows 'Sequence Annotation (fab32-fg10) (Finished at 17:34)' with an 'OK' button. The status bar at the very bottom indicates '[998] Insert'.

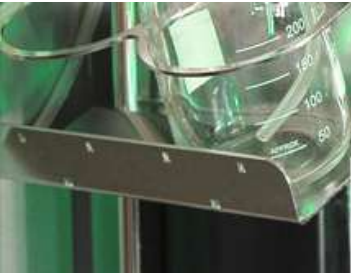


The user interface

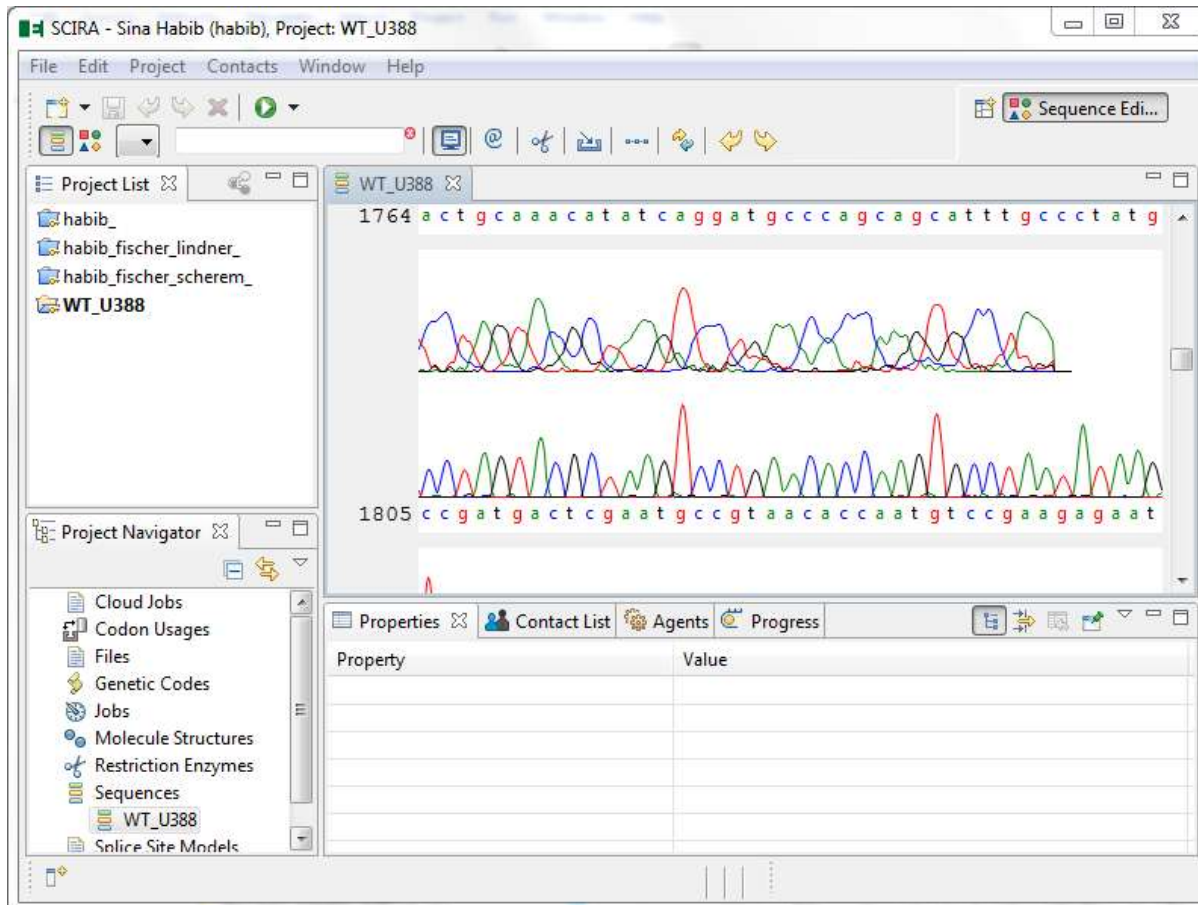


The screenshot displays the SCIRA software interface. The main window shows a 3D ball-and-stick model of a protein structure, labeled 'GFP 3D structure'. The interface includes a menu bar (File, Edit, Project, Contacts, Window, Help), a toolbar with icons for file operations and a 'Spacefill' dropdown, and a 'Project List' sidebar on the left. Below the sidebar is a 'Project Nav...' section with a tree view of project components. At the bottom, there is a 'Contact List' table.

Last Name	First Name	Login Name	Organization	City	Country
Admin	Andy	admin	Test		
Editor	Eddie	editor	Test		
Fischer	Markus	fischer	Intelechon G		



The user interface



SCIRA - Sina Habib (habib), Project: WT_U388

File Edit Project Contacts Window Help

Sequence Edi...

Project List

- habib_
- habib_fischer_lindner_
- habib_fischer_scherem_
- WT_U388

WT_U388

1764 a c t g c a a a c a t a t c a g g a t g c c c a g c a g c a t t t g c c c t a t g

1805 c c g a t g a c t c g a a t g c c g t a a c a c c a a t g t c c g a a g a g a a t

Properties Contact List Agents Progress

Property	Value

Cloud Jobs
Codon Usages
Files
Genetic Codes
Jobs
Molecule Structures
Restriction Enzymes
Sequences
WT_U388
Snlice Site Models

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Distributed computing

- Server can recruit clients for computation tasks
- Automatic load balancing and distribution of a task to multiple clients
- Leverage your LAN for bioinformatics problems

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Security is paramount

- Data between client and server is encrypted
- Fine-grained rights and user management
- Control over
 - data flow
 - data access
 - program execution

How to get it

- Subscribe to the beta test
- Entelechon will offer a subscription model:
 - Hosted service
 - Pay as you use the software
 - Invite other users free of charge
- Licensing for in-house usage available
 - As hosted service or in-house hosting

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Thank you

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