

GENOMEPRO 3.0

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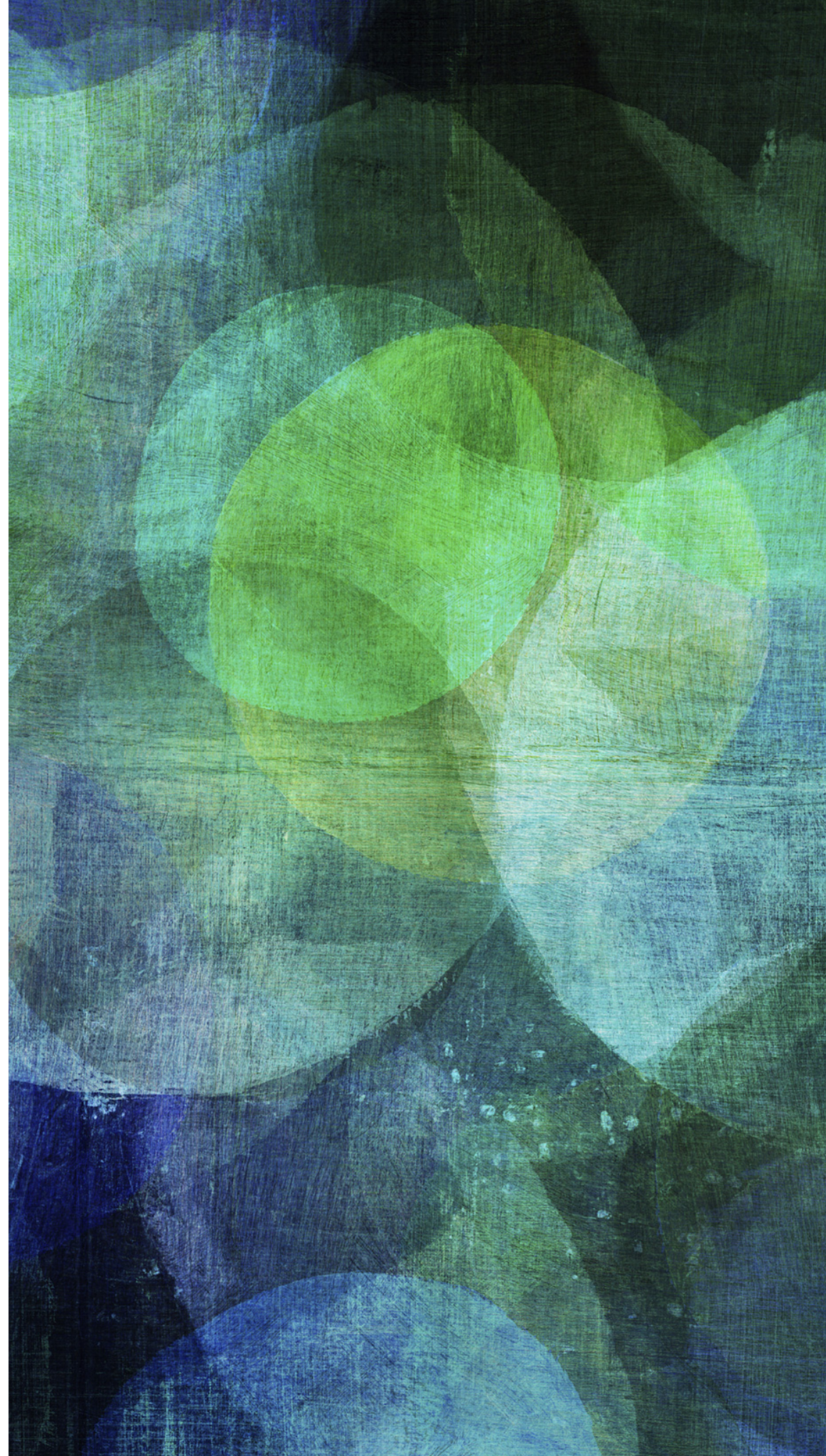
THE PROBLEM

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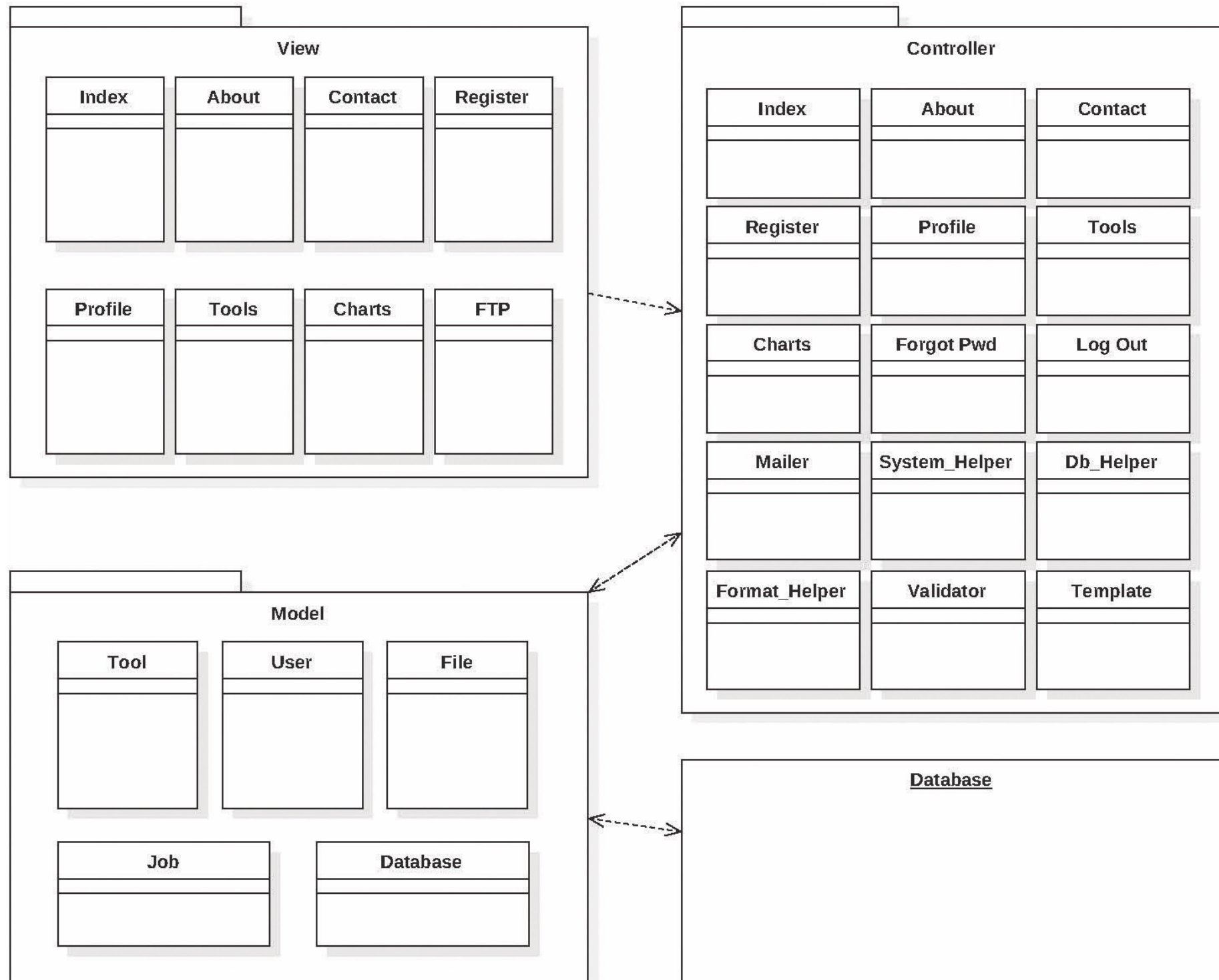
- Modern biological, medical, and biomedical researcher involves analyzing genomic data
- But there is too much!
- A single human genome is...
 - ~3 billion base pairs
 - ~200 gigabytes raw

THE SOLUTION

GenomePro 3.0



MODEL VIEW CONTROLLER



TOOLS PAGE

Submit a Job

Select tool

Genome Signatures
Repeated Sequences
Genome Probes
Unique Sequences

Select files

DNA files:
201602011319_fasta.txt
SORTED:
201602011319_fasta.txt.sorted

Submit

Upload Files To Your Account

Choose File

no file selected

Clear

Upload

Tools Description

Tools Helper

FAQ

Genome Signatures : Choose multiple genome files and see the differences between them, including what is contained in one that isn't contained in the other. The time it takes to complete this job depends exponentially upon the number of files involved.

Repeated Sequences : Run this tool on any valid genome file to view the repeated sequences contained within the file. Because of the complexity of the software, the bigger the file, the longer the processing time to complete the job. Please be weary of this when selecting this job to run on your file.

Genome Probes : This tool will tell you if your probes (sequences) are present or not in your genome files. It will also give you information such as how many times the probes appear and in which lines they are located.

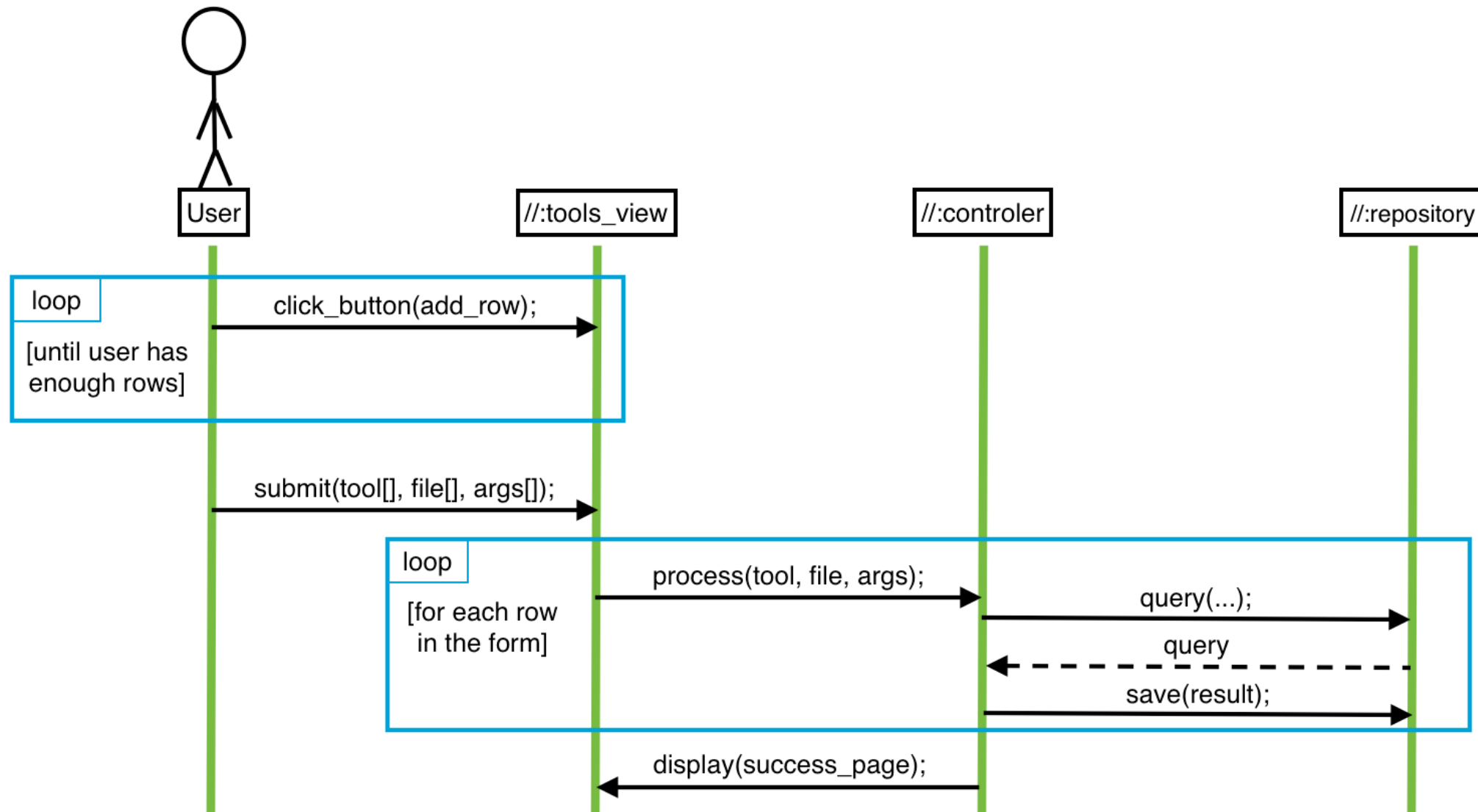
Unique Sequences : Run this tool on files from your map source to verify the existence of unique sequences within the file.

Extract Fasta/Fastq : The extract tool takes any file in FASTA or FASTQ format and extracts sub-sequences of specific length given by the user. You can choose to extract only, extract and sort by alphabetical order, or extract, sort, and generate a map.

Sort Sequences : This tool can sort data in alphabetical order. It can only be used on EXT formatted files that are created by using our extract tools.

Generate Maps : This tool generates maps.

SUBMITTING A JOB



PROFILE PAGE

GenomePro

[Home](#) [About](#) [Contact](#) [Profile](#) [Tools](#) [Charts](#) [FTP](#) [Logout](#)

Logged in as: dgonz293

Welcome

Daniel Gonzalez



No file chosen

Member Since: 01-31-2016

Jobs Submitted: 15

Update Your Profile

dgonz293@fiu.edu

Password

Confirm Password

Daniel

Gonzalez

Enter a description here...

Pending Jobs

You have no pending jobs. You can view your most recently completed jobs below.

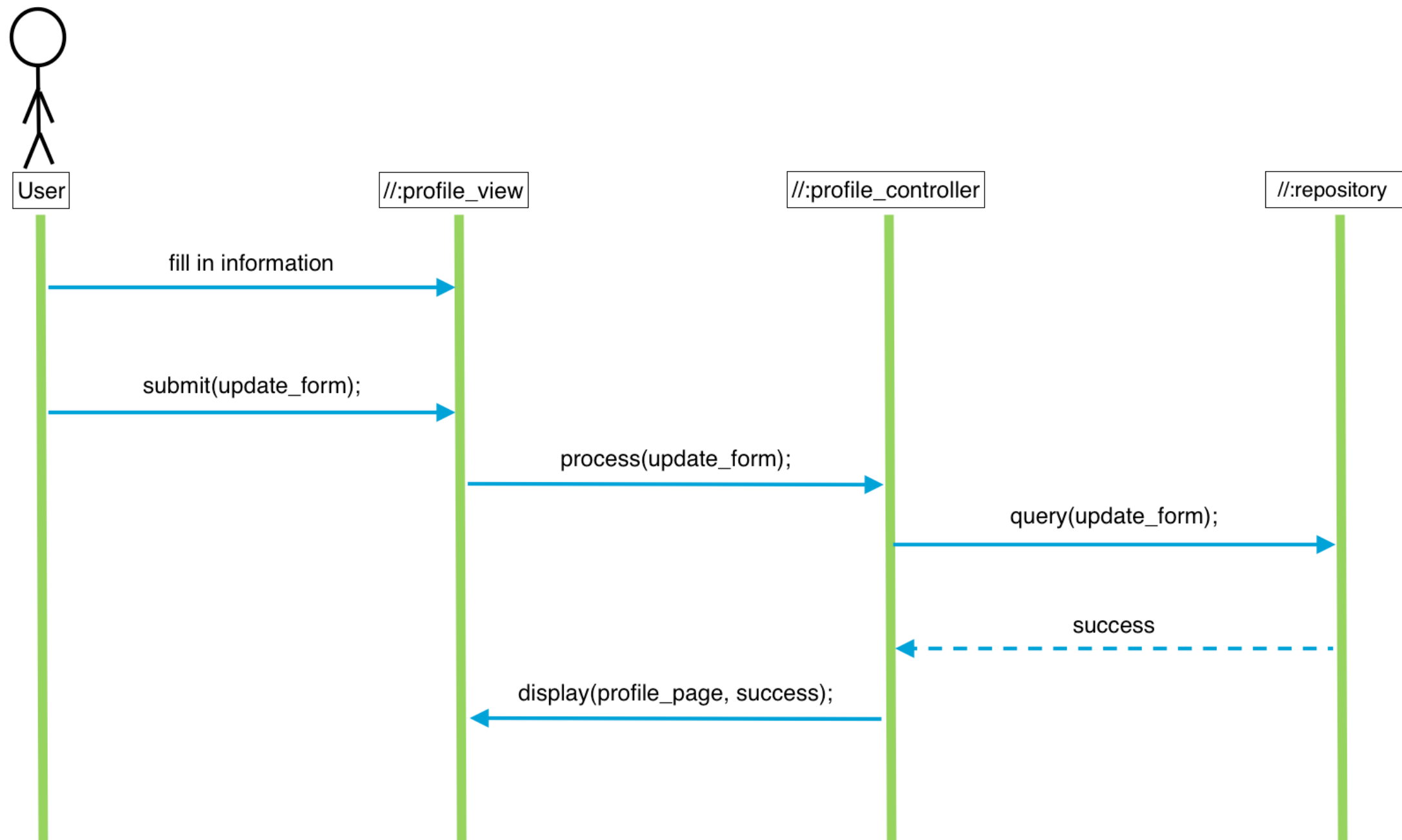
Job History

Tip: click on any JOB ID to View Results | click on any header for sorting

JOB ID	DESCRIPTION	DATE	TIME
369	Repeated Sequences	04-19-2016	5:54 PM
368	Repeated Sequences	04-19-2016	5:54 PM
367	Unique Sequences	04-19-2016	5:21 PM
337	Repeated Sequences	03-07-2016	3:55 PM
336	Sort Sequences	02-28-2016	11:25 PM
335	Sort Sequences	02-28-2016	10:51 PM
334	Unique Sequences	02-28-2016	3:28 AM
330	Repeated Sequences	02-14-2016	10:14 PM
329	Sort Sequences	02-12-2016	1:36 AM
328	Sort Sequences	02-12-2016	1:36 AM
327	Repeated Sequences	02-12-2016	1:35 AM
326	Repeated Sequences	02-12-2016	1:34 AM
321	Generate Maps	02-01-2016	1:29 PM
318	Sort Sequences	02-01-2016	1:27 PM

Clear Job History

UPDATING YOUR PROFILE





THE FUTURE & GENOMEPRO 4.0

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- Full social-media functionality
 - "Sharing" of job results
 - Networking connections
 - Broadcasting announcements
- Color-coded tools and files
- Distributed parallel processing
 - Facilitated modularity through MVC
- More tools!



Thank you!

- Daniel Gonzalez