SevenBridges

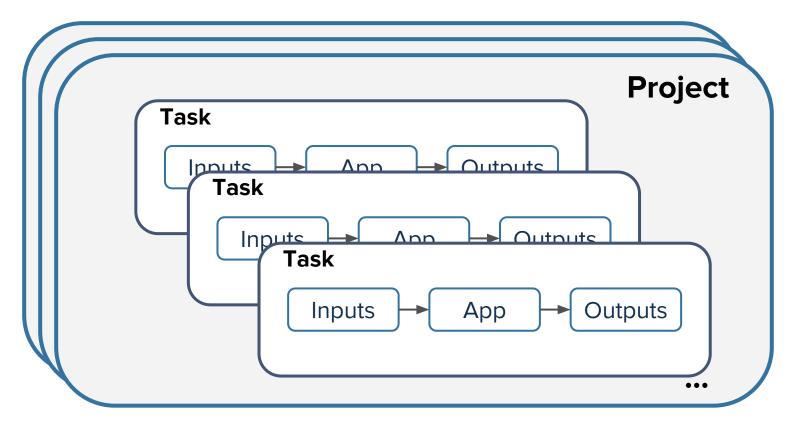
Cancer Genomics Cloud

milan.kovacevic@sbgenomics.com July, 2018.

Cancer Genomics Cloud

- The Cancer Genomics Cloud CGC is a scalable cloud-based environment for analyzing genomics data
- Securely store, analyze, and share data amongst team members
- Collaborate more efficiently
- Main GOAL → Help researchers to get to results faster
 in reproducible
 and reliable manner

Cancer Genomics Cloud



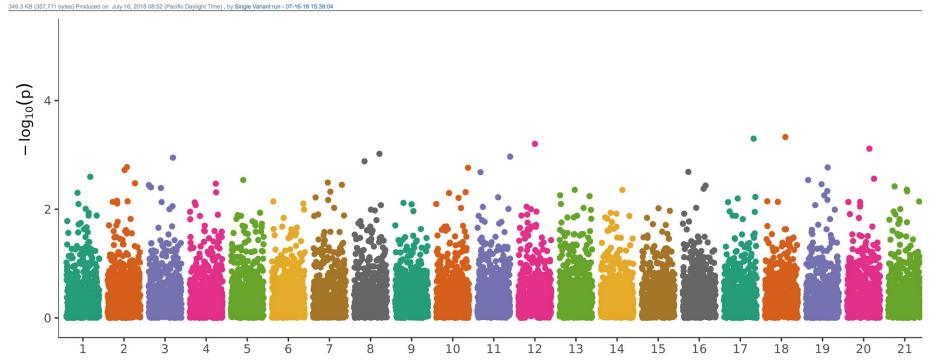


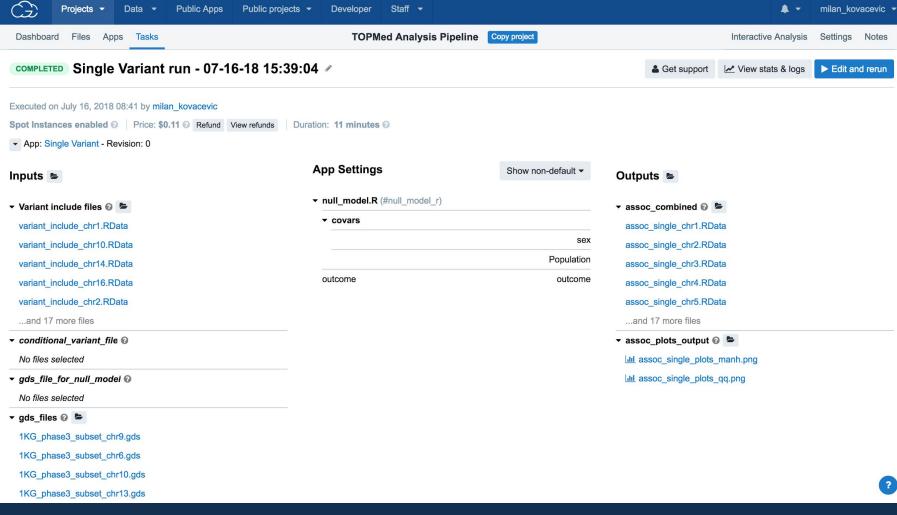
Dashodard Files Apps lasks Interactive Analysis Settings Notes

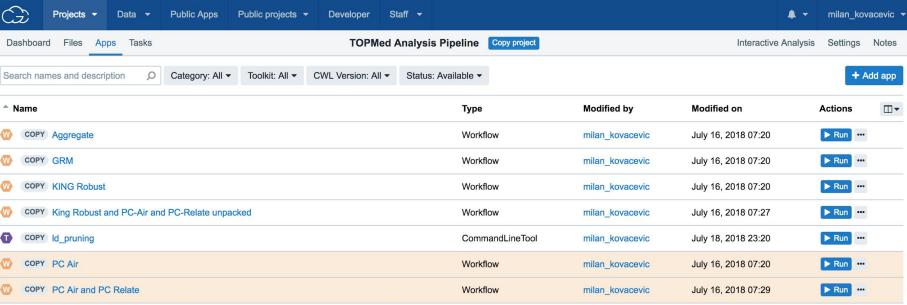
② Copy ▼ STags ③ ···

Files

assoc_single_plots_manh.png /







COPY PC Relate Workflow July 16, 2018 07:21 ▶ Run ••• milan kovacevic ▶ Run ••• COPY Single Variant Workflow milan_kovacevic July 16, 2018 07:20 ▶ Run ••• **COPY** Sliding Window Workflow milan_kovacevic July 16, 2018 07:21 COPY vcf2gds CommandLineTool milan kovacevic July 18, 2018 23:20 ▶ Run ••• COPY VCF to GDS Workflow milan kovacevic July 16, 2018 07:19 ▶ Run ••• ▶ Run ••• COPY VCF to GDS and GRM Workflow milan kovacevic July 16, 2018 07:30 Showing 1-15 of 15 < >

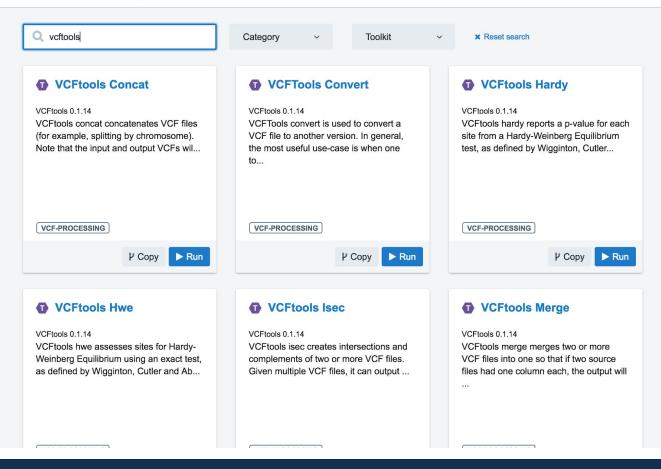
Add apps to "TOPMed Analysis Pipeline"



Projects

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Create New App



Add apps to "TOPMed Analysis Pipeline"

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Public Apps

Projects

My Apps

Create New App



Rabix Composer

Try out Rabix Composer, our new desktop editor. Create CWL 1.0 apps which are portable and which enable enhanced functionalities for workflow development. Enjoy an improved UI with better debugging during development. Learn more.

Download (macOS)

Need it for Windows or Linux?



Workflow

Workflows are chains of interconnected tools.

Create a Workflow

sbg:draft2 only. For CWL 1.0 apps, use Rabix Composer

Learn how to build a workflow



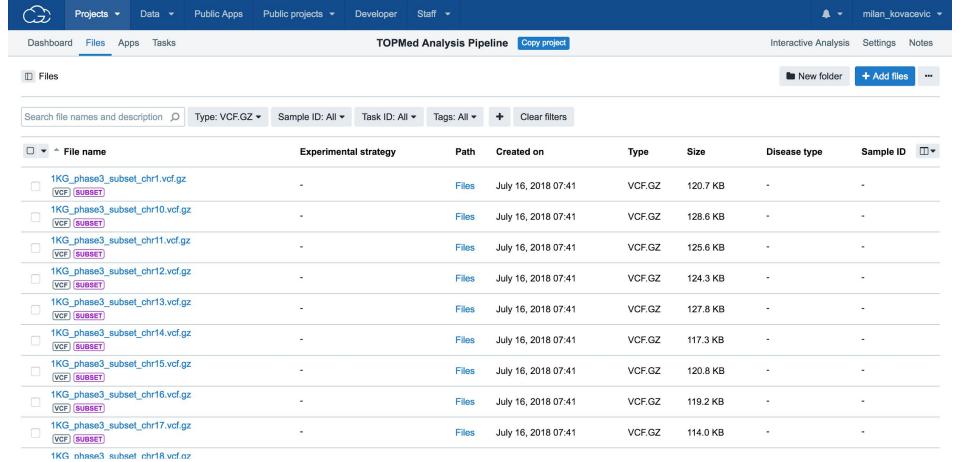
Tool

Tools are programs for processing data on the Platform.

Create a Tool

sbg:draft2 only. For CWL 1.0 apps, use Rabix Composer.

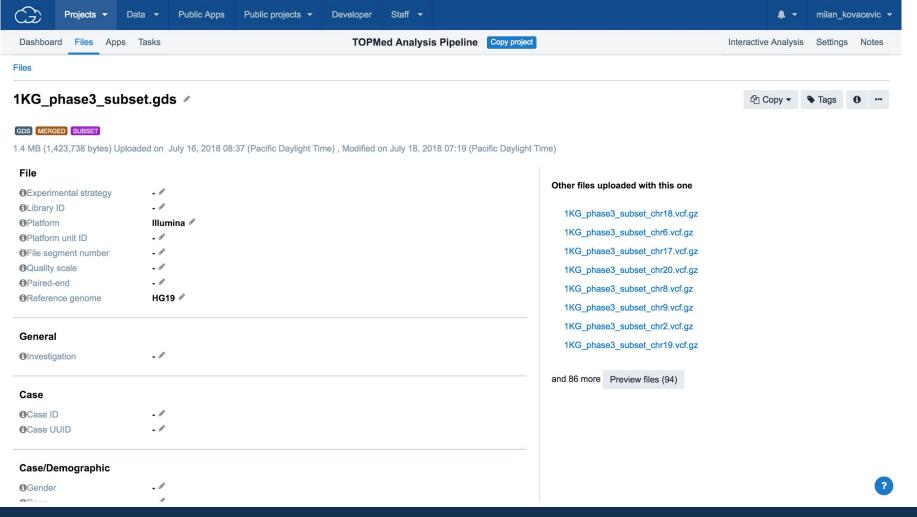
Learn about bringing your own tools

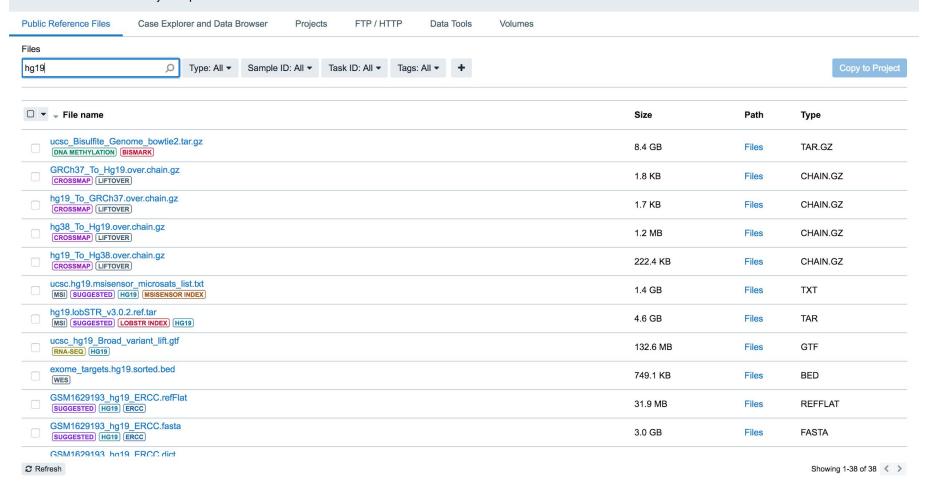


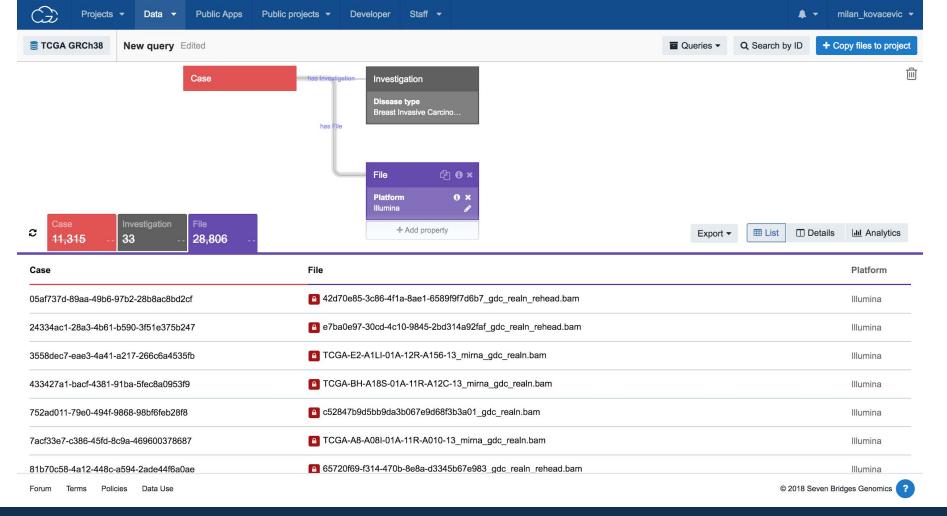
□ 2018 Seven Bridges

Showing 1-22 of 22 < >

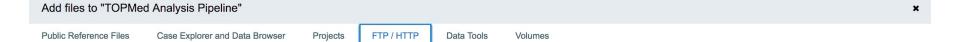
2 Refresh

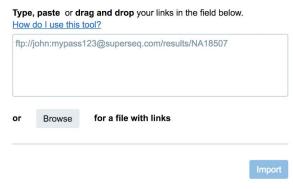






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Add files to "TOPMed Analysis Pipeline"

Public Reference Files

Case Explorer and Data Browser

Projects

FTP / HTTP

Data Tools

Volumes

Command Line Uploader

Upload your private data using fast and secure upload client, taking advantage of parallelization where possible.

Download

Learn more

Desktop Uploader

Upload your private data from a personal computer or hard drive to any of your existing projects.

Download (macOS)

Need it for Windows or Linux? Learn more

SBFS (Seven Bridges File System) BETA

Mount your projects and use files locally.

Important note: before installing SBFS, please install FUSE for macOS.

To install SBFS, run the following command:

curl https://static.sbgenomics.com/sbfs/install.sh
-sSf | sudo sh

Or download the executable file for macOS.

Need it for Linux? (not available for Windows)
Learn more

Upload files via the API

Upload files using the Seven Bridges Python library.

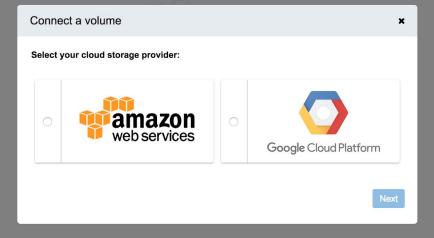
```
files = [
    '/foo/bar/baz.bam
    '/foo/bar/qux.fastq'
]
for file in files:
    api.files.upload(project='my-project',
path=file)
```

Learn more



Volumes

No volumes connected



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Policies Data Use

Forum

Terms

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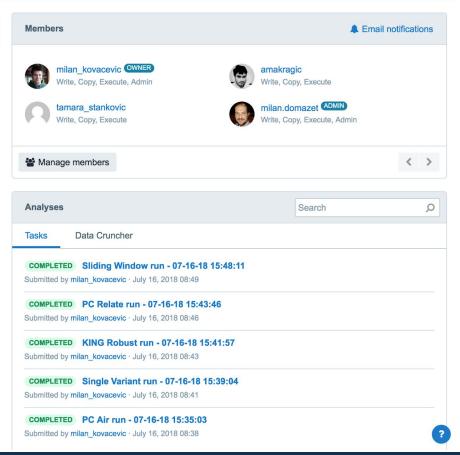
Dashboard Files Apps Tasks

TOPMed Analysis Pipeline

Copy project

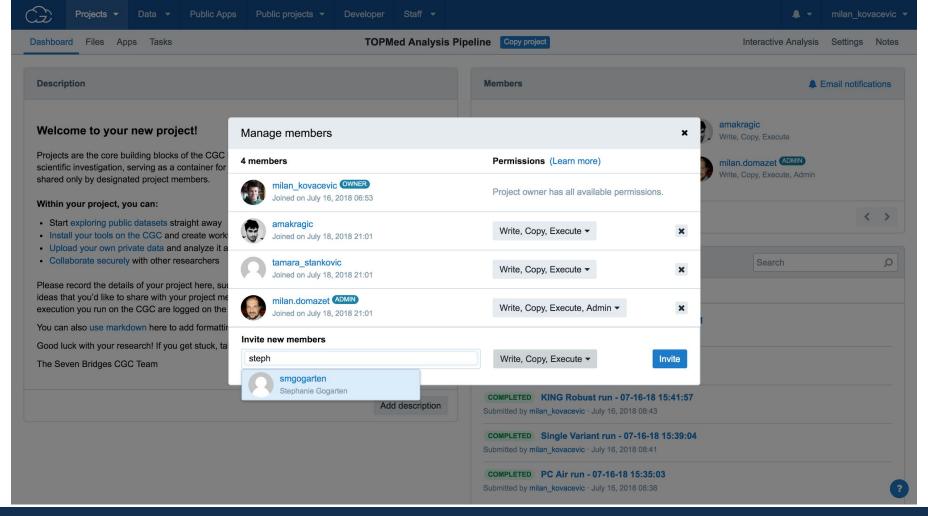
Interactive Analysis Settings Notes

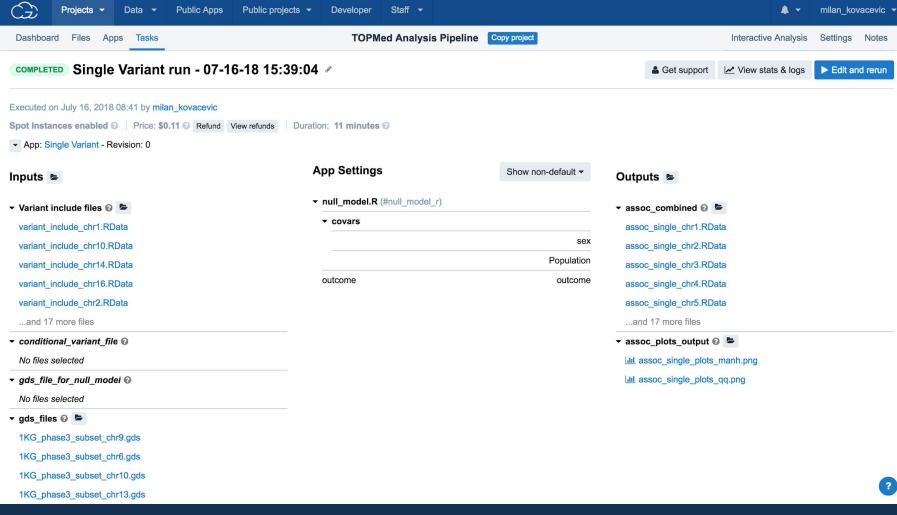
Description Welcome to your new project! Projects are the core building blocks of the CGC Platform. Each project corresponds to a distinct scientific investigation, serving as a container for its data, analysis pipelines, and results. Projects are shared only by designated project members. Within your project, you can: · Start exploring public datasets straight away · Install your tools on the CGC and create workflows · Upload your own private data and analyze it along with public datasets · Collaborate securely with other researchers Please record the details of your project here, such as its aims, experimental context, and any other ideas that you'd like to share with your project members. Remember that details of each pipeline execution you run on the CGC are logged on the task page. This notepad is just for your own notes. You can also use markdown here to add formatting to your notes. Good luck with your research! If you get stuck, take a look at the Knowledge Center The Seven Bridges CGC Team



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Add description



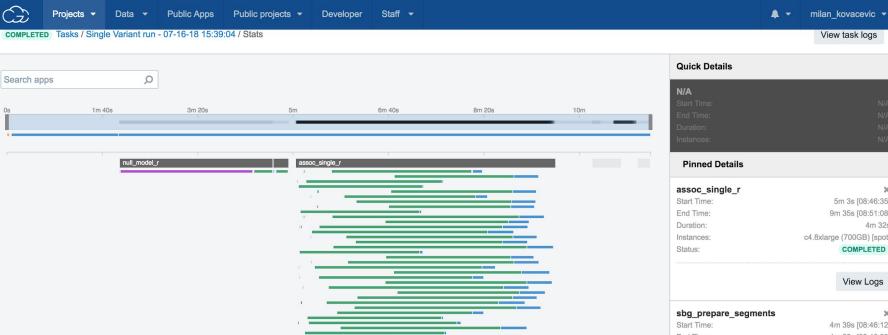


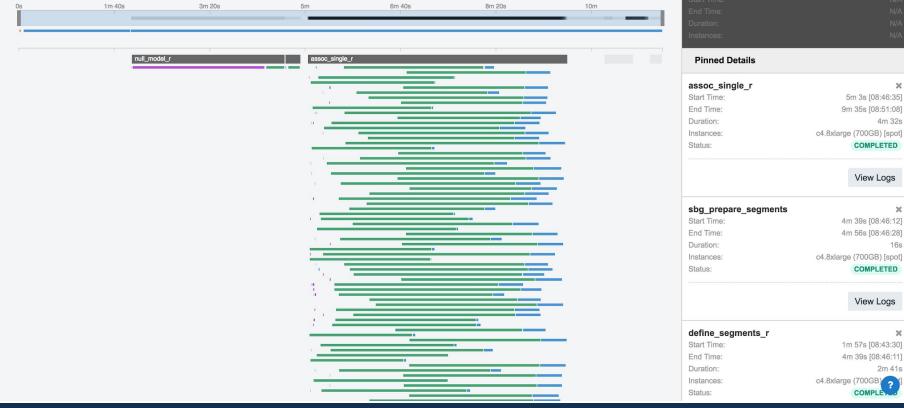
2018 Seven Bridges sevenbridges.com

COMPLETED Tasks / Single Variant run - 07-16-18 15:39:04 / Stats

View task logs







Task logs ×

Search directories	Ω
root_assoc_single_r_129_s	
root_assoc_single_r_12_s	
root_assoc_single_r_130_s	
root_assoc_single_r_131_s	
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root_assoc_single_r_135_s	
root_assoc_single_r_136_s	
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i cmd.log	
cwl.output.json	
cwl.output.json	
job.err.log	
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i job.err.log i job.json i job.tree.log i sbg.worker.log i root_assoc_single_r_138_s i root_assoc_single_r_139_s	
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Dashboard Files Apps Tasks

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TOPMed Analysis Pipeline

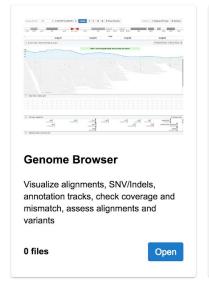
Copy project

Interactive Analysis

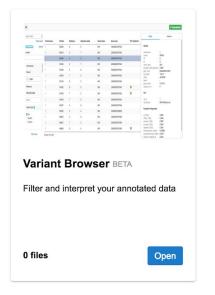
Settings Notes

Explore genomics data

Understand complex genomics data with interactive analysis tools.

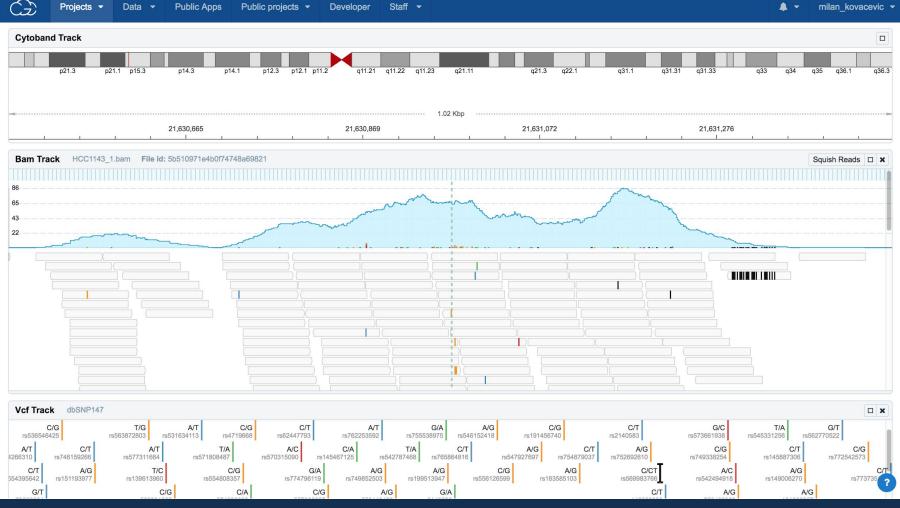






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Dashboard Files Apps Tasks

Data Cruncher Interactive Analyses

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Interactive Analysis

SAVED Structural Variant Interactive Analysis 🕜

₽ Copy

Session started on May 11, 2018 06:06 by anaDsbg Price: \$0.14 | Duration: 19 minutes View Sessions

Files Settings

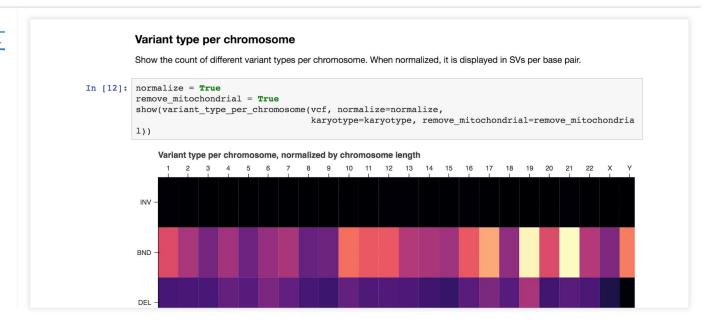
Analysis files:

Structural_Variation_Intractive_Analysi...

current_pathway.png

Produced by this analysis

No files



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Dashboard

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Data Use

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Settings

Notes

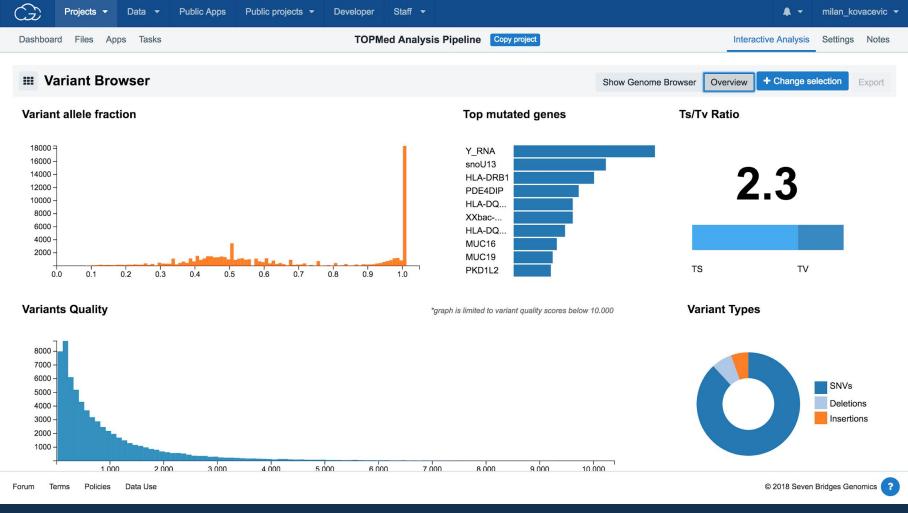
Interactive Analysis

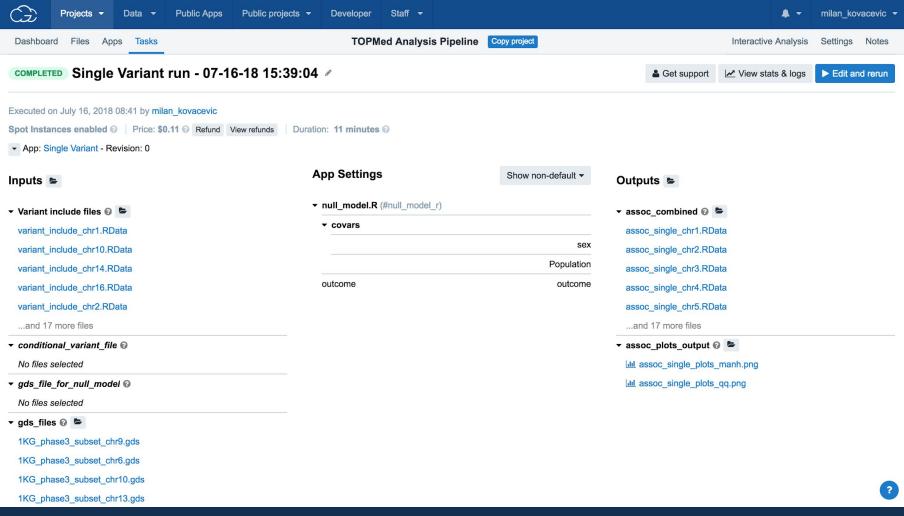
Variant Browser Show Genome Browser Overview + Change selection Export Search Filters 0 Chr Position Ref Alt Gene name Zygosity Features count □ -Reset search 3 764625 **ACTG** AC090044.1 Heterozygous 2 Α 2 filters set Clear all CT... С CNTN6 3 1363304 Heterozygous 4 Location 3 3217128 AT Α **CRBN** Homozygous 10 02 3 AG BHLHE40-AS1 4940288 Α Homozygous 5 **3** 3 7172236 AA... GRM7 Heterozygous 11 Α more... 3 7600819 CT C 0 Homozygous 12 Position ΑT 3 9519363 SETD5 15 Α Heterozygous Ref TG... 10 3 9743398 Т 0 Homozygous Alt TG 3 10075900 Т 0 Heterozygous 8 0 ^ Variant class 3 10083526 CT C 0 Homozygous 9 Insertion Snv 10105661 CT C FANCD2 3 Heterozygous Deletion 3 10142749 TA 10 0 Heterozygous

TOPMed Analysis Pipeline

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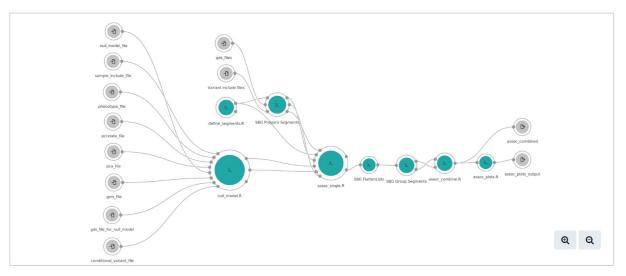




Copy of Single Variant (Latest revision), by milan_kovacevic on July 16, 2018 07:20

Description

No description.



Basic Information

Revision 0 ▼

CWL Version v1.0

Contributors: milan kovacevic

App Id: milan_kovacevic/topmed/single-variant

Edit with Rabix Composer

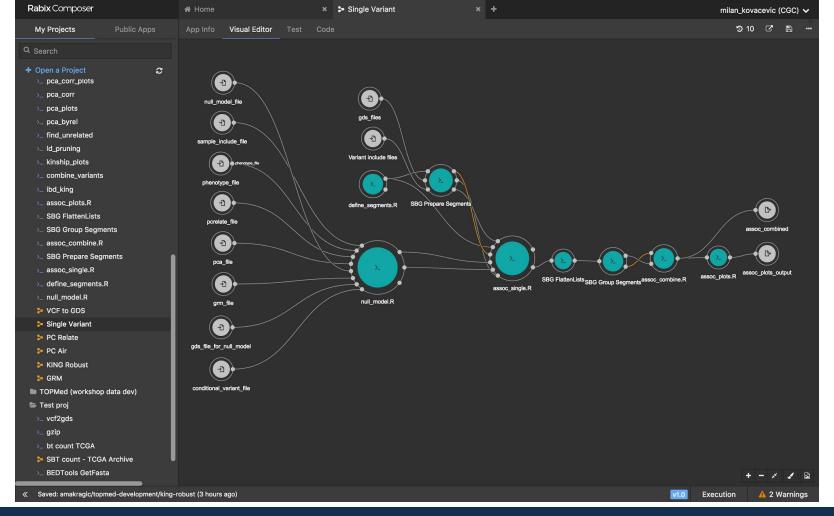
▶ Run

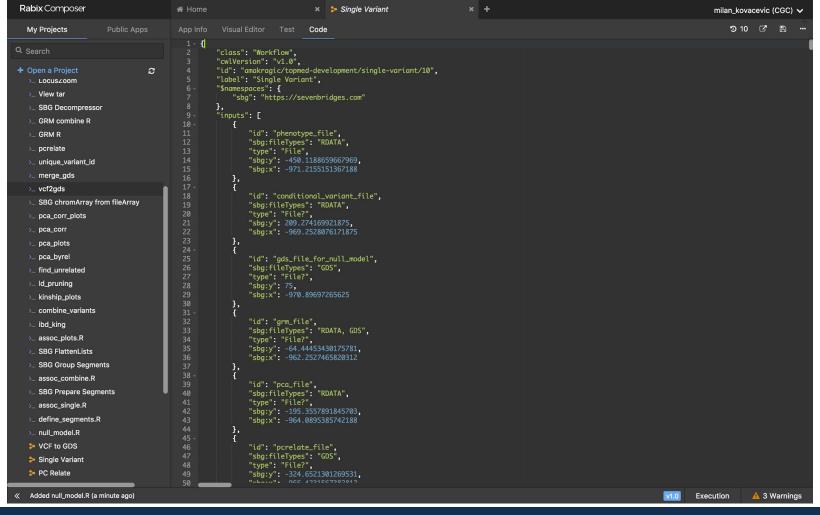
Workflow steps >

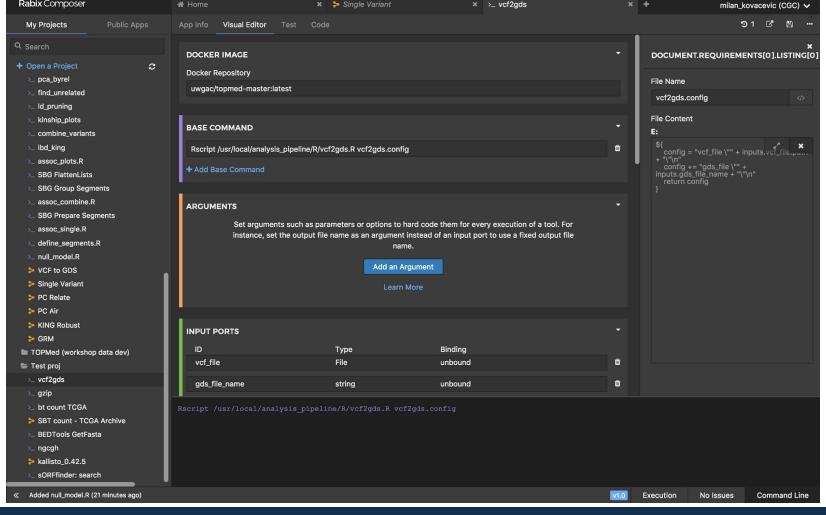
null_model.R >
define_segments.R >
assoc_single.R >
SBG Prepare Segments >
assoc_combine.R >
SBG Group Segments >
SBG FlattenLists >
assoc_plots.R >

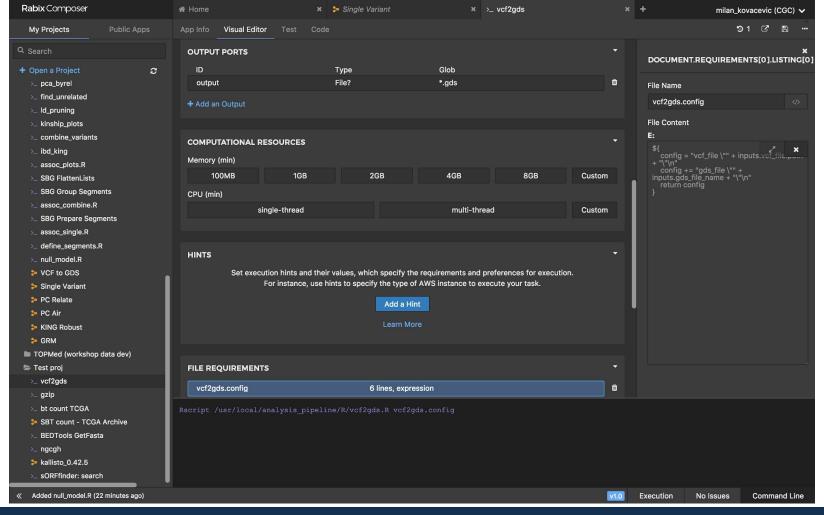
Ports

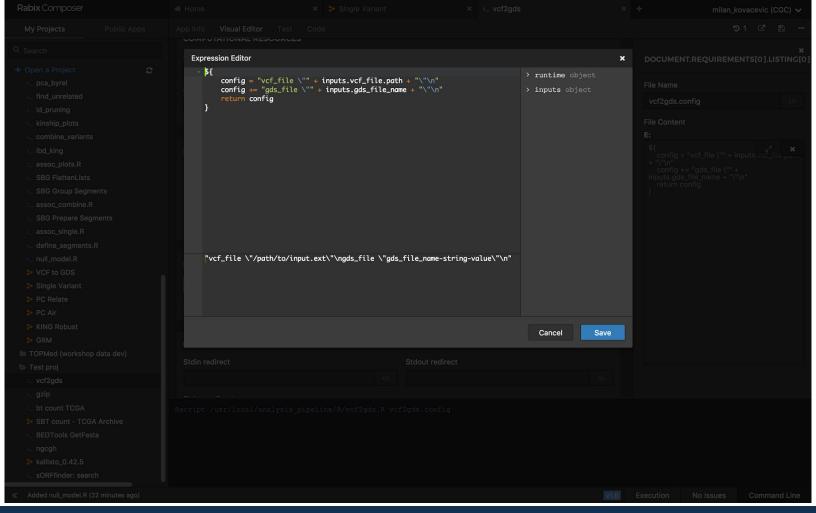
Inputs App Settings Outputs











Links

- CGC
- CGC Docs
- Rabix Composer
- Seven Bridges



Questions?