

Attachment A – Screen Shots



NCI Cancer Genomics Cloud Pilots - User Feedback Survey

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Public reporting burden for this collection of information is estimated to average 15 minutes per response, including the time for reviewing instructions, searching existing data sources, gathering and maintaining the data needed, and completing and reviewing the collection of information. An agency may not conduct or sponsor, and a person is not required to respond to, a collection of information unless it displays a currently valid OMB control number. Send comments regarding this burden estimate or any other aspect of this collection of information, including suggestions for reducing this burden to: NIH, Project Clearance Branch, 6705 Rockledge Drive, MSC 7974, Bethesda, MD 20892-7974, ATTN: PRA (0925-XXXX). Do not return the completed form to this address.



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1. Please provide your institutional affiliation.

2. What is your role at your institution?

- Principal Investigator
- Investigator
- Post-doc / Fellow
- Student
- Other (please specify)

3. How would you describe your primary expertise?

- Clinical care / clinical research
- Bench / basic biology
- Bioinformatics / genomics – analysis, integration of data using existing tools, scripting languages
- Computational biology / systems biology– development of novel algorithms
- Other (please specify)

**5. This survey is in response to work you performed on which Cancer Genomics Cloud (CGC) platform?
(Select only one - please complete a separate survey for each CGC platform you used)**

- Broad Institute (FireCloud)
- Institute for Systems Biology
- Seven Bridges Genomics

6. What kinds of tasks did you perform?

- Query TCGA Data
- Upload locally-generated genomic data to analyze in conjunction with TCGA data
- Perform TCGA data processing or analyses using CGC-provided or user-uploaded tools
- Install new analysis tool(s) to test tools performance on large-scale genomic data set and/or to conduct novel research
- Store and share analyses with collaborators
- Other (please describe)

9. Please indicate if you agree or disagree with the following statements.

	Strongly Agree	Agree	Neutral	Disagree	Strongly Disagree
The system improved my ability to store my analysis results/provenance in a reproducible manner so that the same method could be used with other data.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
The system improved my ability to correlate patient's molecular data with clinical data.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
The system made it possible for me to run analyses which would have been difficult or time consuming otherwise.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
My research benefited from insights I gained while using the system.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>

10. Which of these TCGA data sets did you use? (Select all that apply)

- Gene Expression Array
- Copy Number Array
- Whole Genome Sequence (WGS)
- Whole Exome Sequence (WXS)
- Methylation
- RNA-Seq
- I did not use any TCGA data
- Other (please specify)

11. Which additional TCGA data sets would you like to access through this platform? (Select all that apply)

- Radiology
- Pathology
- Proteomics
- Other (please specify)

12. Did you upload local data?

13. Did you use an Application Programming Interface (API) to access data in the system?

14. Did you use APIs to access analysis tools or pipelines?

15. Which of the following analyses did you perform? (Select all that apply)

- RNA-Seq Analysis
- Exome Analysis
- Whole Genome Analysis
- Transcription Analysis / Assembly
- Other (please specify)

16. Did you upload local pipelines/tools to the CGC?

If yes, please describe.

17. Are you willing to share pipelines/tools you have developed to the CGC?

- Yes, willing to share
- Not sure
- At a later date
- No
- Yes, already shared as open source (please provide the URLs to GitHub or other repositories)

18. What additional open source bioinformatics pipelines/tools would you like incorporated in the CGC?

19. Please add your comments about whether you would use this platform again, and what tools and functions you found most useful.

Done

