2022-6-3 Meeting notes

Date

03 Jun 2022

Attendees

Committee Member	Present	Absent
Kuffel, Gina (NIH/NCI) [C]	X	
Pihl, Todd (NIH/NCI) [C]		X
Unknown User (leblancak)		X
Otridge, John (NIH/NCI) [C]		X
Kim, Erika (NIH/NCI) [E]		X
Sommers, Connie (NIH/NCI) [E]	X	
Debbie Knapp	X	
Toby Hecht	X	
Unknown User (parchmentr)		X

Goals

- Discuss updates to ICDC and define emerging strategies and priorities

SharePoint Site

https://nih.sharepoint.com/sites/NCI-CBIIT-FNL-ICDC-ICDCLeadershipGroups

Outstanding Action Items

None

Agenda

Item	Who	Talking Points

DGAB Updates	Kuffel, Gina (NIH/NCI) [C]	• 33 TB of data are now available in ICDC (five-fold increase since January)
		• PRECINCT has used templates available from the ICDC Data Model Explorer (DME) for the fist ever load of a study via submitter-generated loading files
		  ◦ Initial version of data is available in Dev tier
		  ◦ Waiting on significant data updates from study owners before proceeding with a reload of the study in updated and somewhat expanded form

BPSC Updates	Kuffel, Gina (NIH/NCI) [C]	• 2022 BPSC Review Article
		  ◦ Outline completed
		  ◦ Preliminary section assignments have been made
		  ◦ Communicate deadline of August 1, 2022
		  ◦ Communicate that future funding hinges upon this publication

May Steering Committee Updates	Unknown User (parchmentr)	• Minutes to be posted • Next meeting is ?

ICDC Site Updates	Kuffel, Gina (NIH/NCI) [C]	• Next software release for ICDC targets July 7th
		  ○ ICDC Static News Page
		  ○ Data Availability Landscape (DAL)
		  ○ Gene annotations for JBrowse

ICDC Next Phase Planning	Unknown User (hechtt)	• 2 focus groups met ○ Ideas from the ICDC brainstorming sessions final.docx

Minutes (Not Verbatim)

Previous ICDC Use Cases from Steering Committee

1. Genomic correlates across platforms (DNA, RNA, protein).

2. Correlating multi-omics data with clinical annotation and phenotypes, particularly outcomes.

3. Comparative analyses of canine and human. Examples include:

    1. Search for conserved mutations between canine and human tumors

    2. Disease diagnosis (e.g. cancer type) and classification mapping between canines and humans

    5. Gene expression changes and mutational profiles associated with therapeutic response and outcome

    6. How do sporadic tumors in non-human mammals compare to sporadic human tumors?

    7. Correlations and model building from radiomic and pathomic features extracted from medical and histopathologic images with outcomes and genomics, as is currently being widely done with human images

    8. Develop biomarkers of response and resistance in humans by analyzing the responses and genomic signatures in dogs.

Previous Meeting Minutes (Not Verbatim)

Toby - Can canine bladder cancer be a good model for invasive human bladder cancer? Maybe running differential expression in dogs at various stages vs. human data at different stages of disease obtained from the GDC and then comparing expression patterns and gene signatures. Real focus is comparative genomics.

Ralph - Possibly raise as a discussion point to the SC. Does this cancer in both species survive therapy to resist disease using same pathways? Is there biological convergence?

Toby - Look at dogs in ICDC and see what the genes are in dogs that are more resistant to glioma vs. dogs that are not and see if those up or down regulated genes have human homologs.

Toby - Real data in ICDC can now be used to answer real biological questions.

Ralph - Will put use case into SC meeting agenda.

Action items

- [ ] Kuffel, Gina (NIH/NCI) [C] to send email to Debbie about importance of review article.