2016 ITCR Program Annual Meeting Poster Session
5:10 - 7:30 p.m., Monday, June 13, 2016
Yellowstone Room, 2001
75 Ames Street Building

ITCR Posters – New Projects

1. **Galaxy-P**: recent developments and emerging applications
   *Pratik D. Jagtap, James E. Johnson, Thomas McGowan, Innocent Onsongo, Benjamin Lynch, Candace R. Guerrero, Kevin Murray, Lloyd M. Smith, Michael R. Shortreed, Anthony J. Cesnik, Lennart Martens, Adrian D. Hegeman and Timothy J. Griffin*

2. **Cravat 4.2**: informatics tools for high-throughput analysis of exome variants
   *Collin Tokheim, Christopher Douville, David Masica, Rick Kim, Rohit Bhattacharya, Noushin Niknafs, Derek Gygax, Kyle Moad, Michael Ryan, Rachel Karchin*

3. PDX Integrator - A new resource for cancer research
   *Terrence Meehan*, Helen Parkinson

4. Informatics tools for tumor heterogeneity in multiplexed fluorescence images
   *Dan Spagnolo, Rekha Gyanchandani, Yousef Al-Kofahi, Andrew Stern, Tim Lezon, Albert Gough, Dan Meyer, Fiona Ginty, Brion Sarachan, Jeffrey Fine, Adrian Lee, D. Lans Taylor, S. Chakra Chennubhotla*

5. Informatic tools for single-nucleotide analysis of RNA-seq
   *Zhuangli Liang, Qing Zhang, Jaegyoon Ahn, Xinshu Xiao*
IMAT Posters

6. Single-cell barcode chips for highly multiplexed miRNA and protein profiling
   Nayi Wang, Yao Lu, Minsuk Kwak, Maria Kleppe, Steve C. Chapin, Ross Levine, Jun Lu, Patrick S. Doyle*, and Rong Fan*

7. Single-cell sequencing reveals distinct genomic profiles in epithelial and mesenchymal tumor cells
   Jessica Sang*, Kyungheon Lee, Hyun Jung Chung, Gavin Zhou, Hakho Lee, Ralph Weissleder, Sunney Xie

8. Highly Multiplexed FISH for In Situ Genomics
   John Lafrate*, Hunter Elliott*

ITCR Posters – Ongoing Projects

9. Informatics for routine personalized cancer therapy
   Safa Fathiamini, Amber M. Johnson, Jia Zeng, Alejandro Araya, Vijaykumar Holla, Ann M Bailey, Beate C Litzenburger, Nora S Sanchez, Yekaterina Khotskaya, Hua Xu, Funda Meric-Bernstam, Elmer V Bernstam*, Trevor Cohen

10. The Digital Slide Archive and HistomicsTK: Open-Source Resources for Digital Pathology Management and Analysis
    Lee AD Cooper*, Deepak Chittajallu, Brian Helba, Sanghoon Lee, Mohammed Khalilia, Michael Nalisnik, Jonathan Beezley, Zach Mullen, David Manthey, David A Gutman

11. Cancer Imaging Phenomics Toolkit (CapTk)
    Satrhak Pati, Mark Bergman, Despina Kontos, Ragini Verma, Taki Shinohara, Paul Yushkevich, Yong Fan, Christos Davatzikos*

12. Quantitative Image Informatics for Cancer Research

13. The UCSC Xena system for integrating and visualizing functional genomics data
    Jingchun Zhu, Brian Craft, Mary Goldman*, Teresa Swatloski, Melissa Cline, David Haussler
14. Trinity CTAT: A Community Resource for De Novo and Reference-based RNA-Seq Analysis
Timothy Tickle*, Asma Bankapur, Carrie Ganote, Ben Fulton, Itay Tirosh, Jenny Chen, Thomas Doak, Robert Henschel, Nathalie Pochet, Catherine Wu, Brian Haas*, Aviv Regev

15. OmniSearch: a semantic tool for discovering microRNAs’ critical roles in human cancers
Jingshan Huang*

16. Cloud-based Image Biomarker Optimization Platform (C-BIBOP)
Jayashree Kalpathy-Cramer*, Artem Mamonov, Sandy Napel, Binsheng Zhao, Dmitry Goldgof, Robert Gillies, Bruce Rosen

17. Modeling functional gene regulation in cancer with public ChIP-seq profiles
Chongzhi Zang, Shenglin Mei, Clifford Meyer, Qiu Wu, Jingyu Fan, Rongbin Zheng, Qian Qin, Muyuan Zhu, Binbin Wang, Myles Brown, and X. Shirley Liu*

18. Pathology Image Informatics Platform (PIIP)
Anant Madabhushi*, Anne Martel, Metin Gurcan, Yu Zhou, Dan Hosseinzadeh, Craig Madho

19. Open-source diffusion MRI for neurosurgical planning
Isaiah Norton, Fan Zhang, and Lauren O’Donnell*

20. Linking Diverse Network Sources to Analysis, Visualization, and Publication: Applications of the NDEx Framework
Rudolf T. Pillich*, Jing Chen, Vladimir Rynkov, David Welker and Dexter Pratt

21. GenePattern Notebooks: an integrative analytical environment for cancer research
Michael Reich*, Thorin Tabor, Peter Carr, David Eby, Helga Thorvaldsdóttir, Barbara Hill, Ted Liefeld, Pablo Tamayo, Jill P. Mesirov

22. mint and annotatr: integrating and annotating DNA methylation and hydroxymethylation data
Raymond G. Cavalcante, Yanxiao Zhang, Yongseok Park, Snehal Patil, Laura S. Rozek, and Maureen A. Sartor*
23. The Biomedical Evidence Graph to Discover Novel Relations in Cancer Genomics
   Kyle Ellrott, Ryan Spangler, James Durbin, Jeena Lee, Malisa Smith, Chris Wong, Teresa Swatloski, Yulia Newton, Duncan McColl, Joshua Stuart

24. WebMeV: Software for Next Generation Genomic Data Analysis
   Yaoyu Wang*, Antony Partensky, Lev Kuznetsov, Jalil Farid, John Quackenbush

25. Interactive Statistical Resource for Proteomic Analyses
   Bobbie-Jo Webb-Robertson*, Lisa Bramer, Kelly Stratton, Markus Kobold, Jeff Jensen, Mathew Thomas, Amanda White

   Abhyuday Jagannatha and Hong Yu*

27. Modeling and Validating HL7 FHIR Profiles Using Semantic Web Shape Expressions
   Harold R. Solbrig, Eric Prud'hommeaux, Deepak K. Sharma, Christopher G. Chute, Guoqian Jiang

ITCR Posters - Collaborative Projects

28. Integrating TCGA Clinical Data using metadata-driven tools and NLP
   Richard C. Kiefer, Guoqian Jiang, Michael K. Davis, Melissa Castine, Girish Chavan, Guergana Savova, and Rebecca Jacobson

29. Cravat/MuPIT - NDEX Collaboration
   Dexter Pratt, Rick Kim, Rudolf T. Pillich, Derek Gygax, Jing Chen, Michael Ryan*, Vladimir Rynkov, David Welker and Rachel Karchin*

30. 3DSlicer Pathology and FeatureScape for Linked Radiology/Pathology Image Analysis Competitions
   Jonas Almeida, Nicole Aucoin, Erich Bremer, Tammy DiPrima, Andrey Fedorov, Yi Gao, Jayashree Kalpathy-Cramer, Ron Kikinis, Tahsin Kurc, Arten Mamonov, Steve Pieper, Jean-Christophe Fillion-Robin, Bruce Rosen, Allen Tannenbaum