



The Elizabeth H.
and James S. McDonnell III

**McDONNELL
GENOME INSTITUTE**
at Washington University

GenViz Module 0: Introductions

Malachi Griffith, Obi Griffith, Zachary Skidmore
Genomic Data Visualization and Interpretation

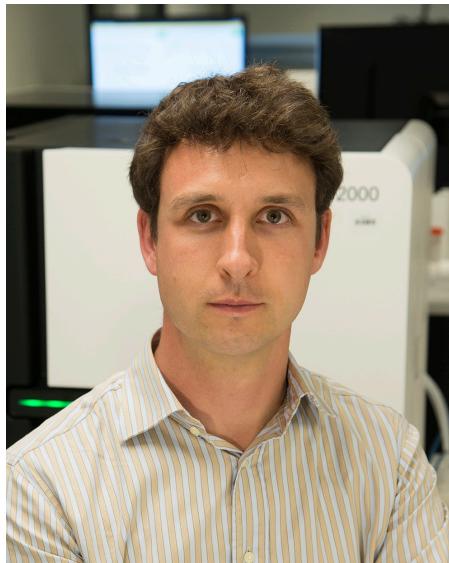
September 11-15, 2017
Berlin

Introductions to course instructors



Malachi Griffith, PhD

Assistant Professor of Medicine
Assistant Professor of Genetics
Assistant Director, MGI



Obi Griffith, PhD

Assistant Professor of Medicine
Assistant Professor of Genetics
Assistant Director, MGI



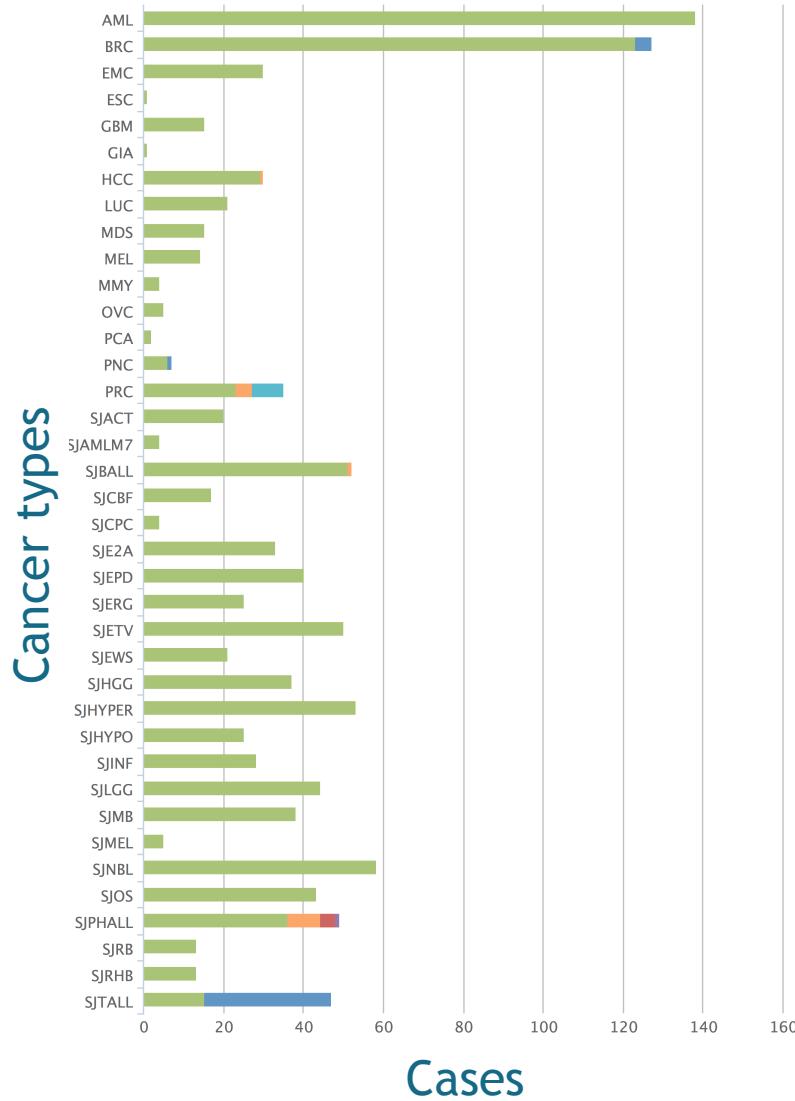
Zachary Skidmore, MSc

Staff Scientist, MGI

GenVisR creator

McDonnell Genome Institute, Washington University School of Medicine

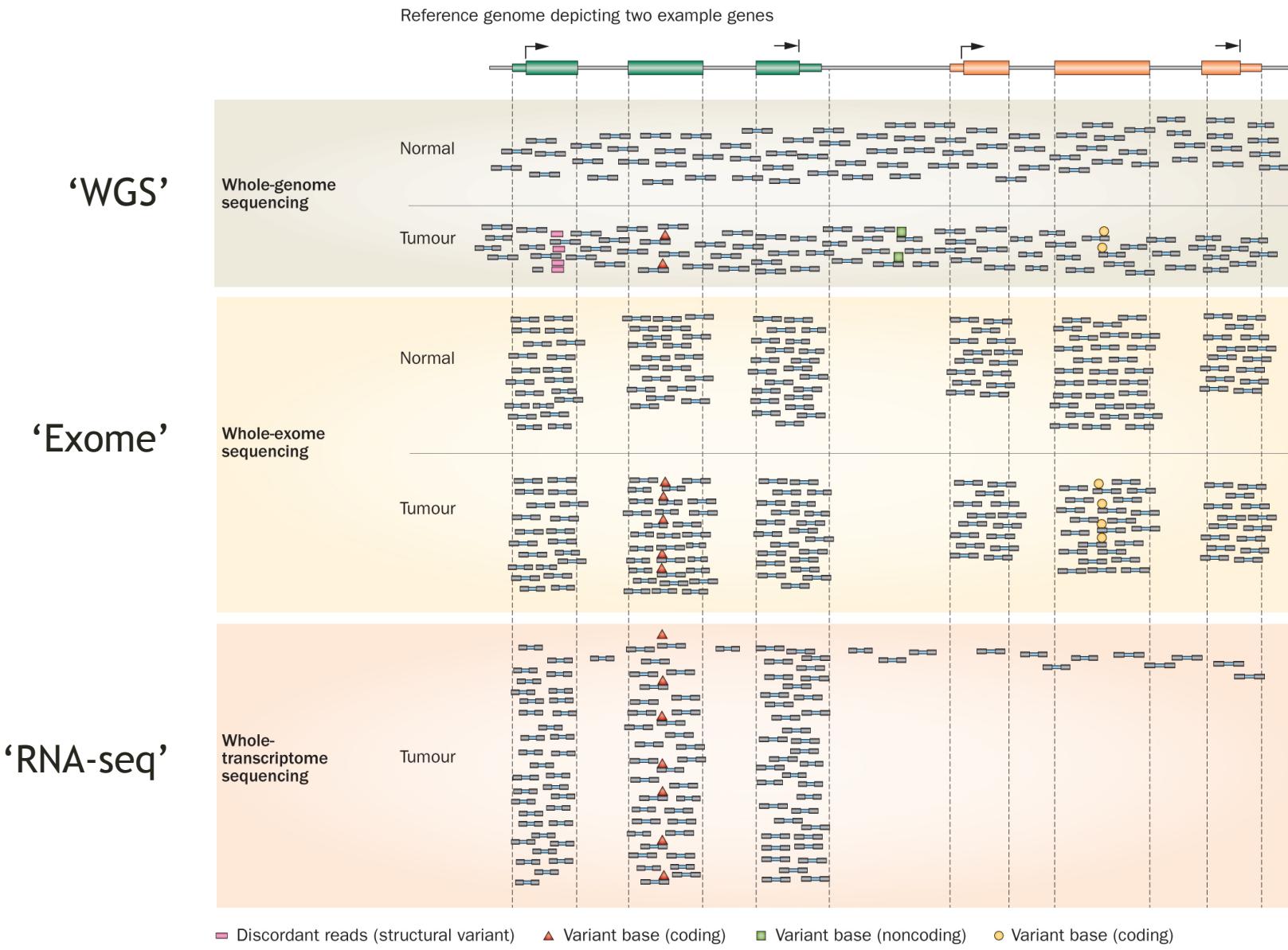
The McDonnell Genome Institute has pursued the field of genomics since inception:
>>1000 whole genomes, >5000 exomes, >1000 transcriptomes for dozens of tumor types



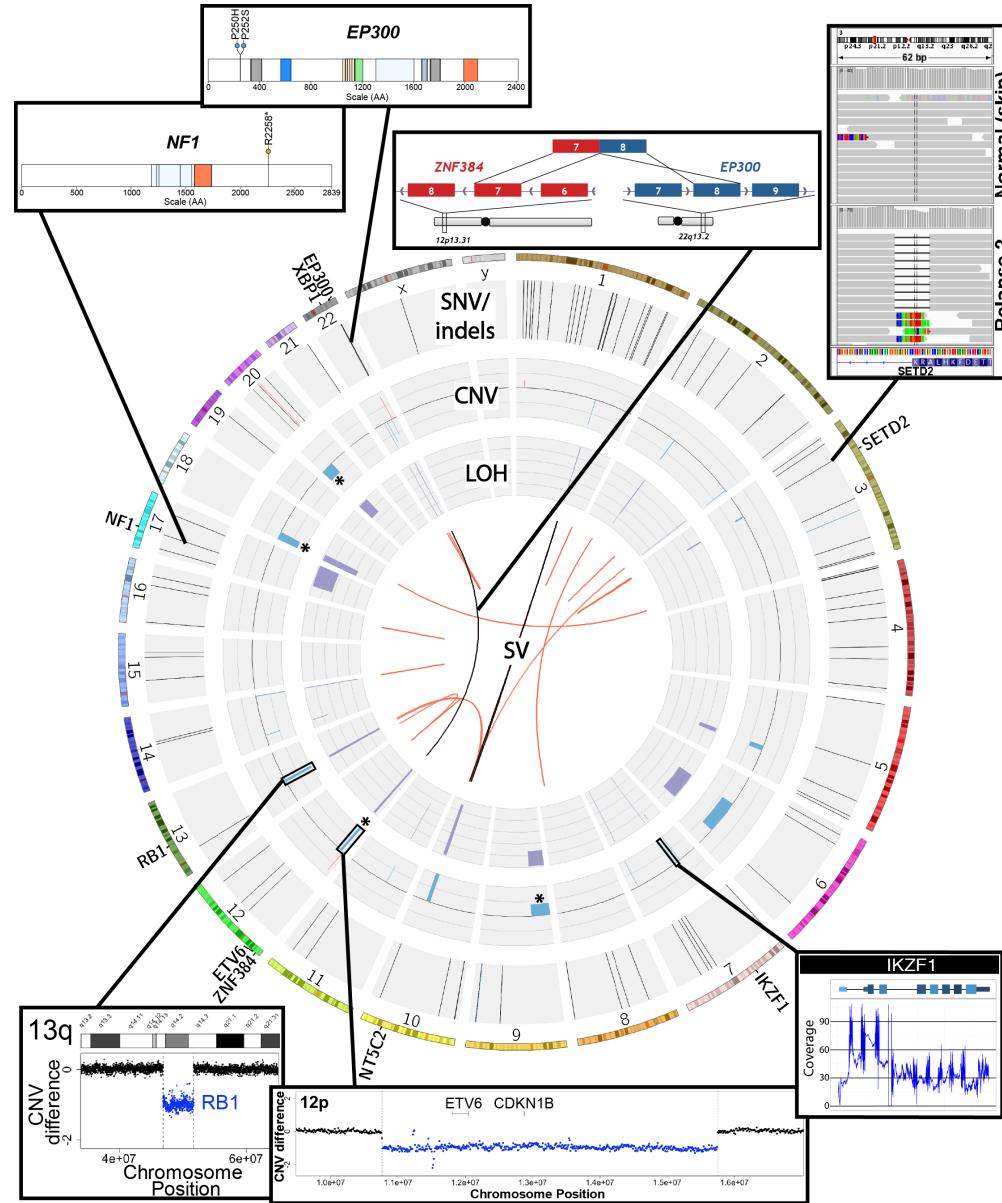
MG - 1000+ tumor whole genomes, many more
exomes, X10 & NovaSeq will accelerate this!

- Human Genome Project
- First to sequence and analyze a tumor whole genome sequence (Ley et al, 2008)
- Major contributor to TCGA, PCGP, etc.
- Most comprehensively sequenced single patient tumor ever published (Griffith et al, 2015)
- Early proof-of-principle for cancer precision medicine (Griffith et al, 2016)
- Analysis and tools for first personalized cancer vaccine design in humans (Carreno et al, 2015)
- Many other widely used tools

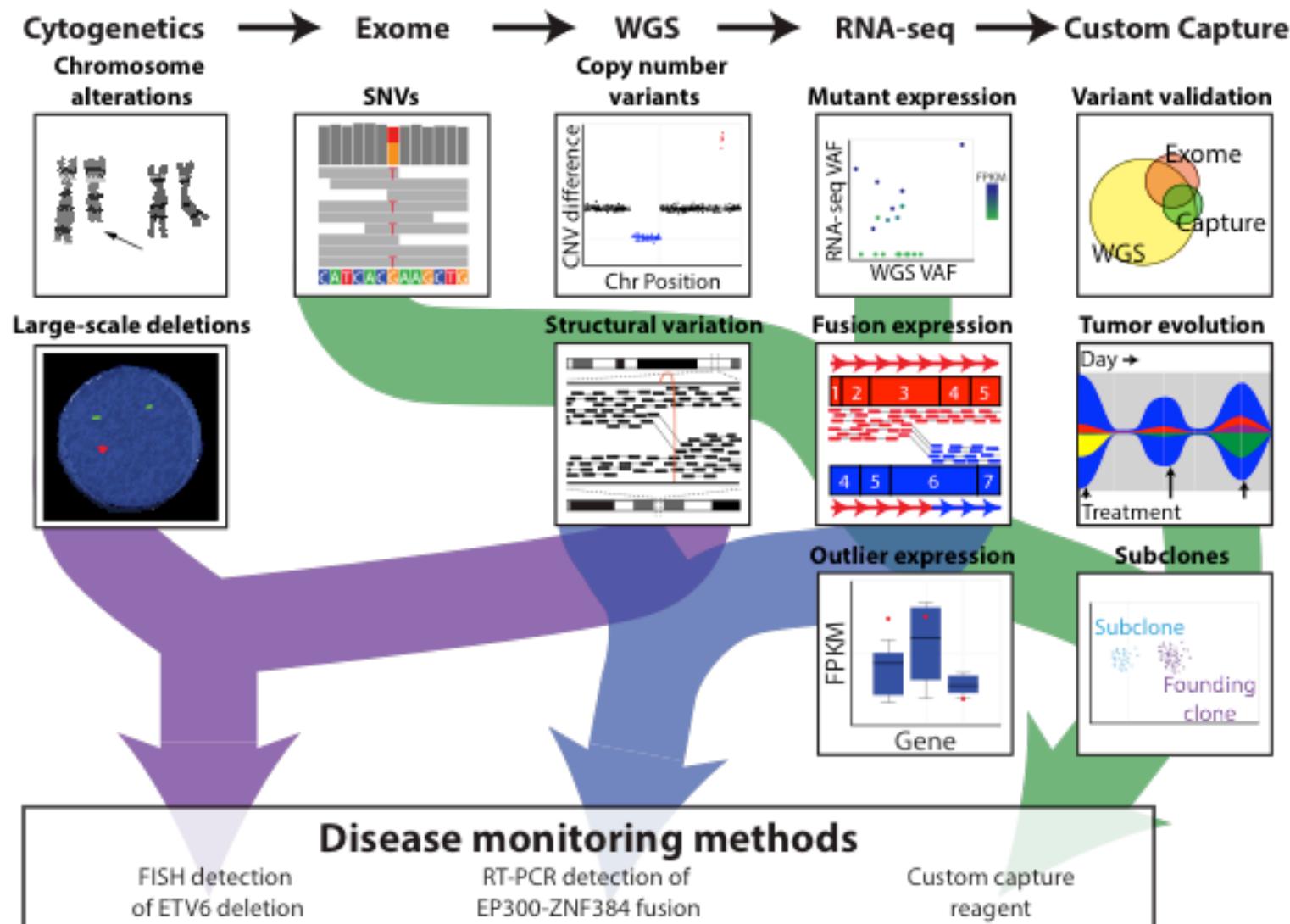
Whole genome, exome, transcriptome and other ‘omic’ sequencing allows us to detect and confirm many different variant types



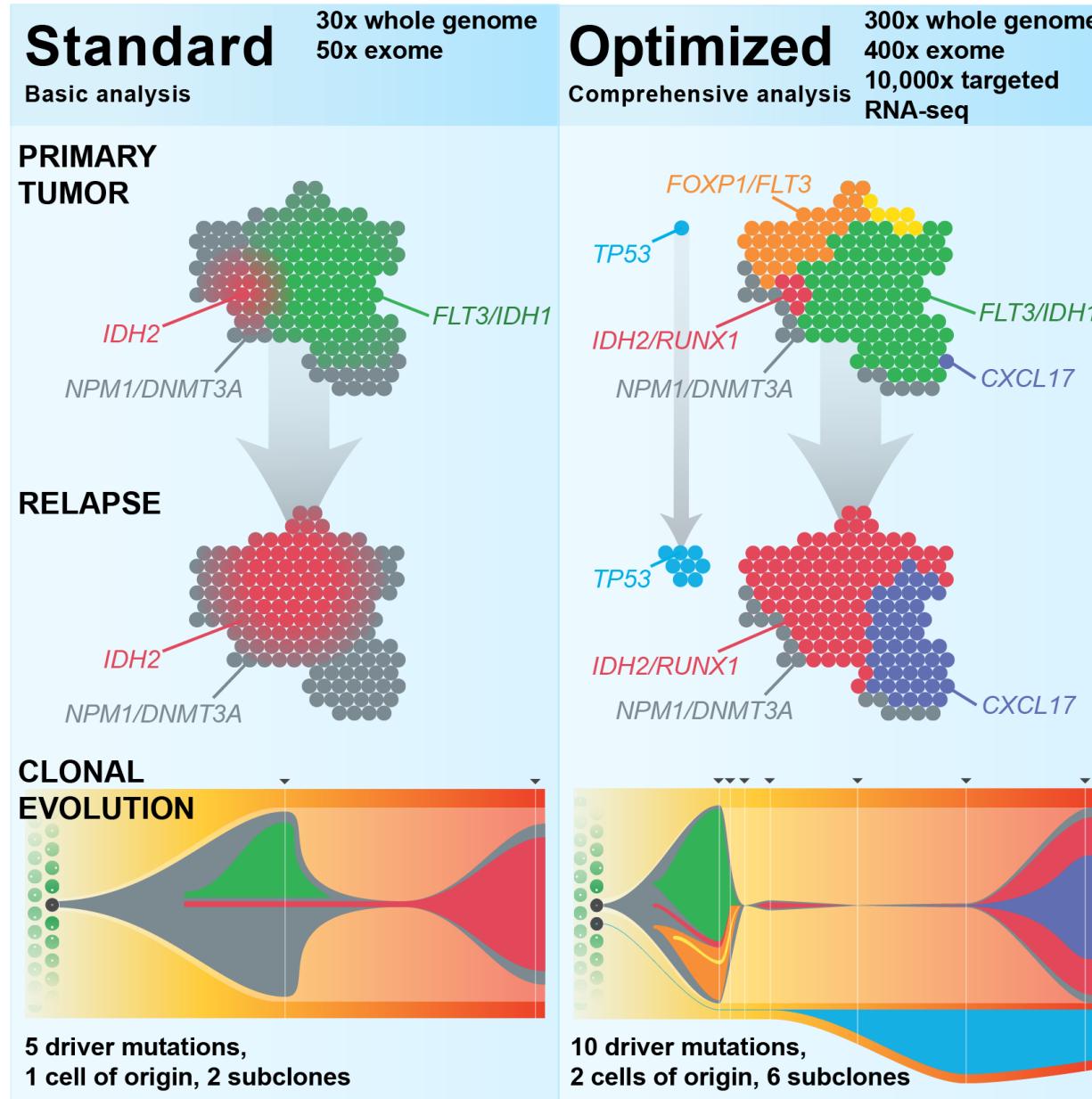
SNVs, Indels, CNVs, SVs, fusions, LOH, expression changes, methylation changes, and more



Comprehensive and integrative analysis methods are needed



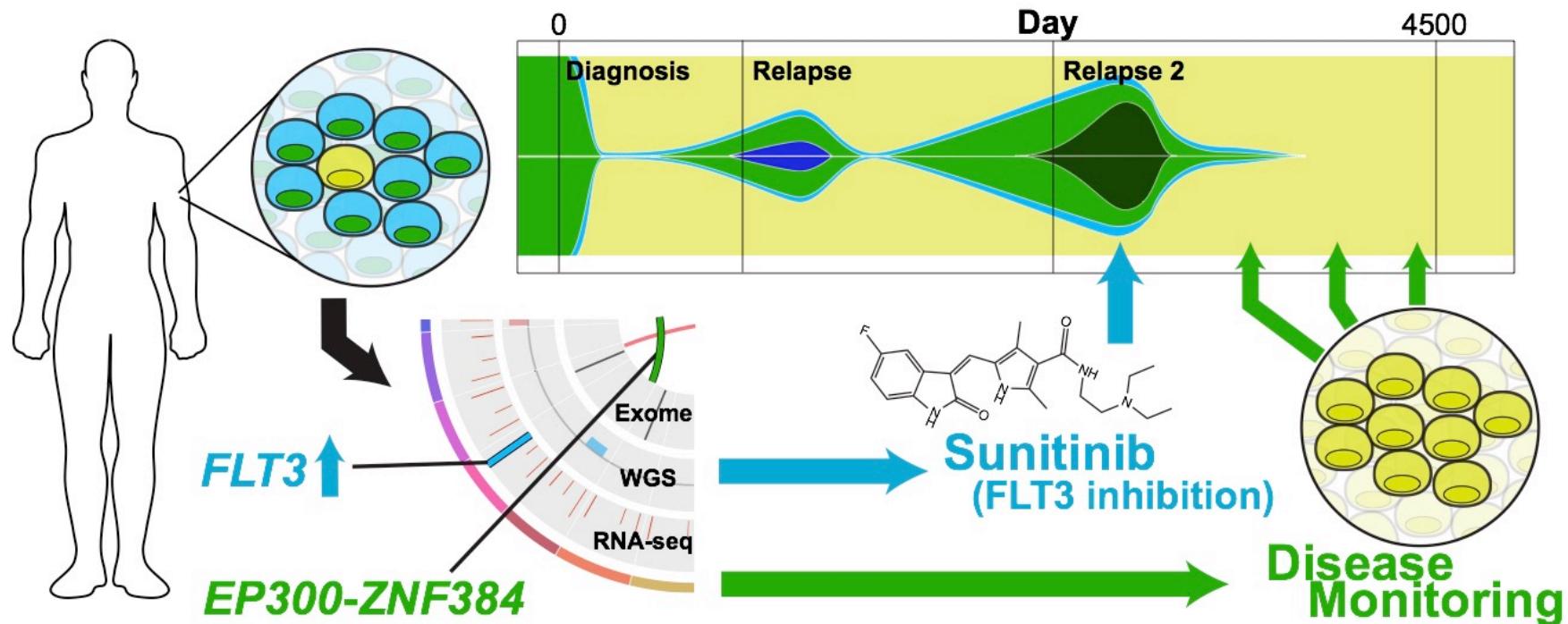
Each study often requires considerable customization



Griffith et al. 2015

Kilannin Krysiak

Personalized medicine requires personalized strategies



CrossMark

ELSEVIER

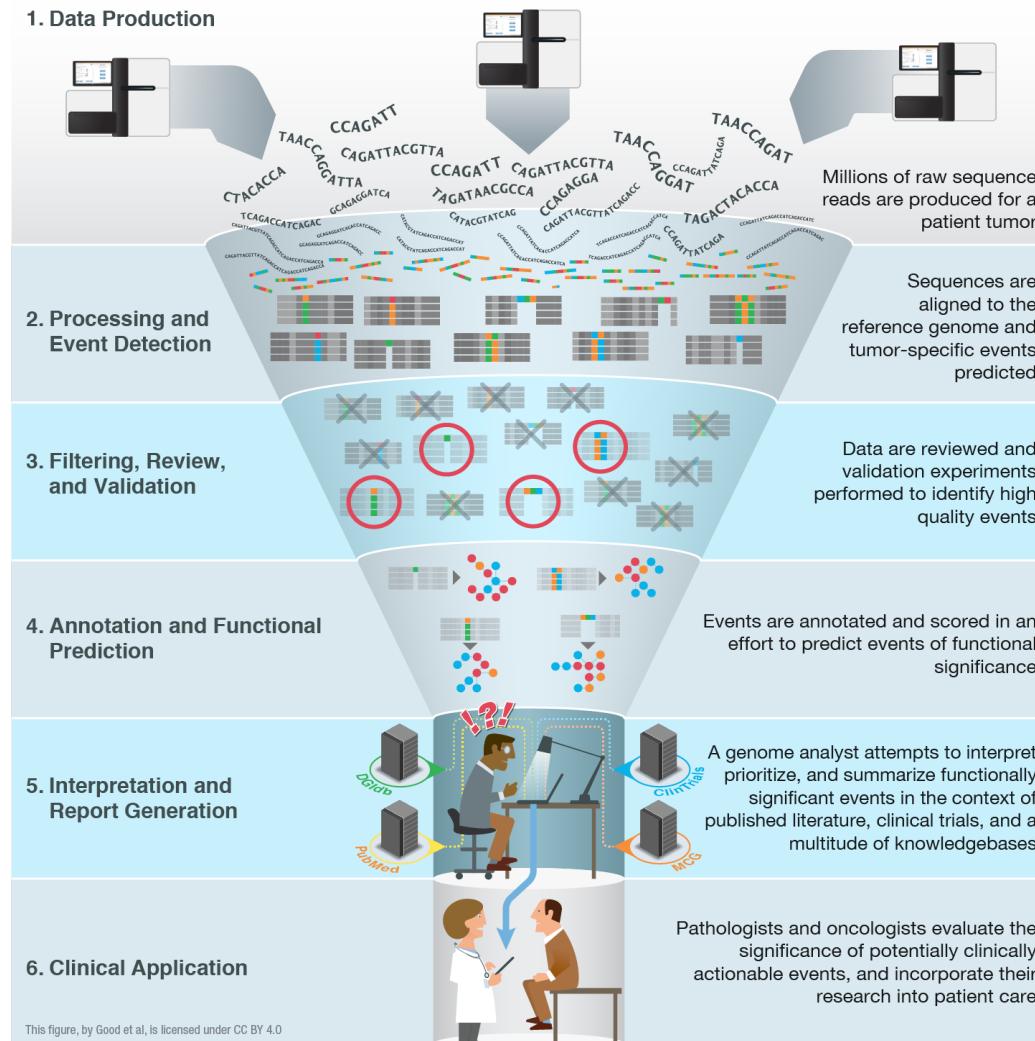
Experimental Hematology 2016;44:603–613

**Experimental
Hematology**

Comprehensive genomic analysis reveals *FLT3* activation and a therapeutic strategy for a patient with relapsed adult B-lymphoblastic leukemia

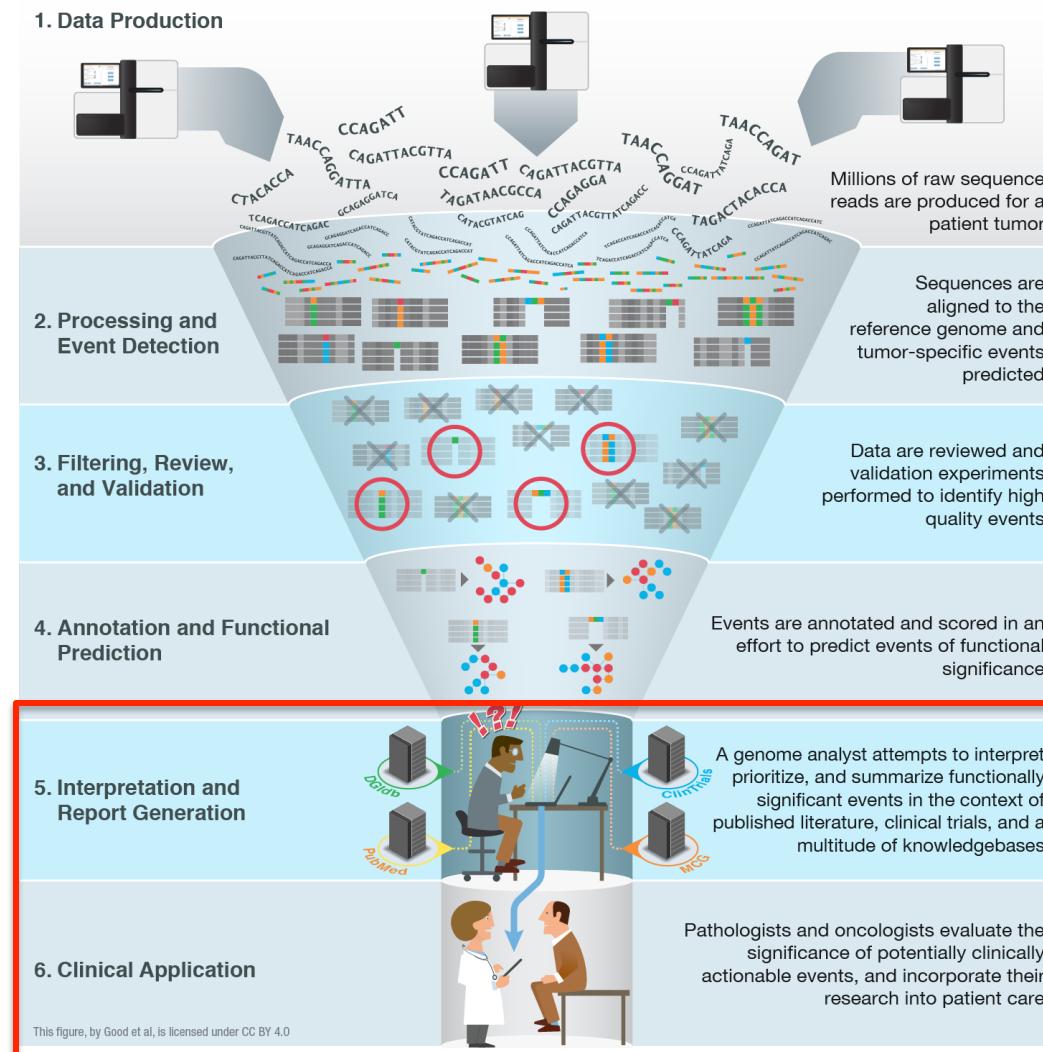
[Griffith et al. 2016](#)

High-throughput sequencing has been largely automated allowing rapid identification of somatic and germline variants



Good BM, Ainscough BJ, McMichael JF, Su AI, Griffith OL. 2014. Genome Biology. 15(8):438.

Interpretation and visualization of genomic alterations remains the bottleneck for realizing precision medicine



Good BM, Ainscough BJ, McMichael JF, Su AI, Griffith OL. 2014. Genome Biology. 15(8):438.

The Griffith lab is focused on developing methods to address this bottleneck for precision medicine in cancer

- Cancer genome analysis
 - AML
 - [Optimizing cancer genome analysis](#)
 - Breast cancer
 - [Immunotherapy](#) (cancer vaccines)
 - STAT1-/- mouse model
 - Targeted sequencing of 625 ER+ with long-term follow-up
 - Liver cancer
 - Small cell lung cancer
 - OSCC
 - Etc...
- Precision Medicine for Cancer
 - [Genomics Tumor Board](#)
 - [Case Reports](#) and [Clinical Trials](#)
- Education projects
 - [RNA-seq analysis and cloud computing](#)
 - [CSHL](#) and [CBW](#)
 - [Genomic Data Visualization/Interpretation](#)
- Tool development

Where tools/resources do not exist we build them



www.dgidb.org

Search genes for known
and potentially druggable
interactions



<https://github.com/griffithlab/pVAC-Seq>

Personalize vaccine design



www.docm.info

Filter against highly
curated set of mutations
known to cause cancer



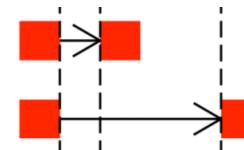
<https://github.com/griffithlab/GenVisR>

Create genomic visualizations



www.civicdb.org

Identify highly curated summaries
of clinical interpretations for
variants in cancer



regtools

<https://github.com/griffithlab/regtools>

Identify regulatory variants

Encourage best practices for software development

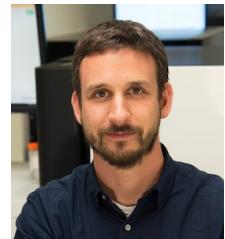
The screenshot shows the GitHub organization page for 'The Griffith Lab'. At the top, there's a header with a search bar, pull requests, issues, and a glist. Below the header, there's a profile picture of two men and the text 'The Griffith Lab' and 'Academic Lab of Obi and Malachi Griffith'. A link to their website is provided. The main navigation bar includes 'Repositories' (which is selected), 'People 25', 'Teams 21', 'Projects 0', and 'Settings'. Below the navigation, there's a search bar, filters for 'Type: All' and 'Language: All', and a button to 'Customize pinned repositories'. A green 'New' button is also present. On the left, three repository cards are listed: 'dgi-db' (Rails frontend to The Genome Institute's drug gene interaction database, Ruby, 23 stars, 14 forks, updated 2 days ago), 'pVAC-Seq' (A cancer immunotherapy pipeline, Python, 37 stars, 33 forks, updated 2 days ago), and 'GenVisR' (Genome data visualizations, R, 95 stars, 37 forks, updated 2 days ago). To the right, there's a 'Top languages' section with a pie chart and a 'People' section showing 25 members with their profile pictures.

- All code deposited in Github
 - 35 repos for different software/projects
 - Virtually all public and open-source
 - Test-driven, code review, pull requests, etc

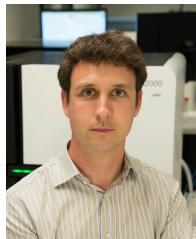
<https://github.com/griffithlab>

<https://github.com/genome>

Acknowledgements: Griffith Lab group members



Malachi
Griffith



Obi
Griffith



Benjamin
Ainscough



Erica
Barnell



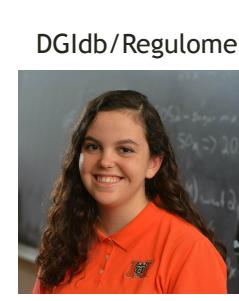
Katie
Campbell



Kaitlin
Clark



Adam
Coffman



Kelsy
Cotto

CIViC/
Regulome

Regtools/
pVAC-seq

Lymphoma

pVAC-seq

pVAC-
seq/CIViC

CIViC/
Lymphoma

CIViC

HCC



Arpad
Danos



Yang-Yang
Feng



Felicia
Gomez



Jasreet
Hundal



Susanna
Kiwala



Kilanin
Krysiak



Lynzey
Kujan



Jason
Kunisaki

CIViC

CIViC
Lymphoma

genVisR
HCC/SCLC

CIViC/Komen

HCC/SCLC

DGIdb
SCLC

Director
Informatics



Josh
McMichael



Cody
Ramirez



Zachary
Skidmore



Nick
Spies



Lee
Trani



Alex
Wagner



Jason
Walker

Acknowledgements: McDonnell Genome Institute

McDonnell Genome Institute @ Washington University School of Medicine

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Susan Dutcher
Tim Ley

Bob Fulton
Lucinda Fulton
Ira Hall
Dave Larson
Chris Maher
Lukas Wartman

Matt Callaway
Chris Miller
Jason Walker

Genomic Data Visualization and Interpretation

- Course goals - by the end of the course we hope you will:
 - Have a solid understanding of basic computational biology techniques for interpreting data
 - Be familiar with a variety of web resources (e.g., genome browsers and portals) to aid in the interpretation of omic data
 - Be able to use R graphical programs for data visualization (e.g., ggplot2, GenVisR) and interactive visualization (e.g., shiny)
 - Be able to perform, visualize, and interpret expression, differential expression and pathway analysis
 - Be able to assess a variant's biological and clinical significance (e.g., VEP, ClinVar, and CIViC)
- What this course does not cover:
 - Upstream genome analysis (alignment, variant calling, assembly, etc, etc)
 - Linux command line and other core bioinformatics skills
- This is a brand new workshop for us - feedback welcome!

Advanced Sequencing Technologies and Applications at CSHL

The screenshot shows the homepage of the Cold Spring Harbor Laboratory Meetings & Courses Program. At the top left is the CSHL logo and the text "Cold Spring Harbor Laboratory MEETINGS & COURSES PROGRAM". Below the logo are five small images: a lake view with a building, people playing frisbee, a sailboat on the water, two people working at a table, and a large DNA helix sculpture. A dark blue navigation bar below these images contains three links: "Home", "Meetings", and "Courses". Underneath the navigation bar are two larger images: one showing several people in a laboratory setting, and another showing four people gathered around a table in a workshop or lab environment. At the bottom of the page is a light blue footer menu with the following items: Welcome, Travel & Location, Application, Sponsors & Stipends, Information, Payments, Policies, and a blank space.

Welcome Travel & Location Application Sponsors & Stipends Information Payments Policies

Advanced Sequencing Technologies & Applications

November 7 - 18, 2017

Application Deadline: July 15, 2017

Instructors:

Obi Griffith, Washington University School of Medicine

Malachi Griffith, Washington University School of Medicine

Elaine Mardis, Washington University School of Medicine

W. Richard McCombie, Cold Spring Harbor Laboratory

Aaron Quinlan, University of Utah

<http://meetings.cshl.edu/courses.aspx?course=C-SEQTEC&year=17>

Canadian Bioinformatics Workshop Series

2017 Workshop Program

One Early Application Fee Deadline for All Workshops: April 3rd, 2017



High-Throughput Biology: From Sequence to Networks

March 20 - 26, 2017 - Cold Spring Harbor, New York

INSTRUCTORS: Guillaume Bourque, Mathieu Bourgey, Florence Cavalli, Michael Hoffman, Veronique Voisin, Juri Reimand, Jared Simpson, Fouad Yousif, Robin Haw, Obi Griffith, and Malachi Griffith



Infectious Disease Genomic Epidemiology

May 1 - 3, 2017 - Vancouver, BC

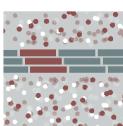
INSTRUCTORS: Will Hsiao, Gary Van Domselaar, Ed Taboada, Andrew McArthur, Robert Beiko, Jennifer Gardy



Bioinformatics of Genomic Medicine

May 10 - 11, 2017 - Downtown Toronto, ON

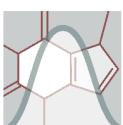
INSTRUCTORS: Guillaume Bourque, Michael Brudno, Anna Goldenberg, Andrei Turinsky, and Carl Virtanen



Informatics on High-Throughput Sequencing Data

May 25 - 26, 2017 - Downtown Toronto, ON

INSTRUCTORS: Guillaume Bourque, Mathieu Bourgey, Florence Cavalli, and Jared Simpson



Informatics and Statistics for Metabolomics

June 6-7, 2017 - Downtown Toronto, ON

INSTRUCTORS: David Wishart and Jeff Xia



Introduction to R

June 12, 2017 - Downtown Toronto, ON

INSTRUCTOR: Boris Steipe



Bioinformatics for Cancer Genomics

May 29 - June 2, 2017 - Toronto, Ontario

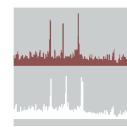
INSTRUCTORS: Trevor Pugh, Anna Goldenberg, Andrew McPherson, Francis Ouellette, Juri Reimand, Jared Simpson, Fouad Yousif, Robin Haw, Fong Chun Chan, and Lincoln Stein



Exploratory Analysis of Biological Data using R

June 13 - 14, 2017 - Downtown Toronto, ON

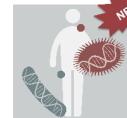
INSTRUCTOR: Boris Steipe



Epigenomic Data Analysis

June 15 - 16, 2017 - Montreal, QC

INSTRUCTORS: Guillaume Bourque, Martin Hirst, David Bujold, and Misha Bilenky



Microbiome Summer School

June 19 - 22, 2017 - Quebec City, QC

INSTRUCTORS: Jacques Corbeil, Robert Beiko, Will Hsiao, Morgan Langille, Fiona Brinkman, John Parkinson, Frédéric Raymond, Marie-Pierre Dubé, Anna Goldenberg, François Laviolette, Alexandre Drouin, Mario Marchand, and Chloé-Agathe Azencott



Pathway and Network Analysis of -omics Data

June 26 - 28, 2017 - Downtown Toronto, ON

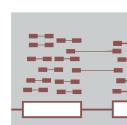
INSTRUCTORS: Gary Bader, Michael Hoffman, Quaid Morris, Juri Reimand, Lincoln Stein, Robin Haw, and Veronique Voisin



Cloud Computing in Bioinformatics with Big Data

July 5 - 6, 2017 - Downtown Toronto, ON

INSTRUCTORS: Francis Ouellette, Mark Phillips, George Mihaiescu, Christina Yung, and Solomon Shorser



Informatics for RNA-Seq Analysis

July 10 - 12, 2017 - Downtown Toronto, ON

INSTRUCTORS: Obi Griffith, Malachi Griffith, Fouad Yousif, and Brian Haas

Student introductions

- Please introduce yourself: Name, affiliation and area of research
- Student poll
 - Are you doing genomics research?
 - Do you consider yourself a bioinformatician?
 - What kind of NGS data are you working with?
 - WGS?
 - Exome?
 - RNAseq?
 - Epigenome?
 - Other?
 - What organism do you work with?
 - Did you bring data?

Student poll continued

- Are you familiar with linux/command line?
 - Intermediate?
 - Expert?
- Do you sometimes write code?
 - What language?
- Are you familiar with R?
 - Intermediate?
 - Expert?
- Are you familiar with ggplot?
 - Intermediate?
 - Expert?
- Do you use git/github?