



Cold
Spring
Harbor
Laboratory

Advanced Sequencing Technologies & Bioinformatics Analysis (Virtual)

<http://meetings.cshl.edu/courses.html>

Introductions to Bioinformatics instructors

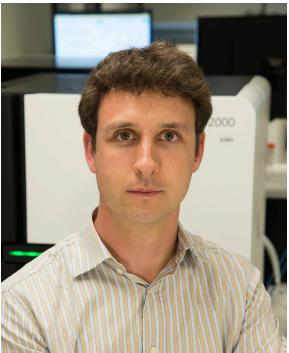


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Megan Richters
PhD candidate

PETTI LAB



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Simone Longo
Graduate Student

 **GRIFFITH LAB**

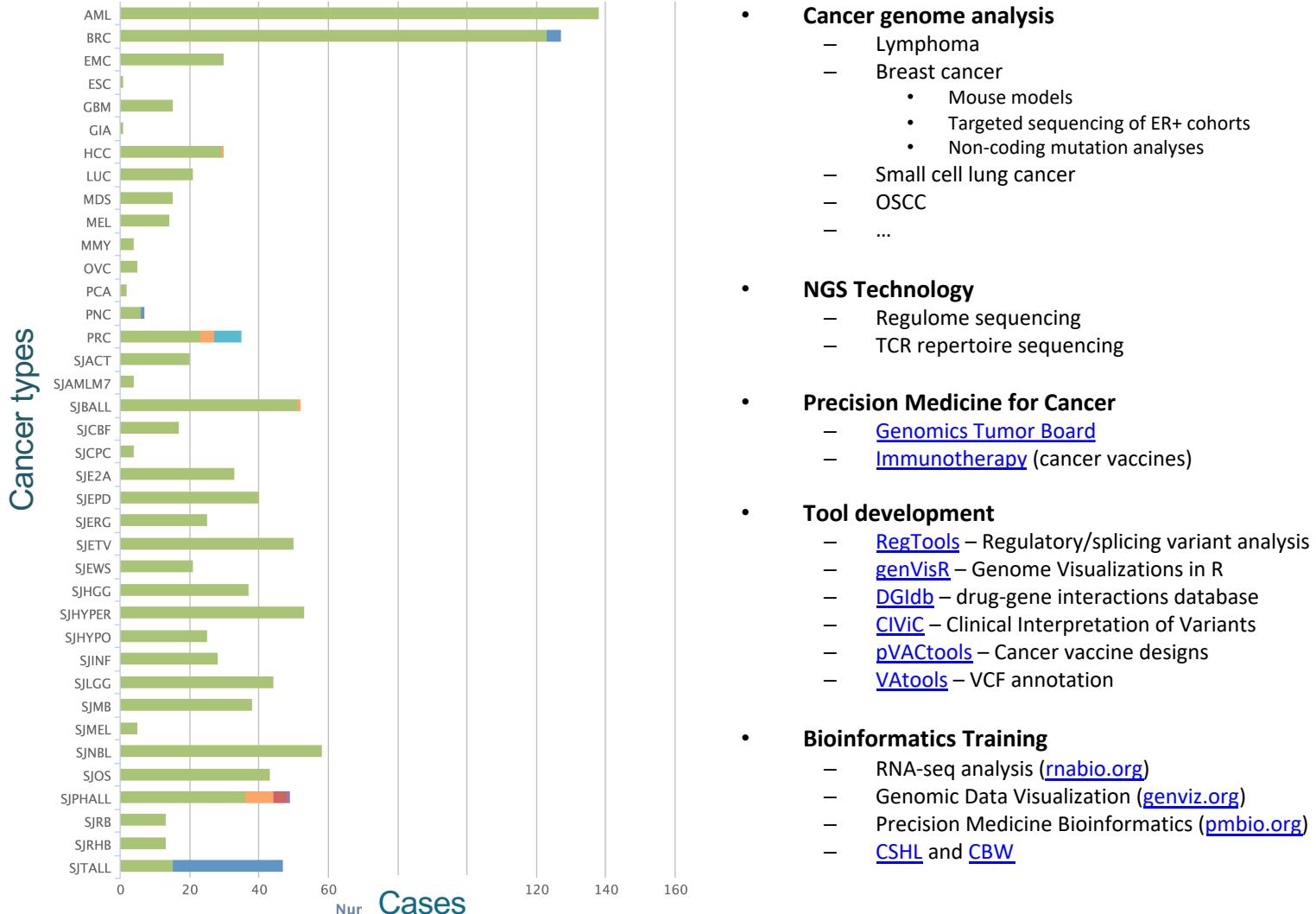
griffithlab.org rnabio.org genviz.org pmbio.org

 Washington University in St. Louis
SCHOOL OF MEDICINE

QUINLAN LAB @ UU

 THE
UNIVERSITY
OF UTAH

Griffith Lab activities are cancer genomics (informatics) focused: new discovery, translation, method development and training



- **Cancer genome analysis**
 - Lymphoma
 - Breast cancer
 - Mouse models
 - Targeted sequencing of ER+ cohorts
 - Non-coding mutation analyses
 - Small cell lung cancer
 - OSCC
 - ...
- **NGS Technology**
 - Regulome sequencing
 - TCR repertoire sequencing
- **Precision Medicine for Cancer**
 - [Genomics Tumor Board](#)
 - [Immunotherapy](#) (cancer vaccines)
- **Tool development**
 - [RegTools](#) – Regulatory/splicing variant analysis
 - [genVisR](#) – Genome Visualizations in R
 - [DGIdb](#) – drug-gene interactions database
 - [CIVIC](#) – Clinical Interpretation of Variants
 - [pVACtools](#) – Cancer vaccine designs
 - [VAtools](#) – VCF annotation
- **Bioinformatics Training**
 - RNA-seq analysis ([rnabio.org](#))
 - Genomic Data Visualization ([genviz.org](#))
 - Precision Medicine Bioinformatics ([pmbio.org](#))
 - [CSHL](#) and [CBW](#)

www.griffithlab.org

Introduction to SEQTEC Informatics – philosophy and goals

Do “the bioinformatics” for someone, and you help them for a day. Teach someone to do bioinformatics, and you help them for a lifetime.

- Ancient Chinese proverb

- Course goals
 - Learn concepts and develop skills for sequence analysis
 - Build the foundation for tackling your own analysis challenges
 - Learn to think like a bioinformatician
 - Have fun

Course outline

Monday - Introduction to technologies

Tuesday - Bioinformatics basics and NGS data fundamentals

Wednesday - RNAseq expression analysis

Thursday - RNAseq differential expression analysis

Friday - Single cell RNAseq

Course format for a typical day

- Lecture
- BREAK
- Lunch
- Practical exercises
- BREAK
- Practical exercises
- Wrap-up and Q&A

Student poll

Not counting the pre-requisites and materials for this course:

- Do you consider yourself a bioinformatician?
- Are you familiar with linux/command line?
 - Intermediate?
 - Expert?
- Do you sometimes write code?
- Are you familiar with R?
 - Intermediate?
 - Expert?
- Do you use git/github?
- What organism do you work with?
- Are you interested in bulk RNAseq (Yes), scRNAseq (No), or both (hand)?
- Who has a dual monitor setup?

An overview of bioinformatics

Adam Siepel

Professor, Watson School of Biological Sciences; Chair, Simons Center
for Quantitative Biology; Cold Spring Harbor Laboratory

Opinion | [Open Access](#) | Published: 29 July 2019

Challenges in funding and developing genomic software: roots and remedies

[Adam Siepel](#) 

[Genome Biology](#) 20, Article number: 147 (2019) | [Cite this article](#)

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