# ZOE JUNE F. ASSAF, PH.D.

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## HIGHLIGHTS OF QUALIFICATIONS

Scientist with >10 years of experience in genomics and cell-free DNA diagnostic testing

- Expert in the analysis & interpretation of genomic data (WGS, WES, RNAseq, targeted NGS)
- Fluent programmer in *R/Bioconductor* (primary); also familiar with *bash , Python, SQL, Java, C++, Perl*
- Expert in NGS assay development for monitoring cell-free tumor DNA in cancer patients
- Builder of bioinformatics pipelines on Unix & cloud computing systems (bwa, samtools, GATK, etc*)*
- Highly trained geneticist with a background in statistics, probability, and modeling in genomics
- Successful contributor and manager of collaborations with pharmaceutical and academic partners
- Demonstrated experience working on interdisciplinary teams to generate impactful publications

## EDUCATION

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| Ph.D. | Genetics, Stanford University, 2010-2016 |
| B.A. | Molecular and Cell Biology, U.C. Berkeley, 2003-2007 |

## INDUSTRY AND ACADEMIC RESEARCH EXPERIENCE

**Genentech**, South San Francisco CA
gRED Translational Medicine | Oncology Biomarkers | Data Science Group
Principal Scientist, Bioinformatics (06/2021 –Present)
Senior Scientist, Bioinformatics (01/2019 –06/2021)

- Drive the application of bioinformatics and analytics methods to large clinical biomarker datasets, including the use of machine learning methods with high throughput NGS genomic data to identify biomarkers predictive of survival and response to therapy
- Lead circulating tumor DNA (ctDNA) analysis efforts within the Oncology Biomarker Development department, including educating team members on current ctDNA technologies, applying advanced analytics to ctDNA datasets, and collaborating effectively within and across departments
- Support biomarker and diagnostic development efforts in Genentech's oncology pipeline, including the identification of predictive biomarkers of treatment response and execution on companion diagnostic strategies for programs in clinical development
- Effectively interact with cross functional teams, and manage internal and external scientific collaborations with key opinion leaders and investigators
- Publish regularly and well in high-impact biomarker and oncology research journals

**Natera**, San Carlos CA (01/2017 –01/2019)
Senior Bioinformatician, Research & Development

- Supported the genomics research and development of Natera's cell-free DNA oncology test –
    - Used whole-exome sequence data to design personalized assays of circulating tumor DNA

    - Implemented novel sample quality-control metrics, including a maximum likelihood algorithm to detect sample contamination
    - Generated new hypotheses to explain unexpected variations in error rates across studies, and tested hypotheses via error rate and read mapping simulations
    - Routinely built bioinformatics pipelines on Unix and remote high-performance compute clusters, including read quality control, read mapping, and variant calling
    - Designed data visualization pipelines in R, including one used by entire oncology team to share results with bench scientists, pharmaceutical partners, and academic collaborators
    - Used diverse data types and sources (WES, WGS, microarrays, dbSNP, gnomad, TCGA, Ensembl, UCSC genome browser, 1000 genome, etc)
    - Bioinformatics Lead on scientific collaborations with pharmaceutical partners, including managing bioinformatics analyses and communication of results to partners
    - Co-author contributor to academic collaborations
- Bioinformatics Lead on teams improving Natera's FDA-approved cell-free DNA prenatal tests –
    - Analyzed high-throughput genomic data, including building and running simulations to improve indel-calling algorithms
    - Led the bioinformatics research effort for improving the preimplantation genetic test for aneuploidy in embryos (Spectrum) and the prenatal screen of single-gene disorders (Vistara)
- Developed/maintained Natera's version-controlled software for massively-multiplexed-PCR panel design in *Java*, including algorithm improvements for research projects and core products.

**Stanford University** (2010 - 2016)
Genetics Ph.D. Student, advised by DA Petrov

- Studied mutation rates, patterns, and fates in the genomes of real and modeled populations
- Discovered novel patterns of mutation, including co-occurrence of mutations at long genomic distances (~1kb), persistent effects of neighbor-dependent mutations in genes, and mutational biases which changed with local GC-content (published in Genome Research, Dec. 2017).
- Built a new mathematical model to describe how deleterious mutations can slow adaptation, and validated it with forward simulations of genome evolution (published in PNAS, May 2015).
- Experimentally generated a dataset of *de novo* ('new') mutations which was the largest such genomic dataset to exist in any model organism.
- Developed computational pipelines to process Whole Genome Sequencing DNA data in a high performance computing environment, including quality control, read mapping, and variant calling.
- Communicated my research via oral presentations at domestic and international scientific conferences (10+ presentations, including at SMBE and TAGC).
- Won an NSF GRFP award, a prestigious graduate student fellowship.

**UC Berkeley** (2008 - 2010)
Staff Research Associate, advised by ZA Cande

- Used molecular approaches to study cytoskeletal dynamics in multiple eukaryotic species
- Co-authored 4 papers (as 2nd author), including work which discovered that *Giardia intestinalis* has a functioning actin cytoskeleton despite the absence of classic actin-binding proteins (PNAS 2011).

## TECHNICAL SKILLS

- **NGS:** read quality control, mapping, variant calling, error rate modeling, maximum likelihood

- **Data:** whole-exome, whole-transcriptome, whole-genome, microarrays, 1000 genome, dbSNP, gnomad, TCGA, etc.
- **Bioinformatics software**: PicardTools, bwa, novoalign, samtools, GATK, Varscan, Mutect, bcftools, snpEff, Bioconductor for R, etc. Also experienced in DNAnexus.
- **Programming languages**: [1] R/Bioconductor, bash, SQL [2] Python, Perl, Java, C++, git, Shiny for R.

## PUBLICATIONS (18 published, 1 under review)

1. Solange Peters, Shirish M. Gadgeel, Tony Mok, Ernest Nadal, Saadettin Kilickap, Aurélie Swalduz, Jacques Cadranel, Shunichi Sugawara, Chao-Hua Chiu, Chong-Jen Yu, Mor Moskovitz, Tomohiro Tanaka, Rhea Nersesian, Sarah M. Shagan, Margaret Maclennan, Michael Mathisen, Vijay Bhagawati-Prasad, Cheick Diarra, Zoe June Assaf, Venice Archer, Rafal Dziadziuszko. *Efficacy and safety of entrectinib in patients with ROS1-positive advanced/metastatic non-small cell lung cancer (NSCLC) from the Blood First Assay Screening Trial (BFAST)*. (Accepted at Nature Medicine)
2. Thomas Powles, Amanda Young, Halla Nimeiri, Russell W Madison, Alexander Fine, Daniel R Zollinger, Yanmei Huang, Chang Xu, Ole V Gjoerup, Vasily N Aushev, Hsin-Ta Wu, Alexey Aleshin, Corey Carter, Nicole Davarpanah, Viraj Degaonkar, Pratyush Gupta, Sanjeev Mariathasan, Erica Schleifman, **Zoe June Assaf**, Geoffrey Oxnard and Priti Hegde. *Molecular residual disease detection in resected, muscle-invasive urothelial cancer with a tissue-based comprehensive genomic profiling-informed personalized monitoring assay.* Frontiers in Oncology. 2023 Jul 31:13:1221718. doi: 10.3389/fonc.2023.1221718.
3. *Thomas Powles, ***Zoe June Assaf (*co-first)**, Viraj Degaonkar, Petros Grivas, Maha Hussain, Stephane Oudard, Jürgen E. Gschwend, Peter Albers, Daniel Castellano, Hiroyuki Nishiyama, Siamak Daneshmand, Shruti Sharma, Himanshu Sethi, Alexey Aleshin, Yi Shi, Nicole Davarpanah, Corey Carter, Joaquim Bellmunt, Sanjeev Mariathasan. *Updated Overall Survival by Circulating Tumor DNA Status from the Phase 3 IMvigor010 Trial: Adjuvant Atezolizumab Versus Observation in Muscle-invasive Urothelial Carcinoma*. European Urology, 2023, ISSN 0302-2838, https://doi.org/10.1016/j.eururo.2023.06.007.
4. **Zoe June F. Assaf**, Wei Zou, Alexander D. Fine, Mark A. Socinski, Amanda Young, Doron Lipson, Jonathan F. Freidin, Mark Kennedy, Eliana Polisecki, Makoto Nishio, David Fabrizio, Geoffrey R. Oxnard, Craig Cummings, Anja Rode, Martin Reck, Namrata S. Patil, Mark Lee, David S. Shames & Katja Schulze. *A longitudinal circulating tumor DNA-based model associated with survival in metastatic non-small-cell lung cancer.* Nature Medicine volume 29, pages 859–868 (2023). doi: 10.1038/s41591-023-02226-6. Epub 2023 Mar 16. PMID: 36928816; PMCID: PMC10115641.
5. Bernadett Szabados, Mark Kockx, **Zoe June Assaf**, Pieter-Jan van Dam, Alejo Rodriguez-Vida, Ignacio Duran, Simon J. Crabb, Michiel S. Van Der Heijden, Albert Font Pous, Gwenaelle Gravis, Urbano Anido Herranz, Andrew Protheroe, Alain Ravaud, Denis Maillet, Maria Jose Mendez, Cristina Suarez, Mark Linch, Aaron Prendergast, Charlotte Tyson, Diana Stanoeva, Sofie Daelemans, Miche Rombouts, Sanjeev Mariathasan, Joy S. Tea, Kelly Mousa, Shruti Sharma, Alexey Aleshin, Romain Banchereau, Daniel Castellano, Thomas Powles. *Final Results of Neoadjuvant Atezolizumab in Cisplatin-ineligible Patients with Muscle-invasive Urothelial Cancer of the Bladder*. European Urology. April 2022. ISSN 0302-2838. https://doi.org/10.1016/j.eururo.2022.04.013.
6. *Thomas Powles, ***Zoe June Assaf (*co-first)**, Nicole Davarpanah, Petros Grivas, Maha Hussain, Stephane Oudard, Jürgen E. Gschwend, Peter Albers, Daniel Castellano, Hiroyuki Nishiyama, Siamak Daneshmand, Shruti Sharma, Bernhard G. Zimmermann, Himanshu Sethi, Alexey Aleshin, Jingbin Zhang, Romain Banchereau, David S. Shames, Viraj Degaonkar, Xiaodong Shen, Corey Carter, Carlos

Bais, Joaquim Bellmunt, Sanjeev Mariathasan. *ctDNA guiding adjuvant immunotherapy in urothelial carcinoma.* Nature 595, 432–437 (2021). PMID 34135506.

7. Rafal Dziadziuszko, Tony Mok, Solange Peters, Ji-Youn Han, Jorge Alatorre-Alexander, Natasha Leighl, Virote Sriuranpong, Maurice Pérol, Gilberto de Castro Junior, Ernest Nadal, Filippo de Marinis, Osvaldo Arén Frontera, Daniel S.W. Tan, Dae Ho Lee, Hye Ryun Kim, Mark Yan, Todd Riehl, Erica Schleifman, Sarah M. Paul, Simonetta Mocci, Rajesh Patel**, Zoe June Assaf**, David S. Shames, Michael S. Mathisen, Shirish M. Gadgeel. *Blood First Assay Screening Trial (BFAST) in Treatment-Naive Advanced or Metastatic NSCLC: Initial Results of the Phase 2 ALK-Positive Cohort*. Journal of Thoracic Oncology. Jul 24 2021. PMID: 34311110.
8. Romain Banchereau, Ning Leng, Oliver Zill, Ethan Sokol, Gengbo Liu, Dean Pavlick, Sophia Maund, Li-Fen Liu, Edward Kadel, III, Nicole Baldwin, Suchit Jhunjhunwala, Dorothee Nickles, **Zoe June Assaf**, Daniel Bower, Namrata Patil, Mark McCleland, David Shames, Luciana Molinero, Mahrukh Huseni, Shomyseh Sanjabi, Craig Cummings, Ira Mellman, Sanjeev Mariathasan, Priti Hegde, and Thomas Powles. *Molecular determinants of response to PD-L1 blockade across tumor types.* Nature Communications. 12, 3969 (2021). PMID: 34172722
9. Kater AP, Wu JQ, Kipps T, Eichhorst B, Hillmen P, D'Rozario J, Assouline S, Owen C, Robak T, de la Serna J, Jaeger U, Cartron G, Montillo M, Dubois J, Eldering E, Mellink C, Van Der Kevie-Kersemaekers AM, Kim SY, Chyla B, Punnoose E, Bolen CR, **Assaf ZJ**, Jiang Y, Wang J, Lefebure M, Boyer M, Humphrey K, Seymour JF. *Venetoclax Plus Rituximab in Relapsed Chronic Lymphocytic Leukemia: 4-Year Results and Evaluation of Impact of Genomic Complexity and Gene Mutations From the MURANO Phase III Study.* Journal of Clinical Oncology. 2020 Sep 28:JCO2000948. PMID: 32986498.
10. Reinert T, Henriksen TV, Christensen E, Sharma S, Salari R, Sethi H, Knudsen M, Nordentoft I, Wu HT, Tin AS, Heilskov Rasmussen M, Vang S, Shchegrova S, Frydendahl Boll Johansen A, Srinivasan R, **Assaf ZJ**, Balcioglu M, Olson A, Dashner S, Hafez D, Navarro S, Goel S, Rabinowitz M, Billings P, Sigurjonsson S, Dyrskjøt L, Swenerton R, Aleshin A, Laurberg S, Husted Madsen A, Kannerup AS, Stribolt K, Palmelund Krag S, Iversen LH, Gotschalck Sunesen K, Lin CJ, Zimmermann BG, Lindbjerg Andersen C. *Analysis of Plasma Cell-Free DNA by Ultradeep Sequencing in Patients With Stages I to III Colorectal Cancer.* JAMA Oncology. 2019 May 9;5(8):1124–31. PMID: 31070691.
11. Christensen E, Birkenkamp-Demtröder K, Sethi H, Shchegrova S, Salari R, Nordentoft I, Wu HT, Knudsen M, Lamy P, Lindskrog SV, Taber A, Balcioglu M, Vang S, **Assaf ZJ**, Sharma S, Tin AS, Srinivasan R, Hafez D, Reinert T, Navarro S, Olson A, Ram R, Dashner S, Rabinowitz M, Billings P, Sigurjonsson S, Andersen CL, Swenerton R, Aleshin A, Zimmermann B, Agerbæk M, Lin CJ, Jensen JB, Dyrskjøt L. *Early Detection of Metastatic Relapse and Monitoring of Therapeutic Efficacy by Ultra-Deep Sequencing of Plasma Cell-Free DNA in Patients With Urothelial Bladder Carcinoma*. Journal of Clinical Oncology. 2019 Jun 20;37(18):1547-1557. PMID: 31059311.
12. Coombes RC, Page K, Salari R, Hastings RK, Armstrong A, Ahmed S, Ali S, Cleator S, Kenny L, Stebbing J, Rutherford M, Sethi H, Boydell A, Swenerton R, Fernandez-Garcia D, Gleason KLT, Goddard K, Guttery DS, **Assaf ZJ**, Wu HT, Natarajan P, Moore DA, Primrose L, Dashner S, Tin AS, Balcioglu M, Srinivasan R, Shchegrova SV, Olson A, Hafez D, Billings P, Aleshin A, Rehman F, Toghill BJ, Hills A, Louie MC, Lin CJ, Zimmermann BG, Shaw JA. *Personalized Detection of Circulating Tumor DNA Antedates Breast Cancer Metastatic Recurrence*. Clinical Cancer Resesearch. 2019 Jul 15;25(14):4255-4263. PMID: 30992300.
13. **Assaf ZJ**, Tilk S, Park J, Siegal ML, Petrov DA. *Deep Sequencing of Natural and Experimental Populations of Drosophila melanogaster Reveals Biases in the Spectrum of New Mutations.* Genome Research (Dec **2017**). 27(12):1988-2000. PMID: 29079675.

14. Wilson BA*, Garud NR*, Feder AF*, **Assaf ZJ* (*co-first)**, Pennings PS. *The population genetics of drug resistance evolution in viral, bacterial, and eukaryotic pathogens.* Molecular Ecology (**2016**). Jan; 25(1):42-66. PMID: 26578204. Review.
15. **Assaf ZJ**, Petrov DA, Blundell JR. *Obstruction of adaptation in diploids by recessive, strongly deleterious alleles.* Proceedings of the National Academy of Sciences (**2015**). 19;112(20)E2658-66. PMID: 25941393
16. Carpenter ML, **Assaf ZJ**, Gourguechon S, Cande WZ. Nuclear inheritance and genetic exchange without meiosis in the binucleate parasite Giardia intestinalis. Journal of Cell Science (2012). 125(Pt 10):2523-32. PMID: 22366460
17. Paredez AR, **Assaf ZJ**, Sept D, Timofejeva L, Dawson SC, Wang CJ, Cande WZ. An actin cytoskeleton with evolutionarily conserved functions in the absence of canonical actin-binding proteins. Proceedings of the National Academy of Sciences (2011). 108(15):6151-6. PMID: 21444821 | PubMed
18. Harper NC*, Rillo R*, Jover-Gil S*, **Assaf ZJ**, Bhalla N, Dernburg AF. Pairing centers recruit a Polo-like kinase to orchestrate meiotic chromosome dynamics in C. elegans. Developmental Cell (2011). 21(5):934-47. PMID: 22018922 ( * contributed equally to this work)
19. Fritz-Laylin LK, **Assaf ZJ**, Chen S, Cande WZ. Naegleria gruberi de novo basal body assembly occurs via stepwise incorporation of conserved proteins. Eukaryotic Cell (2010). 9(6):860-5. PMID: 20400468