GODWIN YUNG

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EDUCATION

Harvard University, Cambridge, MA
Ph.D. in Biostatistics   *May 2016*
Thesis: "Statistical Methods for Analyzing Genetic Sequencing Association Studies"
Advisor: Xihong Lin

Harvard University, Cambridge, MA
M.A. in Biostatistics   *May 2013*

Reed College, Portland, OR
B.A. in Mathematics   *May 2010*
Thesis: "An Algorithm For The Calibration Of Fourier Transform Mass Spectrometry Signals To Improve Peptide Identification"
Advisor: Albyn Jones

WORK EXPERIENCE

Genentech, South San Francisco, CA
Principal Statistical Methodologist   *Jul 2020 – Present*

Takeda Pharmaceutical Company, Cambridge, MA
Principal Statistician   *Mar 2019 – Jun 2020*
Senior Statistician   *Jun 2016 – Mar 2019*
- Lead statistician for TOURMALINE-MM2, a phase 3 study of a proteasome inhibitor in newly diagnosed multiple myeloma.
- Program statistician for Takeda and Shattuck Lab's phase 1 investigation of two agonist redirected checkpoints in multiple cancers.
- Unblinded statistician for a matched historical control phase 2 study in metachromatic leukodystrophy, tasked with identifying prognostic factors for propensity score matching.
- Served as an internal consultant on 40+ projects, primarily for other statisticians and across various therapeutic areas (oncology, rare disease, vaccines, neuroscience, gastroenterology, safety). Projects include:
  - proposing and evaluating complex, innovative trial designs (eg, multiple endpoints, multiple interim analyses, multiple populations, and/or sample size re-estimation);
  - proving strong type I error control via methods in multiple testing (eg, partition principle, graphical method);
  - supporting an NDA by authoring a white paper on adjusting overall survival in the presence of treatment switching (eg, inverse probability weighting, marginal structural model);
  - applying statistical learning algorithms to delineate subgroups of patients who exhibit differential efficacy or safety profile (eg, best subset selection, group lasso, CART); and
  - providing intuitive yet robust responses to agency questions on survival analysis.
- Conducted independent research in survival, multiplicity, adaptive designs, and causal inference.
- Participated in post-marketing scientific publications by performing data analysis and contributing to medical writing.
- Aided pricing and market access efforts by communicating results of clinical trials to doctors and foreign reimbursement agencies (eg, real world evidence, comparative effectiveness studies).

- Provided statistical review for 100+ Investigator Initiated Sponsored Research study protocols.
- Lectured in a company-wide series on basic statistics.
- Active member in 4 working groups: statistics in cancer immunotherapy (lead), big data and biomarker predictive, complex innovative trial design, and oncology estimand (cross-industry).
- Organizer for departmental bi-weekly seminar series and summer internship program.

Harvard University, Cambridge, MA
Graduate Researcher   *Jun 2012 – May 2016*
- Developed an unsupervised machine learning algorithm to combine multiple functional annotations to predict the functional status of genetic variants.
- Developed a weighted generalized linear mixed model for the analysis of secondary outcomes in case-control genetic sequencing studies.
- Investigated the application of naïve generalized linear models for the analysis of secondary outcomes in case-control studies.
- Collaborated with Brigham and Women's Hospital, Massachusetts General Hospital, and Hong Kong Polytechnic University in genetics research.

Takeda Pharmaceutical Company, Cambridge, MA
Intern   *Summer 2014*
- Developed a resampling-based method for testing associations between high dimensional and sparse genomic data and treatment response.
- Applied method to real sequencing data and identified a promising genetic pathway.
- Performed realistic simulations to investigate variability in tumor assays.
- Simulation results were later used to evaluate and change practice at Takeda.

Brigham and Women's Hospital, Boston, MA
Research Trainee   *Jan 2012 – Jun 2012*
- Received training in genetics laboratory techniques (eg, gene cloning, DNA sequencing, in vitro transcription/translation, western blot, protein binding microarray).
- Learned quickly and performed experiments independently to determine the DNA binding specificities of transcription factors.

University of Southern California, Los Angeles, CA
Biostatistics Systems Programmer   *Sep 2010 – Jun 2011*
- Wrote a search algorithm in Python to locate three-dimensional bell curves in mass spectra and created a probabilistic model to differentiate between high and low quality bell curves.

University of California Los Angeles, Los Angeles, CA
Project Manager   *Summer 2009*
- Led 3 other undergraduates and proposed a calibration method based using Bayesian inference to improve measurements from tandem mass spectrometers.

Carnegie Mellon University, Pittsburgh, PA
Undergraduate Researcher   *Summer 2008*
- Wrote code in Excel VBA to simulate call centers with skills-based routing, a strategy that appoints incoming calls to the most suitable agent rather than the first agent available.

PUBLICATIONS

[*]First-author

Lin Lab[*], **Yung G**[*], Ionita-Laza I, Lin X. (*submitted*) A multivariate mixed model framework for predicting functional regions in the human genome.

Facon T, Venner CP, …, **Yung G**, et al. (2021) Oral ixazomib, lenalidomide, and dexamethasone for newly diagnosed transplant-ineligible multiple myeloma patients. *Blood* <https://doi.org/10.1182/blood.2020008787>.

Degtyarev E[*], Rufibach K[*], Shentu Y[*], **Yung G**[*], Casey M, Englert S, Liu F, Liu Y, Sailer O, Siegel J, Sun S, Tang R, Zhou J. (2020) Assessing the impact of COVID-19 on the clinical trial objective and analysis of oncology clinical trials—Application of the estimand framework. *Statistics in Biopharmaceutical Research* <https://doi.org/10.1080/19466315.2020.1785543>.

Yung G[*], Liu Y. (2019) Sample size and power for the weighted log-rank test and Kaplan-Meier based tests with allowance for non-proportional hazards. *Biometrics* 1-12 <https://doi.org/10.1111/biom.13196>.

Garderet L, Laubach JP, Stoppa AM, Hari P, Cavo M, Ludwig H, Mateos MV, Luptakova K, Lin J, **Yung G**, Van De Velde H, Berg D, Moreau P, Richardson PG. (2018) Association between response kinetics and outcomes in relapsed/refractory multiple myeloma: analysis from TOURMALINE-MM1. *Leukemia*.

Kumar SJ, Laubach JP, Giove TJ, Quick M, Neuwirth R, **Yung G**, Rajkumar SV, Richardson PG. (2017) Impact of concomitant dexamethasone dosing schedule on bortezomib-induced peripheral neuropathy in multiple myeloma. *British Journal of Haematology* 178:756-763.

Yung G[*], Lin X. (2016) Validity of using ad hoc methods to analyze secondary traits in case-control association studies. *Genetic Epidemiology* 40:732-473.

Chan L, Lin X, **Yung G**, Lui T, Chiu YM, Wang F, Tsui NBY, Cho WCS, Yip SP, Siu PM, Wong SCC, Yung BYM. (2015) Novel structural co-expression analysis linking NPM1-associated ribosomal biogenesis network to chronic myelogenous leukemia. *Nature Scientific Reports* 5: 10973.

PRESENTATIONS

"Innovative adaptive designs for investigational drug development in small populations", *ICSA Applied Statistics Symposium*, Virtual Conference, December 2020.

"The optimal randomization ratio in time-to-event trials is not 1:1", *ASA Biopharmaceutical Section Regulatory-Industry Statistics Workshop (Poster Session)*, Virtual Conference, September 2020.

"The optimal randomization ratio in time-to-event trials is not 1:1", *Joint Statistical Meetings*, Virtual Conference, August 2020.

"Power calculations for common, nonparametric tests in survival", *Joint Statistical Meetings,* Denver, CO, August 2019.

"A multi-dimensional integrative scoring framework for predicting functional regions in the human genome", *Joint Statistical Meetings*, Vancouver, Canada, August 2018.

"The cost of comparing survival curves using multiple measures", *Joint Statistical Meetings,* Baltimore, MD, August 2017.

"Optimal test for rare variant effects on secondary traits in case-control sequencing studies", *Joint Statistical Meetings*, Seattle, WA, August 2015.

"Secondary trait analysis for case-control association studies in the presence of covariates", *Joint Statistical Meetings*, Boston, MA, August 2014.

"Secondary trait analysis for case-control association studies in the presence of covariates", *Eastern North American Region*, Baltimore, MD, March 2014.

COMPUTER SKILLS

Authored software: npsurvSS in R (5000+ downloads from CRAN)
Expert in Python, R
Proficient in C++, Java, SAS, SQL, Stata
Experience with Maple, Matlab, Visual Basic

SUPERVISED PROJECTS

PhD Dissertation
"A multi-dimensional integrative scoring framework for predicting functional regions in the human genome" with Xihao Li, PhD candidate in biostatistics at Harvard University, ongoing.

Takeda Summer Internship
"Principal stratification analyses to assess the treatment effect in a subgroup characterized by an intercurrent event" with Chuyu Deng, PhD candidate in biostatistics at the University of Minnesota, 2020.

"Assessing the feasibility of an incomplete endpoint for interim decision making" with Teng Fei, PhD candidate in biostatistics at Emory University, 2020.

"Quantitative methods for improved benefit-risk assessment" with Jingyao Hou, PhD candidate in biostatistics at the University of Massachusetts Amherst, 2019.

"Incorporating auxiliary data to improve conditional power estimation" with Xin Li, PhD candidate in biostatistics at the George Washington University, 2018.

"Predicting relapse on non-ixazomib proteasome inhibitors" with Yunqi Zhao, PhD candidate in mathematics at Tulane University, 2018.

"Measuring treatment efficacy in mixture of subgroups" with Busola Sanusi, PhD candidate in biostatistics at the University of North Carolina, 2017.

Harvard Medical School's Computationally-Enabled Medicine Course
"Modeling clinical trials" with Jonathan Fried and Nicholas Moore, MD students at Harvard Medical School, 2018.

TEACHING EXPERIENCE

Lecturer, Statistics for Non-statisticians	*Fall 2016*
Teaching assistant, Introduction to Statistical Genetics	*Fall 2015*
Teaching assistant, Applied Longitudinal Analysis	*Spring 2015*
Teaching assistant, Principles of Biostatistics	*Fall 2013*
Teaching assistant, Rates and Proportions	*Spring 2013*

HONORS/AWARDS

Phi Beta Kappa	*2010 – Present*
Best Poster, ASA Biopharmaceutical Section Regulatory-Industry Statistics Workshop	*2020*
National Science Foundation S-STEM	*2009, 2010*
Suzanne Stephens Fogelstrom Scholarship	*2009*