Matteo Sesia

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Academic Positions

Assistant Professor, (June 2020–present). Department of Data Sciences and Operations, Marshall School of Business, University of Southern California.

Education

Ph.D. in Statistics, 2020. Stanford University. Advisor: Emmanuel Candès.
Thesis title: New methods for variable importance testing with applications to genetic studies.

M.S. in Physics of Complex Systems, 2015. Politecnico di Torino & Université Paris-Sud (joint).
Graduated *cum laude* (top final grade and highest honors).

M.A. in Statistics and Applied Mathematics, 2015. Collegio Carlo Alberto.
Graduated *with distinction* (highest honors).

B.S. in Engineering Physics, 2013. Politecnico di Torino.
Graduated *cum laude* (top final grade and highest honors).

Awards

Jerome H. Friedman Applied Statistics Dissertation Award (2020).

International Master's Scholarship, Université Paris-Saclay (2014–2015).

Allievi Honors Program, Collegio Carlo Alberto (2011–2015).

Professional Service

Journal referee: Biometrika, Briefings in Bioinformatics, Statistical Science.

Conference referee: COLT, ISIT, NeurIPS.

Teaching

University of Southern California:

BUAD 310g: Applied Business Statistics (undergraduate), Fall 2020.

Stanford University:

Stats 390: Consulting Workshop (graduate), Summer 2018.

Stats 195: Introduction to R (undergraduate), Spring 2018, Spring 2020.

Publications and Preprints

Publications

[1] S. Bates, M. Sesia, C. Sabatti, E. Candès. Causal inference in genetic trio studies. Proc. Natl. Acad. Sci. U.S.A., to appear (2020). https://arxiv.org/abs/2002.09644

[2] M. Sesia, E. Katsevich, S. Bates, E. Candès, C. Sabatti. Multi-resolution localization of causal variants across the genome. *Nature Commun.*, 11, 1093 (2020). https://doi.org/10.1038/s41467-020-14791-2

[3] M. Sesia, E. Candès. A comparison of some conformal quantile regression methods. *Stat*, 9:e261 (2020). http://dx.doi.org/10.1002/sta4.261

[4] Y. Romano,* M. Sesia,* E. Candès. Deep knockoffs. (* joint first author) *J. Am. Stat. Assoc.*, 2019. https://doi.org/10.1080/01621459.2019.1660174

[5] M. Sesia, C. Sabatti, E. Candès. Rejoinder: "Gene hunting with hidden Markov model knockoffs". *Biometrika*, 106, 35–45 (2019). https://doi.org/10.1093/biomet/asy075

[6] M. Sesia, C. Sabatti, E. Candès. Gene hunting with hidden Markov model knockoffs. *Biometrika*, 106, 1–18 (2019). https://doi.org/10.1093/biomet/asy033

Preprints

[1] M. Sesia, S. Bates, E. Candès, J. Marchini, C. Sabatti. Controlling the false discovery rate in GWAS with population structure. (2020). https://doi.org/10.1101/2020.08.04.236703

[2] C. Chia, M. Sesia, C.-S. Ho, S. Jeffrey, J. Dionne, E. Candès, R. Howe. Interpretable signal analysis with knockoffs enhances classification of bacterial Raman spectra. (2020). https://arxiv.org/abs/2006.04937

[3] Y. Romano,* M. Sesia,* E. Candès. Classification with valid and adaptive coverage. (* joint first author) (2020). https://arxiv.org/abs/2006.02544

Previous Research Experience

Research Intern, Adobe Systems Inc., Summer 2017. Mentor: Yasin Abbasi-Yadkori.
Invented a new adaptive bandit algorithm and proved regret bounds.

Research Intern, École Normale Supérieure Cachan, Spring 2015. Mentor: Nicolas Vayatis.
Studied algorithms for inferring network structure from epidemic diffusion observations.

Research Intern, Collegio Carlo Alberto, Spring 2013. Mentor: Alfredo Braunstein.
Studied message-passing algorithms for approximate inference in systems with quenched disorder.

Presentations

Invited presentations

Gene hunting with knockoffs.
Johns Hopkins University, Mathematical Institute for Data Science. Feb. 18, 2020, in Baltimore, MD.

Developments in knockoff generation and genetic mapping.
USC Marshall School of Business, DSO Department. Jan. 27, 2020, in Los Angeles, CA.

Developments in knockoff generation and genetic mapping.
UC Davis, Department of Statistics. Jan. 6, 2020, in Davis, CA.

Reproducible localization of causal variants across the genome.
Regeneron Pharmaceuticals. Sept. 17, 2019, in Eastview, NY.

Multi-resolution localization of causal variants across the genome.
23andMe. May 21, 2019, in Mountain View, CA.

Reproducible localization of causal variants across the genome.
Stanford University, Statistics Department seminar. July 16, 2019, in Stanford, CA.

Deep knockoffs.
Stanford University, Statistics Industrial Affiliates Meeting. Feb. 22, 2019, in Stanford, CA.

New tools for reproducible variable selection with knockoffs.
Collegio Carlo Alberto, Statistics Seminar. Dec. 19, 2018, in Torino, Italy.

Gene hunting with knockoffs for hidden Markov models.
Université Grenoble Alpes, Bayes in Grenoble Seminar. July 10, 2018, in Grenoble, France.

Contributed presentations

Gene hunting with hidden Markov model knockoffs.
Royal Statistics Society Conference, Sept. 3–6, 2018, in Cardiff, United Kingdom.

Gene hunting with knockoffs for hidden Markov models.
Workshop on Model Selection, Regularization and Inference, July. 12–14, 2018, in Vienna, Austria.

Gene hunting with knockoffs for hidden Markov models.
Computational and Methodological Statistics Conference, Dec. 16–18, 2017, in London, United Kingdom.

Poster presentations

Multi-resolution localization of causal variants across the genome.
American Society for Human Genetics Annual Meeting, Oct. 15–19, 2019, in Houston, TX.

Multi-resolution localization of causal variants across the genome.
Higher-Order Asymptotics and Post-Selection Inference Workshop, Aug. 17–19, 2019, in St. Louis, MO.

Gene hunting with hidden Markov model knockoffs.
American Society for Human Genetics Annual Meeting, Oct. 16–20, 2018, in San Diego, CA.