

# Matteo Sesia

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## ACADEMIC POSITIONS

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

## EDUCATION

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**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

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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

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*Journal referee*: Bayesian Analysis, Biometrika, Briefings in Bioinformatics, Statistical Science.

*Conference referee*: COLT, ISIT, NeurIPS.

## TEACHING

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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

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### 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

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**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

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### 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.