

# Matteo Sesia

Marshall School of Business, DSO Department, Bridge Hall 308, Los Angeles, CA 90089  
sesia@marshall.usc.edu — <https://msesia.github.io>

## ACADEMIC POSITIONS

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**Assistant Professor**, (June 2020–present). Department of Data Sciences and Operations, 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*: Biometrika, Briefings in Bioinformatics.

*Conference referee*: COLT, ISIT.

## 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.

## PUBLICATIONS AND PREPRINTS

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### Publications

- [1] **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>

- [2] **M. Sesia**, E. Candès. A comparison of some conformal quantile regression methods. *Stat*, 9:e261 (2020). <http://dx.doi.org/10.1002/sta4.261>
- [3] Y. Romano\*, **M. Sesia**\*, E. Candès. Deep knockoffs. (\* equal contribution) *J. Am. Stat. Assoc.*, 2019. <https://doi.org/10.1080/01621459.2019.1660174>
- [4] **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>
- [5] **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] 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>
- [2] Y. Romano\*, **M. Sesia**\*, E. Candès. Classification with valid and adaptive coverage. (\* equal contribution) 2020. <https://arxiv.org/abs/2006.02544>
- [3] S. Bates, **M. Sesia**, C. Sabatti, E. Candès. Causal inference in genetic trio studies. 2020. <https://arxiv.org/abs/2002.09644>

## TEACHING EXPERIENCE

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**Principal Instructor**, Stanford University.

Responsibilities included: designing the curriculum, preparing material, lecturing, evaluating assignments.

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

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

**Teaching Assistant**, Stanford University.

Responsibilities varied, including: preparing assignments, leading sessions, occasionally lecturing, assisting students during office hours, evaluating assignments, coordinating team of teaching assistants.

Stats 366: Modern Statistics for Modern Biology (graduate level), Summer 2019.

Stats 315A: Modern Applied Statistics I (graduate level), Winter 2018.

Stats 315B: Modern Applied Statistics II (graduate level), Spring 2017, Spring 2019.

CS 229: Machine Learning (graduate level), Spring 2016.

Stats 216: Introduction to Statistical Learning (graduate level), Winter 2016, Summer 2016.

Stats 202: Data Mining and Analysis (graduate level), Fall 2016.

Stats 191: Introduction to Applied Statistics (undergraduate level), Winter 2019.

Stats 141: Biostatistics (undergraduate level), Fall 2019.

Stats 60: Introduction to Statistical Methods (undergraduate level), Fall 2017.

## 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.