

# **Curriculum Vitae**

## **Seung Hoan Choi**

Broad Institute of MIT and Harvard  
75 Ames Street, Rm #10013D  
Cambridge, MA 02142  
E-mail: schoi@broadinstitute.org  
Cell: 6176202894

### **Professional Interests**

Statistical Analysis in Genetic and Genomic data, Whole Genome Sequencing Analysis, Big Data Cloud Computing, Genetics in Cardiovascular disease, RNA-Sequencing Analysis Methods

### **Education**

Boston University, Ph.D. in Biostatistics (May 2016)	Boston, MA
Supervised by Drs. Josée Dupuis, Kathryn L. Lunetta, Anita L. Destefano	
Boston University, M.A. in Biostatistics (May 2011)	Boston, MA
Supervised by Dr. Anita L. Destefano	
The State University of New York at Stony Brook, B.S. in Applied Math & Statistics and Mathematics (Dec. 2008)	
Supervised by Dr. Stephen Finch	Stony Brook, NY

### **Research Experience**

2021-present	Computational Scientist, Cardiovascular Disease Initiative, Broad Institute of MIT and Harvard
2016-2021	Postdoctoral Associate (Mentored by Dr. Patrick T. Ellinor), Cardiovascular Disease Initiative, Broad Institute of MIT and Harvard
2009-2016	Research Assistant, Department of Biostatistics, Boston University
2007-2008	Research Assistant, Department of Applied Math & Statistics. The State University of New York at Stony Brook

### **Teaching Experience**

2020	Cardiovascular genetics onboarding program (Rare variant analysis and Cloud-computing)
2013-2015	Course Grader ( <b>BS723</b> : Introduction to statistical Computing, <b>BS858</b> : Statistical Genetics I), Department of Biostatistics, Boston University
2012-2014	Teaching Assistant ( <b>Statistical Genetics Section in SIBS</b> : Summer Institute for Training in Biostatistics), Department of Biostatistics, Boston University
2008	Teaching Assistant ( <b>AMS315</b> : Data Analysis, <b>AMS210</b> : Linear Algebra), Department of Applied Math & Statistics, The State University of New York at Stony Brook

### **Organizing group meeting**

2021-present	All of Us demonstration project for GWAS
2016-2019	Whole genome sequencing analysis meeting for atrial fibrillation
2019-2020	Cardiovascular genetics meeting

## Research Support

### NHLBI BioData Catalyst Fellow Program

Choi (PI)

2020/04/01- 2021/04/01 (\$69,733)

### Whole-genome sequencing reveals genetics of atrial fibrillation

The objective of this proposal is to build a cloud computing environment to identify the heritability of atrial fibrillation using whole genome sequencing data. we will identify protein-disruptive deleterious variants and conduct the gene-based association tests with atrial fibrillation.

### NHLBI TOPMed Analysis Support Program

Choi (PI)

2017/04/01- 2018/04/01 (\$100,000)

### Leveraging whole genome sequencing data to understand atrial fibrillation and electrocardiographic traits

The objective of this proposal is to leverage data from the NHLBI Trans-Omics Precision Medicine whole genome sequencing program to expand ongoing analyses of atrial fibrillation, identify causal variation related to both fibrillation and cardiac conduction, and contrast the genetic architecture of atrial fibrillation and electrocardiographic traits.

## Awards and Honors

2016	Best Poster Presentation, <b>Cohorts for Heart and Aging Research in Genomic Epidemiology, Houston</b>
2015	Best Poster Presentation, <b>Genome Science Institute Research Symposium, Boston University</b>
2013	CHARGE Rotterdam meeting travel award, <b>Framingham Heart Study</b>
2012	CHARGE Reykjavik meeting travel award, <b>Framingham Heart Study</b>
2009-2016	Graduate Research Assistant Scholarship Program, <b>Boston University</b>
2008	Cum Laude, <b>The State University of New York at Stony Brook</b>
2008	Undergraduate Research and Creativity Activity Summer Research Fellowship, <b>The State University of New York at Stony Brook</b>

## Poster Presentations

2019	Monogenic and Polygenic Contributions to Atrial fibrillation Risk: Results from a National Biobank, <b>American Heart Associate, Philadelphia, PA</b>
2018	Association between titin loss-of-function variants and early-onset atrial fibrillation, <b>The American Society of Human Genetics, San Diego, CA</b>
2016	Evaluation of Logistic Regression Models and Effect of Covariates for Case-Control Study in RNA-Seq Analysis. <b>Cohorts for Heart and Aging Research in Genomic Epidemiology, Houston, TX</b>
2015	Evaluation of Logistic Regression Models and Effect of Covariates for Case-Control Study in RNA-Seq Analysis. <b>Genome Science Institute Research Symposium, Boston, MA</b>
2014	Six novel loci associated with circulating VEGF levels identified by a meta-analysis genome-wide association study. <b>The American Society of Human Genetics, San Diego, CA</b>
2013	Genetic Variants associated with incidence of late-onset Alzheimer's disease in Caucasians. <b>Alzheimer's Association International Conference, Boston, MA</b>
2013	Genetic Variants associated with incidence of late-onset Alzheimer's disease in Caucasians. <b>Cohorts for Heart and Aging Research in Genomic Epidemiology, Rotterdam, Netherland</b>
2012	Pathway Analysis of Genes Identified by Genome Wide Association Study of Circulating Vascular Endothelial growth factors Levels. <b>Cohorts for Heart and Aging Research in Genomic Epidemiology, Reykjavik, Iceland</b>
2011	Pathway Analysis of Genes Identified by Genome Wide Association Study of Circulating Vascular Endothelial growth factors Levels. <b>Genome Science Institute Research Symposium, Boston, MA</b>
2009	Growth Mixture Modeling as an Exploratory Analysis Tool in Longitudinal QTL. <b>Undergraduate Research and Creative Activity, Stony Brook, NY</b>

## **Recent publications related atrial fibrillation**

1. Halford JL, Weng LC, **Choi SH**, Jurgens SJ, Morrill VN, Khurshid S, Trinquart L, Benjamin EJ, Ellinor PT, Lubitz SA. Associations Between Alcohol Intake and Genetic Predisposition With Atrial Fibrillation Risk in a National Biobank. *Circ Genom Precis Med.* 2020 Dec;13(6):e003111. doi: 10.1161/CIRCGEN.120.003111. Epub 2020 Nov 6. PubMed PMID: 33156697; PubMed Central PMCID: PMC7738370.
2. **Choi SH**, Jurgens SJ, Weng LC, Pirruccello JP, Roselli C, Chaffin M, Lee CJ, Hall AW, Khera AV, Lunetta KL, Lubitz SA, Ellinor PT. Monogenic and Polygenic Contributions to Atrial Fibrillation Risk: Results From a National Biobank. *Circ Res.* 2020 Jan 17;126(2):200-209. doi: 10.1161/CIRCRESAHA.119.315686. Epub 2019 Nov 6. PubMed PMID: 31691645; PubMed Central PMCID: PMC7007701.
3. Tucker NR, Chaffin M, Fleming SJ, Hall AW, Parsons VA, Bedi KC Jr, Akkad AD, Herndon CN, Arduini A, Papangeli I, Roselli C, Aguet F, **Choi SH**, Ardlie KG, Babadi M, Margulies KB, Stegmann CM, Ellinor PT. Transcriptional and Cellular Diversity of the Human Heart. *Circulation.* 2020 Aug 4;142(5):466-482. doi: 10.1161/CIRCULATIONAHA.119.045401. Epub 2020 May 14. PubMed PMID: 32403949; PubMed Central PMCID: PMC7666104.
4. Pirruccello JP, Bick A, Chaffin M, Aragam KG, **Choi SH**, Lubitz SA, Ho CY, Ng K, Philippakis A, Ellinor PT, Kathiresan S, Khera AV. Titin Truncating Variants in Adults Without Known Congestive Heart Failure. *J Am Coll Cardiol.* 2020 Mar 17;75(10):1239-1241. doi: 10.1016/j.jacc.2020.01.013. PubMed PMID: 32164899; PubMed Central PMCID: PMC7433750.
5. **Choi SH**, Weng LC, Roselli C, Lin H, Haggerty CM, Shoemaker MB, Barnard J, Arking DE, Chasman DI, Albert CM, Chaffin M, Tucker NR, Smith JD, Gupta N, Gabriel S, Margolin L, Shea MA, Shaffer CM, Yoneda ZT, Boerwinkle E, Smith NL, Silverman EK, Redline S, Vasan RS, Burchard EG, Gogarten SM, Laurie C, Blackwell TW, Abecasis G, Carey DJ, Fornwalt BK, Smelser DT, Baras A, Dewey FE, Jaquish CE, Papanicolaou GJ, Sotoodehnia N, Van Wagoner DR, Psaty BM, Kathiresan S, Darbar D, Alonso A, Heckbert SR, Chung MK, Roden DM, Benjamin EJ, Murray MF, Lunetta KL, Lubitz SA, Ellinor PT. Association Between Titin Loss-of-Function Variants and Early-Onset Atrial Fibrillation. *JAMA : the journal of the American Medical Association.* 2018;320(22):2354-64. Epub 2018/12/12. doi: 10.1001/jama.2018.18179. PubMed PMID: 30535219.
6. Khera AV, Chaffin M, Aragam KG, Haas ME, Roselli C, **Choi SH**, Natarajan P, Lander ES, Lubitz SA, Ellinor PT, Kathiresan S. Genome-wide polygenic scores for common diseases identify individuals with risk equivalent to monogenic mutations. *Nat Genet.* 2018;50(9):1219-24. Epub 2018/08/15. doi: 10.1038/s41588-018-0183-z. PubMed PMID: 30104762; PubMed Central PMCID: PMC6128408.
7. Weng LC, Preis SR, Hulme OL, Larson MG, **Choi SH**, Wang B, Trinquart L, McManus DD, Staerk L, Lin H, Lunetta KL, Ellinor PT, Benjamin EJ, Lubitz SA. Genetic Predisposition, Clinical Risk Factor Burden, and Lifetime Risk of Atrial Fibrillation. *Circulation.* 2018;137(10):1027-38. Epub 2017/11/14. doi: 10.1161/circulationaha.117.031431. PubMed PMID: 29129827; PubMed Central PMCID: PMC5840011.
8. Roselli C, Chaffin MD, Weng LC, Aeschbacher S, Ahlberg G, Albert CM, Almgren P, Alonso A, Anderson CD, Aragam KG, Arking DE, Barnard J, Bartz TM, Benjamin EJ, Bihlmeyer NA, Bis JC, Bloom HL, Boerwinkle E, Bottinger EB, Brody JA, Calkins H, Campbell A, Cappola TP, Carlquist J, Chasman DI, Chen LY, Chen YI, Choi EK, **Choi SH**, Christophersen IE, Chung MK, Cole JW, Conen D, Cook J, Crijs HJ, Cutler MJ, Damrauer SM, Daniels BR, Darbar D, Delgado G, Denny JC, Dichgans M, Dorr M, Dudink EA, Dudley SC, Esa N, Esko T, Eskola M, Fatkin D, Felix SB, Ford I, Franco OH, Geelhoed B, Grewal RP, Gudnason V, Guo X, Gupta N, Gustafsson S, Gutmann R, Hamsten A, Harris TB, Hayward C, Heckbert SR, Hernesniemi J, Hocking LJ, Hofman A, Horimoto A, Huang J, Huang PL, Huffman J, Ingelsson E, Ipek EG, Ito K, Jimenez-Conde J, Johnson R, Jukema JW, Kaab S, Kahonen M, Kamatani Y, Kane JP, Kastrati A, Kathiresan S, Katschnig-Winter P, Kavousi M, Kessler T, Ketselaer BL, Kirchhof P, Kleber ME, Knight S, Krieger JE, Kubo M, Launer

LJ, Laurikka J, Lehtimaki T, Leineweber K, Lemaitre RN, Li M, Lim HE, Lin HJ, Lin H, Lind L, Lindgren CM, Lokki ML, London B, Loos RJF, Low SK, Lu Y, Lyytikainen LP, Macfarlane PW, Magnusson PK, Mahajan A, Malik R, Mansur AJ, Marcus GM, Margolin L, Margulies KB, Marz W, McManus DD, Melander O, Mohanty S, Montgomery JA, Morley MP, Morris AP, Muller-Nurasyid M, Natale A, Nazarian S, Neumann B, Newton-Cheh C, Niemeijer MN, Nikus K, Nilsson P, Noordam R, Oellers H, Olesen MS, Orho-Melander M, Padmanabhan S, Pak HN, Pare G, Pedersen NL, Pera J, Pereira A, Porteous D, Psaty BM, Pulit SL, Pullinger CR, Rader DJ, Refsgaard L, Ribases M, Ridker PM, Rienstra M, Risch L, Roden DM, Rosand J, Rosenberg MA, Rost N, Rotter JI, Saba S, Sandhu RK, Schnabel RB, Schramm K, Schunkert H, Schurman C, Scott SA, Seppala I, Shaffer C, Shah S, Shalaby AA, Shim J, Shoemaker MB, Siland JE, Sinisalo J, Sinner MF, Slowik A, Smith AV, Smith BH, Smith JG, Smith JD, Smith NL, Soliman EZ, Sotoodehnia N, Stricker BH, Sun A, Sun H, Svendsen JH, Tanaka T, Tanriverdi K, Taylor KD, Teder-Laving M, Teumer A, Theriault S, Trompet S, Tucker NR, Tveit A, Uitterlinden AG, Van Der Harst P, Van Gelder IC, Van Wagoner DR, Verweij N, Vlachopoulou E, Volker U, Wang B, Weeke PE, Weijns B, Weiss R, Weiss S, Wells QS, Wiggins KL, Wong JA, Woo D, Worrall BB, Yang PS, Yao J, Yoneda ZT, Zeller T, Zeng L, Lubitz SA, Lunetta KL, Ellinor PT. Multi-ethnic genome-wide association study for atrial fibrillation. *Nat Genet*. 2018. Epub 2018/06/13. doi: 10.1038/s41588-018-0133-9. PubMed PMID: 29892015.

### **Recent progress (under review/preprint)**

1. Jurgens SJ\*, Choi SH\*, ..., Lunetta K, Lubitz SA, Ellinor PT. Rare Genetic Variation Underlying Human Traits and Diseases: Results from 200,000 Individuals in the UK Biobank, **bioRxiv** 2020.11.29.402495; doi: <https://doi.org/10.1101/2020.11.29.402495> (*Nat Gen*, under review)
2. Choi SH, Jurgens SJ, ..., Lunetta K, Lubitz SA, Ellinor PT. Rare Coding Variants Associated with Electrocardiographic Intervals Identify Monogenic Arrhythmia Susceptibility Genes – a Multi-ancestry Analysis (*Circ Genom Precis Med*, under review)

### **Complete List of Published Work in My Bibliography:**

<https://www.ncbi.nlm.nih.gov/myncbi/seung.hoan.choi.1/bibliography/43429434/public/>