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Current Position

Assistant Professor
Human Genetics Center
Department of Epidemiology, Human Genetics & Environmental Sciences
School of Public Health
University of Texas Health Science Center at Houston (UTHealth)

Education

- 2010-2014 Postdoctoral Research Fellow, University of Michigan, Ann Arbor, MI.
Center for Statistical Genetics & Department of Biostatistics
- 2005-2010 Ph.D., The University of Texas, Austin, TX.
Electrical and Computer Engineering
Dissertation: Transfer learning for classification of spatially varying data
- 1997-1999 M.S., University of Michigan, Ann Arbor, MI.
Electrical Engineering and Computer Science
- 1993-1999 B.S., KAIST, Daejeon, South Korea.
Electrical Engineering (major) / Computer Science (minor)

Experience

- Oct. 2014 – Current, Assistant Professor
University of Texas Health Science Center, Houston, TX
Human Genetics Center
Department of Epidemiology, Human Genetics and Environmental Sciences
School of Public Health
- Aug. 2010 – Oct. 2014, Postdoctoral Research Fellow
University of Michigan, Ann Arbor, MI
Center for Statistical Genetics & Department of Biostatistics
PIs: Goncalo Abeçasis and Michael Boehnke
- Jun. 2009 – Aug. 2009, Adv. Short-Term Research Opportunity (ASTRO)
Oak Ridge Nat. Lab., Oak Ridge, TN
Computational Sciences and Engineering Division (CSED)
- Jan. 2007 – Aug. 2010, Research Assistant
University of Texas, Austin, TX
Advanced Data Exploration and Analysis Laboratory (IDEAL)

Dec. 1999 – Jun. 2010, Engineer/Senior Engineer
Samsung Electronics, Suwon, South Korea.
Digital Media R&D Center

Jan. 1998 – May. 1999, Research Assistant
University of Michigan, Ann Arbor, MI.
Biomechanics Laboratory

Research Support (Current)

(Pending) 1R01DK11863, NIH/NIDDK. Co-I

- Diabetes Progression with Metabolomic Profiling in Starr County Mexican Americans

OT2OD002748, NIH. Co-I

- The Baylor-Hopkins Clinical Genomics Center for All of Us

1R01DK116378-01, NIH/NIDDK. Co-I

- Microbiome and Worsening Glycemia Among Mexican Americans in Starr County, Texas

1R03DE026509, NIH/NIDCR. Co-I

- Identification of microRNAs associated with cleft lip

UM1HG008898, NIH/NHGRI. Co-I

- Genomic Architecture of Common Disease in Diverse Populations

Research Support (Completed)

1R03DE026208, NIH/NIDCR. Co-I

- Transcripts and Functions Targeted by Non-coding RNAs in Palate Development

CURE Pilot, BCM/CURE. Co-I

- Pilot in Silico Mortality Risk Attribution in Sudep and Sudden Death in the Young (SUDY) to Information Precision Molecular Diagnostics of Sudden Death

PRIME, UTHealth SPH. PI

- Diabetes Progression with Metabolomic and Genomic Profiling in Starr County Mexican Americans

Publications (Journal Articles)

Jun G*, Manning A, Almeida M, Zawistowski M, Wood AR, Teslovich TM, Fuchsberger C, Feng S, Cingolani P, Gaulton KJ, Dyer T, Blackwell TW, Chen H, Chines PS, Choi S, Churchhouse C, Fontanillas P, King R, Lee S, Lincoln SE, Trubetskoy V, DePristo M, Fingerlin T, Grossman R, Grundstad J, Heath A, Kim J, Kim YJ, Laramie J, Lee J, Li H, Liu X, Livne O, Locke AE, Maller J, Mazur A, Morris AP, Pollin TI, Ragona D, Reich D, Rivas MA, Scott LJ, Sim X, Tearle RG, Teo YY, Williams AL, Zollner S, Curran JE, Peralta J, Akolkar B, Bell GI, Burt NP, Cox NJ, Florez JC, Hanis CL, McKeon C, Mohlke KL, Seielstad

M, Wilson JG, Atzmon G, Below JE, Dupuis J, Nicolae DL, Lehman D, Park T, Won S, Sladek R, Altshuler D, McCarthy MI, Duggirala R, Boehnke M, Frayling TM, Abecasis GR, Blangero J. Evaluating the contribution of rare variants to type 2 diabetes and related traits using pedigrees. *Proc Natl Acad Sci U S A*. 2018;115(2):379-84. Epub 2017/12/28. doi: 10.1073/pnas.1705859115. PubMed PMID: 29279374; PMCID: PMC5777025. ***Corresponding**

Herrington DM, Mao C, Parker SJ, Fu Z, Yu G, Chen L, Venkatraman V, Fu Y, Wang Y, Howard TD, **Jun G**, Zhao CF, Liu Y, Saylor G, Spivia WR, Athas GB, Troxclair D, Hixson JE, Vander Heide RS, Wang Y, Van Eyk JE. Proteomic Architecture of Human Coronary and Aortic Atherosclerosis. *Circulation*. 2018;137(25):2741-56. Epub 2018/06/20. doi: 10.1161/CIRCULATIONAHA.118.034365. PubMed PMID: 29915101; PMCID: PMC6011234.

Suzuki A, Abdallah N, Gajera M, **Jun G**, Jia P, Zhao Z, Iwata J. Genes and microRNAs associated with mouse cleft palate: A systematic review and bioinformatics analysis. *Mech Dev*. 2018;150:21-7. Epub 2018/02/24. doi: 10.1016/j.mod.2018.02.003. PubMed PMID: 29475039; PMCID: PMC5906164.

Rashkin S, **Jun G**, Chen S, Genetics, Epidemiology of Colorectal Cancer C, Abecasis GR. Optimal sequencing strategies for identifying disease-associated singletons. *PLoS Genet*. 2017;13(6):e1006811. doi: 10.1371/journal.pgen.1006811. PubMed PMID: 28640830; PMCID: PMC5501675.

Metwalli KA, Do MA, Nguyen K, Mallick S, Kin K, Farokhnia N, **Jun G**, Fakhouri WD. Interferon Regulatory Factor 6 Is Necessary for Salivary Glands and Pancreas Development. *J Dent Res*. 2017;22034517729803. doi: 10.1177/0022034517729803. PubMed PMID: 28898113.

Manning A, Highland HM, Gasser J, Sim X, ..., **Jun G**, ..., Abecasis G, Bell GI, Blangero J, Cox NJ, Duggirala R, Seielstad M, Wilson JG, Dupuis J, Ripatti S, Hanis CL, Florez JC, Mohlke KL, Meigs JB, Laakso M, Morris AP, Boehnke M, Altshuler D, McCarthy MI, Gloyn AL, Lindgren CM. A Low-Frequency Inactivating AKT2 Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. *Diabetes*. 2017;66(7):2019-32. doi: 10.2337/db16-1329. PubMed PMID: 28341696; PMCID: PMC5482074.

Jiang ZD, Ajami NJ, Petrosino JF, **Jun G**, Hanis CL, Shah M, Hochman L, Ankoma-Sey V, DuPont AW, Wong MC, Alexander A, Ke S, DuPont HL. Randomised clinical trial: faecal microbiota transplantation for recurrent *Clostridium difficile* infection - fresh, or frozen, or lyophilised microbiota from a small pool of healthy donors delivered by colonoscopy. *Aliment Pharmacol Ther*. 2017;45(7):899-908. doi: 10.1111/apt.13969. PubMed PMID: 28220514.

Hixson JE, **Jun G**, Shimmin LC, Wang Y, Yu G, Mao C, Warren AS, Howard TD, Heide RSV, Van Eyk J, Wang Y, Herrington DM. Whole Exome Sequencing to Identify Genetic Variants Associated with Raised Atherosclerotic Lesions in Young Persons. *Sci Rep*. 2017;7(1):4091. doi: 10.1038/s41598-017-04433-x. PubMed PMID: 28642624; PMCID: PMC5481334.

Blangero J, Teslovich TM, Sim X, Almeida MA, **Jun G**, Dyer TD, Johnson M, Peralta JM, Manning A, Wood AR, Fuchsberger C, Kent JW, Jr., Aguilar DA, Below JE, Farook VS, Arya R, Fowler S, Blackwell TW, Puppala S, Kumar S, Glahn DC, Moses EK, Curran JE, Thameem F, Jenkinson CP, DeFronzo RA, Lehman DM, Hanis C, Abecasis G, Boehnke M, Goring H, Duggirala R, Almasy L, T2D-GENES Consortium. Omics-squared: human genomic, transcriptomic and phenotypic data for genetic analysis workshop 19. *BMC Proc*. 2016;10(Suppl 7):71-7. doi: 10.1186/s12919-016-0008-y. PubMed PMID: 27980614; PMCID: PMC5133484.

Almeida M, Blondell L, Peralta JM, Kent JW, Jr., **Jun G**, Teslovich TM, Fuchsberger C, Wood AR, Manning AK, Frayling TM, Cingolani PE, Sladek R, Dyer TD, Abecasis G, Duggirala R, Blangero J.

Independent test assessment using the extreme value distribution theory. *BMC Proc.* 2016;10(Suppl 7):245-9. doi: 10.1186/s12919-016-0038-5. PubMed PMID: 27980644; PMCID: PMC5133519.

Nicholson AM, Finch NA, Almeida M, Perkerson RB, van Blitterswijk M, Wojtas A, Cenik B, Rotondo S, Inskeep V, Almasy L, Dyer T, Peralta J, ***Jun G***, Wood AR, Frayling TM, Fuchsberger C, Fowler S, Teslovich TM, Manning AK, Kumar S, Curran J, Lehman D, Abecasis G, Duggirala R, Pottier C, Zahir HA, Crook JE, Karydas A, Mitic L, Sun Y, Dickson DW, Bu G, Herz J, Yu G, Miller BL, Ferguson S, Petersen RC, Graff-Radford N, Blangero J, Rademakers R. Prosaposin is a regulator of progranulin levels and oligomerization. *Nature Communications.* 2016;7:11992. doi: 10.1038/ncomms11992

Fuchsberger C, Flannick J, Teslovich TM, Mahajan A, Agarwala V, Gaulton KJ, Ma C, Fontanillas P, Moutsianas L, McCarthy DJ, Rivas MA, Perry JRB, Sim X, ..., ***Jun G***, ..., Park T, Donnelly P, Morris AD, Hattersley AT, Bowden DW, Collins FS, Atzmon G, Chambers JC, Spector TD, Laakso M, Strom TM, Bell GI, Blangero J, Duggirala R, Tai ES, McVean G, Hanis CL, Wilson JG, Seielstad M, Frayling TM, Meigs JB, Cox NJ, Sladek R, Lander ES, Gabriel S, Burt NP, Mohlke KL, Meitinger T, Groop L, Abecasis G, Florez JC, Scott LJ, Morris AP, Kang HM, Boehnke M, Altshuler D, McCarthy MI. The genetic architecture of type 2 diabetes. *Nature.* 2016;536(7614):41-7. doi: 10.1038/nature18642

Wood AR, Tuke MA, Nalls M, Hernandez D, Gibbs JR, Lin H, Xu CS, Li Q, Shen J, ***Jun G***, Almeida M, Tanaka T, Perry JRB, Gaulton K, Rivas M, Pearson R, Curran JE, Johnson MP, Göring HHH, Duggirala R, Blangero J, McCarthy MI, Bandinelli S, Murray A, Weedon MN, Singleton A, Melzer D, Ferrucci L, Frayling TM. Whole-genome sequencing to understand the genetic architecture of common gene expression and biomarker phenotypes. *Human Molecular Genetics.* 2015;24(5):1504-12. doi: 10.1093/hmg/ddu560.

Williams AL, Genovese G, Dyer T, Altemose N, Truax K, ***Jun G***, Patterson N, Myers SR, Curran JE, Duggirala R, Blangero J, Reich D, Przeworski M. Non-crossover gene conversions show strong GC bias and unexpected clustering in humans. *eLife.* 2015;4:e04637. doi: 10.7554/eLife.04637.

The 1000 Genomes Project Consortium. A global reference for human genetic variation. *Nature.* 2015;526(7571):68-74. doi: 10.1038/nature15393

Sudmant PH*, Rausch T*, Gardner EJ*, Handsaker RE*, Abyzov A*, Huddleston J*, Zhang Y*, Ye K*, ***Jun G***, ..., Sebat J, Batzer MA, McCarroll SA, The Genomes Project C, Mills RE, Gerstein MB, Bashir A, Stegle O, Devine SE, Lee C, Eichler EE, Korb J. An integrated map of structural variation in 2,504 human genomes. *Nature.* 2015;526(7571):75-81. doi: 10.1038/nature15394

Mahajan A, Sim X, Ng HJ, Manning A, Rivas MA, ..., ***Jun G***, ..., Dupuis J, Karpe F, Groop L, Laakso M, Pedersen O, Florez JC, Morris AP, Altshuler D, Meigs JB, Boehnke M, McCarthy MI, Lindgren CM, Gloyn AL, On Behalf of the T2D-GENES Consortium and GoT2D Consortium. Identification and Functional Characterization of G6PC2 Coding Variants Influencing Glycemic Traits Define an Effector Transcript at the G6PC2-ABCB11 Locus. *PLoS Genet.* 2015;11(1):e1004876. doi: 10.1371/journal.pgen.1004876.

Jun G, Wing MK, Abecasis GR, Kang HM. An efficient and scalable analysis framework for variant extraction and refinement from population-scale DNA sequence data. *Genome Research.* 2015;25(6):918-25. doi: 10.1101/gr.176552.114.

Flickinger M, ***Jun G***, Abecasis Gonçalo R, Boehnke M, Kang Hyun M. Correcting for Sample Contamination in Genotype Calling of DNA Sequence Data. *The American Journal of Human Genetics.* 2015;97(2):284-90. doi: <http://dx.doi.org/10.1016/j.ajhg.2015.07.002>.

Vrieze SI, Malone SM, Vaidyanathan U, Kwong A, Kang HM, Zhan X, Flickinger M, Irons D, ***Jun G***, Locke AE, Pistis G, Porcu E, Levy S, Myers RM, Oetting W, McGue M, Abecasis G, Iacono WG. In search of rare variants: Preliminary results from whole genome sequencing of 1,325 individuals with

psychophysiological endophenotypes. *Psychophysiology*. 2014;51(12):1309-20. doi: 10.1111/psyp.12350.

Zhan X, Larson DE, Wang C, Koboldt DC, Sergeev YV, Fulton RS, Fulton LL, Fronick CC, Branham KE, Bragg-Gresham J, **Jun G**, Hu Y, Kang HM, Liu D, Othman M, Brooks M, Ratnapriya R, Boleda A, Grassmann F, Von Strachwitz C, Olson LM, Buitendijk GHS, Hofman A, Van Duijn CM, Cipriani V, Moore AT, Shahid H, Jiang Y, Conley YP, Morgan DJ, Kim IK, Johnson MP, Cantsilieris S, Richardson AJ, Guymer RH, Luo H, Ouyang H, Licht C, Pluthero FG, Zhang MM, Zhang K, Baird PN, Blangero J, Klein ML, Farrer LA, DeAngelis MM, Weeks DE, Gorin MB, Yates JRW, Klaver CCW, Pericak-Vance MA, Haines JL, Weber BHF, Wilson RK, Heckenlively JR, Chew EY, Stambolian D, Mardis ER, Swaroop A, Abecasis GR. Identification of a rare coding variant in complement 3 associated with age-related macular degeneration. *Nature Genetics*. 2013;45(11):1375-81. doi: 10.1038/ng.2758. PubMed PMID: WOS:000326384100020.

Jun G, Ghosh J. Semisupervised learning of hyperspectral data with unknown land-cover classes. *IEEE Transactions on Geoscience and Remote Sensing*. 2013;51(1):273-82. doi: 10.1109/TGRS.2012.2198654. PubMed PMID: WOS:000313963700026.

Fu W, O'Connor TD, **Jun G**, Kang HM, Abecasis G, Leal SM, Gabriel S, Altshuler D, Shendure J, Nickerson DA, Bamshad MJ, Akey JM. Analysis of 6,515 exomes reveals the recent origin of most human protein-coding variants. *Nature*. 2013;493(7431):216-20. doi: 10.1038/nature11690. PubMed PMID: WOS:000313259600038.

Duan Q, Liu EY, Auer PL, Zhang G, Lange EM, **Jun G**, Bizon C, Jiao S, Buyske S, Franceschini N, Carlson CS, Hsu L, Reiner AP, Peters U, Haessler J, Curtis K, Wassel CL, Robinson JG, Martin LW, Haiman CA, Le Marchand L, Matise TC, Hindorf LA, Crawford DC, Assimes TL, Kang HM, Heiss G, Jackson RD, Kooperberg C, Wilson JG, Abecasis GR, North KE, Nickerson DA, Lange LA, Li Y. Imputation of coding variants in African Americans: Better performance using data from the exome sequencing project. *Bioinformatics*. 2013;29(21):2744-9. doi: 10.1093/bioinformatics/btt477. PubMed PMID: WOS:000325997500011.

Tennesen JA, Bigham AW, O'Connor TD, Fu W, Kenny EE, Gravel S, McGee S, Do R, Liu X, **Jun G**, Kang HM, Jordan D, Leal SM, Gabriel S, Rieder MJ, Abecasis G, Altshuler D, Nickerson DA, Boerwinkle E, Sunyaev S, Bustamante CD, Bamshad MJ, Akey JM. Evolution and functional impact of rare coding variation from deep sequencing of human exomes. *Science*. 2012;336(6090):64-9. doi: 10.1126/science.1219240. PubMed PMID: WOS:000306053100043.

Jun G, Flickinger M, Hetrick KN, Romm JM, Doheny KF, Abecasis GR, Boehnke M, Kang HM. Detecting and estimating contamination of human DNA samples in sequencing and array-based genotype data. *American Journal of Human Genetics*. 2012;91(5):839-48. doi: 10.1016/j.ajhg.2012.09.004. PubMed PMID: WOS:000311011400006.

The 1000 Genomes Consortium, An integrated map of genetic variation from 1,092 human genomes. *Nature*. 2012;491(7422):56-65. doi: 10.1038/nature11632. PubMed PMID: WOS:000310434500030.

Vatsavai RR, Symons CT, Chandola V, **Jun G**. GX-means: A model-based divide and merge algorithm for geospatial image clustering. *Procedia Computer Science*. 2011;4:186-95. doi: 10.1016/j.procs.2011.04.020. PubMed PMID: WOS:000299165200019.

Jun G, Ghosh J. Spatially adaptive classification of land cover with remote sensing data. *IEEE Transactions on Geoscience and Remote Sensing*. 2011;49(7):2662-73. doi: 10.1109/TGRS.2011.2105490. PubMed PMID: WOS:000292111800016.

Jun G, Ghosh J. Spatially adaptive semi-supervised learning with Gaussian processes for hyperspectral data analysis. *Statistical Analysis and Data Mining*. 2011;4(4):358-71. doi: 10.1002/sam.10119.

Jun G, Ghosh J. Nearest-manifold classification with Gaussian processes. *Proceedings - International Conference on Pattern Recognition*. 2010:914-7. doi: 10.1109/ICPR.2010.230.

Liu A, **Jun G**, Ghosh J. A self-training approach to cost sensitive uncertainty sampling. *Machine Learning*. 2009;76(2-3):257-70. doi: 10.1007/s10994-009-5131-9. PubMed PMID: WOS:000269013000007.

Publications (Peer-reviewed Conference Proceedings)

Symons CT, Vatsavai RR, **Jun G**, Arel I. Bias selection using task-targeted random subspaces for robust application of graph-based semi-supervised learning. *Proceedings - 2012 11th International Conference on Machine Learning and Applications, ICMLA 2012*. 2012;1:415-20. doi: 10.1109/ICMLA.2012.75.

Jun G, Ghosh J, Radosavljevic V, Obradovic Z. Predicting ground-based aerosol optical depth with satellite images via Gaussian processes. *KDIR 2010 - Proceedings of the International Conference on Knowledge Discovery and Information Retrieval*. 2010:370-5.

Liu A, **Jun G**, Ghosh J. Active learning of hyperspectral data with spatially dependent label acquisition costs. *International Geoscience and Remote Sensing Symposium (IGARSS)*. 2009;5. doi: 10.1109/IGARSS.2009.5417684. PubMed PMID: WOS:000281054102198.

Liu A, **Jun G**, Ghosh J. Spatially cost-sensitive active learning. *Society for Industrial and Applied Mathematics - 9th SIAM International Conference on Data Mining 2009, Proceedings in Applied Mathematics*. 2009;2:810-21.

Jun G, Vatsavai RR, Ghosh J. Spatially adaptive classification and active learning of multispectral data with gaussian processes. *ICDM Workshops 2009 - IEEE International Conference on Data Mining*. 2009:597-603. doi: 10.1109/ICDMW.2009.107. PubMed PMID: WOS:000290247100096.

Jun G, Ghosh J. Spatially adaptive classification of hyperspectral data with Gaussian processes. *International Geoscience and Remote Sensing Symposium (IGARSS)*. 2009;2. doi: 10.1109/IGARSS.2009.5418067. PubMed PMID: WOS:000281054100137.

Jun G, Ghosh J. Multi-class boosting with class hierarchies. *Lecture Notes in Computer Science (including subseries Lecture Notes in Artificial Intelligence and Lecture Notes in Bioinformatics)*. 2009;5519 LNCS:32-41. doi: 10.1007/978-3-642-02326-2_4.

Jun G, Ghosh J. Hybrid hierarchical classifiers for hyperspectral data analysis. *Lecture Notes in Computer Science (including subseries Lecture Notes in Artificial Intelligence and Lecture Notes in Bioinformatics)*. 2009;5519 LNCS:42-51. doi: 10.1007/978-3-642-02326-2_5.

Jun G, Ghosh J. An efficient active learning algorithm with knowledge transfer for hyperspectral data analysis. *International Geoscience and Remote Sensing Symposium (IGARSS)*. 2008;1(1). doi: 10.1109/IGARSS.2008.4778790.

Jun G, Aggarwal JK, Gökmen M. Tracking and segmentation of highway vehicles in cluttered and crowded scenes. *2008 IEEE Workshop on Applications of Computer Vision, WACV*. 2008. doi: 10.1109/WACV.2008.4544017. PubMed PMID: WOS:000258906400026.

Jun G. Home media center and media clients for multi-room audio and video applications. *2005 2nd IEEE Consumer Communications and Networking Conference, CCNC2005*. 2005;2005:257-60.

Software

- muCNV
 - Multi-sample SV genotyping for large-scale WGS data
 - <https://bitbucket.org/gjun/mucnv>
- verifyBamID
 - Detecting and estimating sample contaminations in sequencing data
 - <http://genome.sph.umich.edu/wiki/VerifyBamID>
- verifyIDintensity
 - Detecting and estimating sample contamination in genotype array data
 - <http://genome.sph.umich.edu/wiki/VerifyIDintensity>
- GotCloud
 - Software pipeline for SNP detection and refinement
 - <http://genome.sph.umich.edu/wiki/GotCloud>

Patents

- US Patent 9,342,141 and 8,504,637, KR Patent 1005773620000, Audio/video device, apparatus and method for controlling audio/video device
- US Patent 8,260,843, KR Patent 1007728610000, Apparatus and method for providing remote user interface
- US Patent 8,196,170, KR Patent 1007556950000, Method of connecting to internet via broadcast receiving device and apparatus for the same
- KR Patent 1004777050000, Method for displaying main screen of home media center
- KR Patent 1005974040000, Method and apparatus for transferring home media center's media contents apart from home media center
- KR Patent 1007886520000, Apparatus and method for dialing auto sound

Professional Activities

Editorial Board

- PEERJ, *Editor*

Journal Reviewer

- Bioinformatics (Oxford)
- PLoS Computational Biology
- BMC Bioinformatics
- Genome Research
- Patter Recognition
- Remote Sensing
- IEEE Transactions on Neural Network and Learning Systems
- IEEE Transactions on Image Processing
- IEEE Journal of Selected Topics in Applied Earth Observations and Remote Sensing
- IEEE Geoscience and Remote Sensing Letters

Program Committee

- ACM International Conference on Advances in Geographic Information Systems (ACM SIGSPATIAL)

- International Workshop on Spatial and Spatiotemporal Data Mining (SSTDM), held in conjunction with IEEE International Conference on Data Mining (ICDM)
- International Workshop on Knowledge Discovery from Sensor Data (SensorKDD), held in conjunction with the ACM SIGKDD Conference on Knowledge Discovery and Data Mining (KDD)

Professional Membership

- American Society of Human Genetics (ASHG)
- American Diabetes Association (ADA)
- Institute of Electrical and Electronic Engineers (IEEE)