

Serghei Mangul

CONTACT INFORMATION	Postdoctoral Fellow Institute for Quant. and Comput. Biosciences (QCBio) University of California, Los Angeles Engineering VI 286, UCLA	Cell phone: 404-654-0479 Office phone: 310-206-6069 E-mail: smangul@ucla.edu http://www.sergheimangul.com
RESEARCH INTERESTS	Computational biology, bioinformatics, genomics, immunogenomics, computational genetics, discrete algorithms, bioinformatics education	
EDUCATION	University of California , Los Angeles, CA Postdoctoral Fellow with Prof. Eleazar Eskin	Jan 2013 – present
	Georgia State University , Atlanta, GA Ph.D. in Bioinformatics Advisor: Prof. Alexander Zelikovsky	Aug 2008 – Dec 2012
	Moldova State University , Chisinau, Moldova B.S. in Applied Mathematics	Sep 2003 – Jul 2007
SELECTED AWARDS AND FELLOWSHIPS	Collaboratory Fellowship, QCBio Institute, UCLA ISCB Best Oral Presentation at NGS 2018, Barcelona, Spain ASHG Abstract Reviewers' Choice (top 10% of submitted abstracts) Second Century Initiative Bioinformatics University Doctoral Fellowship Long Program Fellowship, GEN2011, IPAM, UCLA Molecular Basis of Disease Fellowship, Georgia State University, Atlanta	Jan 2013 – present April 2018 Oct 2015 Jul 2011 – Dec 2012 Sep 2011 – Dec 2011 Jul 2009 – Jul 2011
GRANTS	Life Technologies Collaborative Research Grant “Software for Robust Transcript Discovery and Quantification” with Prof. Ion Mandoiu at University of Connecticut and Dr. Dumitru Brinza at Life Technologies	Aug 2011 – Feb 2012
	Life Technologies Collaborative Research Grant “Novel transcript reconstruction from Ion Torrent sequencing” with Prof. Ion Mandoiu at University of Connecticut and Dr. Dumitru Brinza at Life Technologies.	Jul 2011 – Dec 2011
PROFESSIONAL EXPERIENCE	University of California, Los Angeles <i>Postdoctoral Scholar</i> , Computer Science Department	Jan 2013 – present
	University of California, Los Angeles <i>Visiting Scholar</i> , Institute for Pure and Applied Mathematics	Sep 2011 – Dec 2011
	Life Technologies <i>Ambassador at UCLA Campus</i> , Life Technologies <i>Bioinformatics Intern</i> , Ion Torrent by Life Technologies <i>Bioinformatics Intern</i> , Applied Biosystems by Life Technologies	Sep 2011 – Dec 2011 May 2011 – Aug 2011 May 2010 – Aug 2010
	Georgia State University Department of Computer Science, Atlanta, GA <i>Research Assistant</i>	Aug 2008 – Dec 2012

TEACHING
EXPERIENCE

- **Introduction to UNIX command line, Instructor**, 3 day workshop to train biomedical researchers in Unix and latest next-generation sequence analysis techniques , Institute for Quant. and Comput. Biosciences (QCB), UCLA, Online version of the course : <https://github.com/QCB-Collaboratory/W1.UNIX.command.line/wiki>, Winter 2013 - present
- **CS M184, Instructor**, “Introduction to Computational and Systems Biology”, University of California, Los Angeles, Winter 2018
- **HG236A, Computational Instructor**, “Advanced Human Genetics Course”, University of California, Los Angeles, Fall 2016
- **CSc 7350, Instructor**, “Programming for Bioinformatics”, Georgia State University, Fall 2010, Spring 2012
- **CSc 2310, Instructor**, “Principles of Computer Programming”, Georgia State University, Spring 2010

PUBLICATIONS

Refereed Journal Articles

The most up-to-date list of publications is available at
<https://scholar.google.com/citations?user=9bgLa50AAAAAJ&hl=en>

51. **S. Mangul**, H. T. Yang, N. Strauli, F. Gruhl, T. Daley, Stephanie Christenson, Agata Wesolowska Andersen, Roberto Spreafico, Cydney Rios, Celeste Eng, Andrew D. Smith, Ryan D. Hernandez, Roel A. Ophoff, Jose Rodriguez Santana, Prescott G. Woodruff, Esteban Burchard, Max A. Seibold, Sagiv Shifman, Eleazar Eskin, Noah Zaitlen, “ROP : Dumpster diving in RNA-sequencing to find the source of 1 trillion reads across diverse adult human tissues”, *Genome biology* 19.1 (2018): 36.
50. Loes M Olde Loohuis, **S. Mangul (joint first author)** , Anil Ori, Guillaume Jospin, David Koslicki, Harry Taegyun Yang, Timothy Wu, Marco P Boks, Catherine Lomen-Hoerth, Martina Wiedau-Pazos, Rita Cantor, Willem M de Vos, Rene S Kahn, Eleazar Eskin, Roel A Ophoff, “Total RNA Sequencing reveals microbial communities in human blood and disease-specific effects.”, *Translational Psychiatry* 8.1 (2018): 96.
49. **S. Mangul**, L. Martin, E. Eskin “Involving undergraduates in genomics research to narrow the education-research gap.” *Nature Biotechnology*, 36, 369371 (2018)
48. **S. Mangul**, L. Martin, A. Hoffmann, M. Pellegrini, E. Eskin, “Addressing the digital divide in contemporary biology: Lessons from teaching UNIX”, *Trends in Biotechnology*, Volume 35, Issue 10, October 2017, Pages 901-903
47. A. Artyomenko, N. Wu (joint first author), **S. Mangul (joint first author)**, E. Eskin, R. Sun and A. Zelikovsky, “Long single-molecule reads can resolve the complexity of the Influenza virus composed of rare, closely related mutant variants”, *Journal of Computational Biology* Vol. 24, No. 6 (2017)
46. Ashis Saha, Yungil Kim, (authors), GTEx Consortium (including **Serghei Mangul**), (authors), Nicholas Van Wittenberghe, Fan Wu, “Co-expression networks reveal the tissue-specific regulation of transcription and splicing.” *Genome research* 27.11 (2017): 1843-1858.
45. Fan Yang, Jiebiao Wang, (authors), GTEx Consortium (including **Serghei Mangul**), (authors), Meng Wang, Nicholas Van Wittenberghe, “Identifying cis-mediators for trans-eQTLs across many human tissues using genomic mediation analysis.” *Genome research* 27.11 (2017): 1859-1871.
44. Alexis Battle, Christopher D Brown, Barbara E Engelhardt, Stephen B Montgomery, GTEx Consortium (including **Serghei Mangul**), “Genetic effects on gene expression across human tissues.” *Nature* 550.7675 (2017): 204-213

43. Meng How Tan, Qin Li, (authors), GTEx Consortium (including **Sergei Mangul**), (authors), Kazuko Nishikura, Jin Billy Li, “Dynamic landscape and regulation of RNA editing in mammals.” *Nature* 550.7675 (2017): 249-254
42. **S. Mangul**, HT Yang, F Hormozdiari, E Tseng, A. Zelikovsky, E. Eskin “HapIso: An Accurate Method for the Haplotype-Specific Isoforms Reconstruction from Long Single-Molecule Reads.” *IEEE Transactions on Nanobioscience (TNB)* 2017
41. E. Kang, L. J. Martin(joint first author), **S. Mangul(joint first author)**, E. Eskin, “Discovering Single Nucleotide Polymorphisms Regulating Human Gene Expression Using Allele-Specific Expression from RNA-seq Data”, *Genetics* 204.3 (2016): 1057-1064., 2017
40. S. Schokrpur, J. Hu, D. L. Moughon, P. Liu, L. C. Lin, K. Hermann, **S. Mangul**, W. Guan, M. Pellegrini, H. Xu, L. Wu
“CRISPR-Mediated VHL Knockout Generates an Improved Model for Metastatic Renal Cell Carcinoma.” *Scientific Reports* 6 (2016).
39. **S. Mangul**, N. Wu, N. Mancuso, A. Zelikovsky, R. Sun and E. Eskin, “Accurate HIV population assembly from ultra-deep sequencing data”, *Bioinformatics*, Bioinformatics, Proc. 17th Annual International Conference on Research in Computational Molecular Biology (ISMB 2014), (**acceptance rate 19%**)
38. **S. Mangul**, S. Al Seesi, A. Caciula, D. Brinza, I. Mandoiu and A. Zelikovsky, “Transcriptome Assembly and Quantification from Ion Torrent RNA-Seq Data”, *BMC Genomics*, 2014
37. **S. Mangul**, A. Caciula, O. Glebova, I. Mandoiu and A. Zelikovsky, “Improved Transcriptome Quantification and Reconstruction from RNA-Seq Reads using Partial Annotations”, *In Silico Biology(ISB) : An International Journal on Computational Molecular Biology*, 2012
36. M. Nicolae, **S. Mangul**, I. Mandoiu and A. Zelikovsky, “Estimation of alternative splicing isoform frequencies from RNA-Seq data”, *Algorithms for Molecular Biology*, 2011
35. I. Astrovskaya, B. Tork, **S. Mangul**, K. Westbrooks, I. Mandoiu, P. Balfe and A. Zelikovsky, “Inferring Viral Spectrum from 454 Pyrosequencing Reads”, *BMC Bioinformatics*, 2011

Refereed conference and workshop articles

34. **S. Mangul**, and D. Koslicki. “Reference-free comparison of microbial communities via de Bruijn graphs.” *Proc. 7th ACM Conference on Bioinformatics, Computational Biology and Biomedicine (ACM-BCB 2016)*
33. **S. Mangul**, HT Yang, F Hormozdiari, E Tseng, A. Zelikovsky, E. Eskin “HapIso: An Accurate Method for the Haplotype-Specific Isoforms Reconstruction from Long Single-Molecule Reads.” *Proc. International Symposium on Bioinformatics Research and Applications (ISBRA 2016)*
32. A. Artyomenko, N. Wu (joint first author), **S. Mangul(joint first author)**, E. Eskin, R. Sun and A. Zelikovsky, “Long single-molecule reads can resolve the complexity of the Influenza virus composed of rare, closely related mutant variants”, *Proc. 20th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2016)*, **acceptance rate 20%**
31. A. Artyomenko, **S. Mangul(joint first author)**, N. Wu, E. Eskin, R. Sun and A. Zelikovsky, “Reconstruction of influenza a virus variants from PacBio reads”, *Proc. 4th Workshop on Computational Advances for Next Generation Sequencing (CANGS 2014)*
30. A. Caciula, O. Glebova, A. Artyomenko, **S. Mangul**, J. Lindsay, I. Mandoiu and A. Zelikovsky, “Simulated Regression Algorithm for Transcriptome Quantification from RNA-Seq Data”, *Proc. 10th International Symposium on Bioinformatics Research and Applications (ISBRA 2014)*
29. **S. Mangul**, S. Al Seesi, A. Caciula, D. Brinza, I. Mandoiu and A. Zelikovsky, “Transcriptome Assembly and Quantification from Ion Torrent RNA-Seq Data”, *Proc. 3rd Workshop on Computational Advances for Next Generation Sequencing (CANGS 2013)*

28. A. Caciula, A. Zelikovsky, **S. Mangul**, J. Lindsay and I. Mandoiu, “Monte-Carlo Regression Algorithm for Isoform Frequency Estimation from RNA-Seq Data”, *Proc. 3rd Workshop on Computational Advances for Next Generation Sequencing (CANGS 2013)*
27. A. Caciula, **S. Mangul**, I. Mandoiu and A. Zelikovsky, “Transcriptome reconstruction from single RNA-Seq reads using expectation maximization algorithm with expected deviation minimization enhancement”, *Proc. 9th International Symposium on Bioinformatics Research and Applications (ISBRA 2013)*
26. **S. Mangul**, A. Caciula, S. Al Seesi, D. Brinza, A. Banday, R. Kanadia, I. Mandoiu and A. Zelikovsky, “Flexible Approach for Novel Transcript Reconstruction from RNA-Seq Data using Maximum Likelihood Integer Programming”, *Proc. 5th International Conference on Bioinformatics and Computational Biology (BICoB 2013)*
25. **S. Mangul**, A. Caciula, D. Brinza, I. Mandoiu and A. Zelikovsky, “TRIP: a method for novel transcript reconstruction from paired-end RNA-Seq reads”, *Highlights from the Eighth International Society for Computational Biology (ISCB) Student Council Symposium (2012)*
24. **S. Mangul**, A. Caciula, S. Al Seesi, D. Brinza, A. Banday, R. Kanadia, I. Mandoiu and A. Zelikovsky, “An Integer Programming Approach to Novel Transcript Reconstruction from Paired-End RNA-Seq Reads”, *Proc. 3rd ACM Conference on Bioinformatics, Computational Biology, and Biomedicine (ACM-BCB 2012)*
23. **S. Mangul**, A. Caciula, I. Mandoiu and A. Zelikovsky, “Novel Transcript Reconstruction from Paired-End RNA-Seq Reads Using Fragment Length Distribution”, *Proc. 2nd Computational Advances in Bio and Medical Sciences (ICCABS 2012)*
22. **S. Mangul**, A. Caciula, I. Mandoiu and A. Zelikovsky, “RNA-Seq based discovery and reconstruction of unannotated transcripts in partially annotated genomes”, *Proc. of Workshop on Computational Advances in Molecular Epidemiology (CAME 2011)*
21. **S. Mangul**, I. Astrovskaya, M. Nicolae, B. Tork, I. Mandoiu and A. Zelikovsky, “Maximum Likelihood Estimation of Incomplete Genomic Spectrum from HTS Data”, *Proc. 11th Workshop on Algorithms in Bioinformatics (WABI 2011)*, Lecture Notes in Bioinformatics, pp.
20. M. Nicolae, **S. Mangul**, I. Mandoiu and A. Zelikovsky, “Estimation of Alternative Splicing isoform Frequencies from RNA-Seq Data”, *Proc. 10th Workshop on Algorithms in Bioinformatics (WABI 2010)*, Lecture Notes in Bioinformatics 6293, pp. 202-214
19. Z. Comarova, **S. Mangul**, “Simulation of emission dispersion as the method of air quality management”, *Proc. Workshop Simulation and Assessment of Chemical Processes in a Multiphase Environment (2008)*, NATO Science for Peace and Security Series, pp. 403-408
18. **S. Mangul**, V. Cazac, L. Fedotova, I. Mangul, “The Specificity of Climate Change in the Dniester River Basin”, *Proc. International Conference Integrated Management of Natural Resources in the Transboundary Dniester River Basin (2004)*

Preprints and/or under review

17. **S. Mangul**, I. Mandric, and others, “Profiling adaptive immune repertoires across multiple human tissues by RNA Sequencing”, bioRxiv (2016): 089235, (under review Nature Communication)
16. **S. Mangul**, L. Martin, M. Distler, E. Eskin, J. Flint, “Towards reproducible, transparent, and systematic benchmarking of omics computational tools.” Open Science Framework (preprint) (under review Nature Genetics)
15. **S. Mangul**, S. V. Driesche, L. S. Martin, K. C. Martin, E. Eskin “UMI-Reducer: Collapsing duplicate sequencing reads via Unique Molecular Identifiers.” bioRxiv (2017): 103267. (under review BMC Bioinformatics)

14. N. LaPierre, **S. Mangul (joint first author)**, M. Alser, I. Mandric, N. C. Wu, D. Koslicki, E. Eskin, “MiCoP: Microbial Community Profiling method capable of detecting low abundance viral and fungal organisms in metagenomic samples” (under review BMC Bioinformatics)
13. C. W. K. Chiang, **S. Mangul**, C. R. Robles, W. W. Kretzschmar, N. Cai, K.S. Kendler, S. Sankararam, J. Flint, “A comprehensive map of genetic variation in the worlds largest ethnic group-Han Chinese”, bioRxiv (2017): 162982. (under review Genome Biology)
12. Diego Arambula, Elizabeth Czornyj, Umesh Ahuja, Blair Paul, Serghei Mangul, Partho Ghosh , Huatao Guo, Jeff F. Miller, “Host control of retroelement-guided protein evolution”, (under review Nature Communication)
11. Suraj P Bhat, Rajendra K Gangalum , **S. Mangul**, Dennis Mock , David J Kim , Raj K. Kashyap, “Cellular Complexity of the Developing Ocular Lens as Dissected by Single Cell Transcriptomics” (under review iScience)

In preparation

10. **S. Mangul**, S. Gusev, N. Zaitlen “Seeing Beyond the Target: Constructing Germline Research Cohorts from Clinical Tumor Sequencing” (in preparation)
9. **S. Mangul**, S. Schaffert, P. Khatri, “Toward decoding complete human immunome. Assemble recombined T and B cell receptor sequences across 70000 individuals”, (in preparation)
8. **S. Mangul**, Eleazar Eskin, Jonathan Flint, “A polygenic burden of ultra-rare deleterious coding variants increased in depressive disorder across Han Chinese women” (in preparation)
7. **S. Mangul**, Catie Grasso, Antoni Ribas, “Convventional sequencing provides affordable immune repetoire screening in cancer patients” (in preparation)

Books and book chapter

6. **S. Mangul**, H. T. Yang, Max A. Seibold, Sagiv Shifman, Eleazar Eskin, Noah Zaitlen, “Hidden treasures in contemporary RNA sequencing”, **book**, in preparation based on the invitation from Springer (SpringerBriefs format)
5. **S. Mangul**, N. C. Wu, E. Nenasteyeva, N. Mancuso, A. Zelikovsky, R. Sun, and E. Eskin, Applications of High-Fidelity Sequencing Protocol to RNA Viruses, **book chapter**, *Computational Methods for Next Generation Sequencing Data Analysis*, Wiley, 2016, pp. 85-104.
4. O. Glebova, Y. TemateTiagueu, A. Caciula, S. Al Seesi, A. Artyomenko, **S. Mangul**, J. Lindsay, I. I Mandoiu, A. Zelikovsky, “Transcriptome quantification and differential expression from NGS Data”, **book chapter**, *Computational Methods for Next Generation Sequencing Data Analysis*, Wiley, 2016, pp. 301-329.
3. I. Astrovsckaya, N. Mancuso, B. Tork, **S. Mangul**, A. Artyomenko, P. Skums, L. Ganova-Raeva, I.I. Mandoiu and A. Zelikovsky “Inferring Viral Quasispecies Spectra from Shotgun and Amplicon Next-Generation Sequencing Reads.” **book chapter**, *Genome Analysis: Current Procedures and Applications* (2014): 231.
2. S. Al Seesi, **S. Mangul**, A. Caciula, I. Mandoiu and A. Zelikovsky “Transcriptome Assembly and Quantication from RNA-Seq Data”, **book chapter**, *Genome Analysis: Current Procedures and Applications*, 2013
1. **S. Mangul**, A. Caciula, I. Mandoiu and A. Zelikovsky “RNA-Seq based transcriptome quantification and reconstruction guided by protein-coding gene annotation”, **book chapter**, *Algorithmic and AI Methods for Protein Bioinformatics*, 2012

UNDERGRADUATE
STUDENTS
SUPERVISED

- Russell Jared, undergraduate student, May 2017 - June 2018. Accepted to **UCLA PhD Bioinformatics Graduate Program**, 1 paper in preparation
- German Shabanets, summer high school student, June 2017 - July 2017. Accepted to **Stanford Undergraduate Computer Science Program**, 1 paper in preparation
- Taylor Shabani, summer high school student, June 2017 - July 2017. Accepted to **Duke Undergraduate Computer Science Program**, 1 paper in preparation
- Jeremy Rotman, QCBio B.I.G. Summer, Jun 2016 – Aug 2016. Accepted to **UCLA PhD Bioinformatics Graduate Program**, 1 papers published
- Harry Yang, undergraduate student, Aug 2015 - Aug 2017. Accepted to **UCLA PhD Bioinformatics Graduate Program**, 4 papers published

In total, I have supervised over **20** undergraduate students. The full list of undergraduates is available at <http://www.sergheimangul.com/undegrads-in-genomics/>

REVIEWER SERVICE

- Reviewer for *Bioinformatics*, *GigaScience*, *BMC Bioinformatics*, *BMC Genomics*, *Direct Biology*, *IEEE/ACM Transactions on Computational Biology and Bioinformatics*
- My open reviews are available at <https://publons.com/author/1492721/serghei-mangul>
- Program committees member of ISMB, RECOMB-Seq, ACM-BCB, ICCABS

SOFTWARE
PACKAGES

- **SBT** - a software platform to mine discarded tumor sequences from clinical sequencing <https://github.com/smangul1/seeing.beyond.target/wiki>
- **ImReP** - a computational method for rapid and accurate profiling of the adaptive immune repertoire from bulk RNA-Seq data, <https://github.com/mandricigor/imrep/wiki>
- **ROP** - a computational protocol to discover the source of all reads, which originate from complex RNA molecules, recombined B and T cell receptors and microbial communities <https://github.com/smangul1/rop/wiki>
- **Needle** - a method for comprehensive virome, mycobiome, and eukaryome profiling on the strain level. Needle combines alignment and assembly strategies, <https://github.com/smangul1/needle/wiki>
- **MiCoP** - a method for detecting low abundance viral and fungal organisms in metagenomic sample, <https://github.com/smangul1/miCoP>
- **Microbe-scope** - a method to visualize the metagenomics data in the form of interactive coverage plots. It allows to detect false positives based on the coverage corresponding microbial genomes, <https://github.com/smangul1/Microbe-scope/wiki>
- **HapIso** - a computational method to reconstruct the haploid transcriptome of a diploid organism from long single molecule reads, <https://github.com/smangul1/HapIso>
- **UMI-Reducer** - a computational protocol allowing to differentiate PCR duplicates from biological duplicates using UMIs. Tool is designed in collaboration with Prof. Kelsey Martin <https://github.com/smangul1/UMI-Reducer/wiki>
- **VGA** - a viral population assembly from ultra-deep sequencing data <http://genetics.cs.ucla.edu/vga/>
- **2SNV** - a method to reconstruct rare and closely related viral mutant variants from long single molecule reads, <http://alan.cs.gsu.edu/NGS/?q=content/2snv>
- **IsoEM** - a method to infer alternative splicing Isoform frequencies from RNA-Seq data <https://dna.engr.uconn.edu/>
- **Vsem** - a method to infer unknown haplotypes and their frequencies. This is an enhancement tool for IsoEM and ViSpA <http://www.cs.gsu.edu/serghei/?q=vsem>
- **Drut** - a method to discover and reconstruct unknown transcripts from RNA-Seq data using partial genome annotations. <http://www.cs.gsu.edu/serghei/?q=drut>
- **Trip** - a method to assemble novel isoform transcript from paired-end RNA-Seq data <http://www.cs.gsu.edu/serghei/?q=trip>
- **MaLTA** - a method to assemble and quantify transcripts from Ion-Torrent RNA-Seq data <http://www.cs.gsu.edu/serghei/?q=malta>

PRESENTATIONS
AND INVITED TALKS

38. **S. Mangul**, Conventional sequencing provides affordable screening of immune receptor repertoires and microbial communities, **Invited talk**, The Computational Biology Institute, George Washington University, Washington, DC, August 30, 2018
37. **S. Mangul**, Dumpster diving in RNA-sequencing to find the source of 1 trillion reads across GTEx human tissues, **Invited talk**, Northwestern University, Division of Pulmonary and Critical Care Medicine, Chicago, IL, July 9, 2018
36. **S. Mangul** ROP: Dumpster diving in RNA-sequencing to find the source of 1 trillion reads across diverse adult human tissues, **Highlight talk**, *17th European Conference on Computational Biology (ECCB 2018)*, Athens, Greece
35. **S. Mangul** ROP: Dumpster diving in RNA-sequencing to find the source of 1 trillion reads across diverse adult human tissues *Highlight talk at 9th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM BCB 2018)*, Washington, DC
34. **S. Mangul**, Involving undergraduates in genomics research to narrow the education-research gap, *21th Annual International Conference on Research in Computational Molecular Biology (ISMB 2018)*, *Education 2018*, Chicago, IL
33. **S. Mangul** Dumpster diving in RNA-sequencing to find the source of 1 trillion reads across diverse adult human tissues, *Highlight talk at RECOMB Satellite Workshop on Massively Parallel Sequencing (RECOMB-Seq 2018)*, Paris, France
32. **S. Mangul** Toward decoding complete human immunome. Assemble recombined T and B cell receptor sequences across 50000 individuals, *Next Generation Sequencing Conference (NGS 2018)*, Barcelona, Spain
31. **S. Mangul** Dumpster diving RNA-sequencing to find the source of 1 trillion reads across diverse adult human tissues, *Highlight talk at Next Generation Sequencing Conference (NGS 2018)*, **best oral presentation**, Barcelona, Spain
30. **S. Mangul**, Profiling immunoglobulin repertoires across multiple human tissues by RNA Sequencing, *3rd Adaptive Immune Receptor Repertoire (AIRR) Community Meeting*, Washington, DC
29. **S. Mangul**, Ultra-sensitive profiling of eukaryotic and viral communities across the US metropolitan areas, *IEEE 7th International Conference on Computational Advances in Bio and Medical Sciences (ICCABS 2017)*, Orlando, FL
28. **S. Mangul** Profiling immunoglobulin repertoires by RNA Sequencing across 8555 samples from 53 GTEx tissues, *American Society of Human Genetics (ASHG 2017)*, Orlando, FL
27. **S. Mangul**, Profiling immunoglobulin repertoires by RNA Sequencing across 8555 samples from 53 GTEx tissues, **Invited talk**, EBI Seminar Series, Hinxton, UK, September 19, 2017
26. **S. Mangul**, Profiling immunoglobulin repertoires across multiple human tissues by RNA Sequencing, *The 13th Basel Computational Biology Conference (BC2 2017)*, Basel, Switzerland
25. **S. Mangul**, Profiling immunoglobulin repertoires by RNA Sequencing across 8555 samples from 53 GTEx tissues, **Invited talk**, Stanford Computational and Systems Immunology Seminar Series, Stanford, CA, August 15, 2017
24. **S. Mangul**, Profiling immunoglobulin repertoires across multiple human tissues by RNA Sequencing, *8th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB 2017)*, *CAME 2017*, Boston, MA
23. **S. Mangul**, Profiling immunoglobulin repertoires across multiple human tissues by RNA Sequencing, *20th Annual International Conference on Research in Computational Molecular Biology (ISMB 2017)*, *HiTSeq 2017*, Prague, Czech Republic
22. **S. Mangul**, Viral and eukaryotic communities of urban ecosystems across the US metropolitan areas, *20th Annual International Conference on Research in Computational Molecular Biology (ISMB 2017)*, *CAMDA 2017*, Prague, Czech Republic

21. **S. Mangul**, Profiling adaptive immune repertoires across 544 individuals from 53 GTEx tissues by RNA Sequencing, *Computational Approaches in Precision Medicine*, Vienna, Austria
20. **S. Mangul**, Profiling Open RNA Sequencing data to study the adaptive immune repertoires, *PSB 2017 Workshop on Open Data for Discovery Science*, Big Island, HI
19. **S. Mangul**, Comprehensive analysis of RNA-sequencing to find the source of every last read across 544 individuals from 53 tissues, *ASHG 2016*, Vancouver, Canada
18. **S. Mangul**, “Dumpster diving in RNA-sequencing to find the source of every last read”, *W3 ECCB 2016*, The Hague, Netherlands
17. **S. Mangul**, “HapIso: An Accurate Method for the Haplotype-Specific Isoforms Reconstruction from Long Single-Molecule Reads”, *Computational challenges of third Generation DNA Sequencing data analysis, ECCB 2016*, Hague, Netherlands
16. **S. Mangul** “Dumpster diving in RNA-sequencing to find the source of every last read”, *UCLA Computational Genomics Summer Institute*, Los Angeles, CA
15. Lisa Gai, **S. Mangul** “Accounting for linkage disequilibrium when estimating the contribution of a genomic region”, *RECOMB-Genetics 2016*, Los Angeles, CA
14. **S. Mangul**, “Examining lost reads to survey the microbiome components of the human body across 43 human sites from 175 individuals”, **invited talk**, *PSB Microbiology Workshop 2016*, Big Island, HI
13. **S. Mangul**, “Haplotype phasing using long single-molecule reads”, **invited talk**, *SMRT Informatics Developers Conference 2016*, San Diego, CA
12. **S. Mangul**, “Examining lost reads to survey the microbiome and immune components of the human body across 43 human sites from 175 individuals”, *18th Annual International Conference on Research in Computational Molecular Biology (ISMB 2015)*, *CAMDA 2015*, Dublin, Ireland
11. **S. Mangul**, “HapIso : An accurate method for the haplotype-specific isoforms reconstruction from long single-molecule reads”, *18th Annual International Conference on Research in Computational Molecular Biology (ISMB 2015)*, *HiTSeq 2015*, Dublin, Ireland
10. **S. Mangul**, “Examining lost reads to survey the microbiome and immune components of the human body across multiple human tissues”, *2015 GTEx Project Community Meeting*, Chicago, IL
9. **S. Mangul**, “Dumpster Diving: Finding the source of every last read”, **oral presentation**, *12th [BC]2 - the Basel Computational Biology Conference (ECCB 2014)*, Basel, Switzerland
8. **S. Mangul**, Comprehensive analysis of RNA-sequencing to find the source of every last read across 544 individuals from 53 tissues, **Invited talk**, Bioinformatics Seminar Series, University of Natural Resources and Life Sciences, Vienna, Austria, August 15, 2014
7. **S. Mangul**, Comprehensive analysis of RNA-sequencing to find the source of every last read across 544 individuals from 53 tissues, **Invited talk**, Population Genetics Seminar Series, Vienna Graduate School of Population Genetics, Vienna, Austria, August 15, 2014
6. **S. Mangul**, “VGA: A method for viral quasispecies assembly from ultra-deep sequencing data”, **invited talk**, *4th Workshop on Computational Advances for Next Generation Sequencing 2014*, Miami, FL
5. **S. Mangul**, “An Integer Programming Approach to Novel Transcript Reconstruction from Paired-End RNA-Seq Reads”, **invited talk**, *Student Council Symposium 2012/ISMB 2012*, Long Beach, CA
4. **S. Mangul**, “Computational Methods for Transcriptome Reconstruction and Quantification using RNA-seq”, **public lecture**, *Center of Molecular Biology, University of Academy of Sciences of Moldova(2012)*, Chisinau, Moldova

3. **S. Mangul**, “Mathematical and Computational Approaches in High- Throughput Genomics”, **public lecture**, *Center of Molecular Biology, University of Academy of Sciences of Moldova(2012)*, Chisinau, Moldova
2. **S. Mangul**, “Its a DNA World: An introduction to the Next Generation Sequencing”, **public lecture**, *Center of Molecular Biology, University of Academy of Sciences of Moldova(2012)*, Chisinau, Moldova
1. **S. Mangul**, “The Next, Next Generation Sequencing - From Semiconductor to Single Molecule”, **info session**, *Life Technologies Info Session at UCLA(2011)*, UCLA ISPE, University of California, Los Angeles, CA

TUTORIALS

- “Human Microbiome Analysis: Computational Techniques and Challenges”, BC2 2015, Basel, Switzerland
- “Human Microbiome Analysis: Computational Techniques and Challenges”, BIBM 2015, Washington, D.C., US
- “Viral Population Analysis: Detection of Rare Variants and Full-length Genomes from Next-generation Sequencing Data”, BIBM 2014, Belfast, UK

SELECTED POSTERS

- **S. Mangul**, N. Strauli, R. Hernandez, R. Ophoff, M. Seibold, E. Eskin, N. Zaitlen, “Dumpster Diving: Finding the source of every last read”, ASHG 2015, Baltimore, MD, **2015 Reviewers Choice (top 10% of posters submitted), selected for Poster walk led by Deanna Church**
- **S. Mangul**, A. Caciula, I. Mandoiu and A. Zelikovsky, “An Integer Programming Approach to Novel Transcript Reconstruction from Paired-End RNA-Seq Reads”, *Poster at 8th International Symposium on Bioinformatics Research and Applications (ISBRA 2012)*, Dallas, TX, **best poster award**
- **S. Mangul**, D. Brinza, F. Hyland, “Orthogonal Error Correction Codes in Next Generation Sequencing”, *Poster at Life Technologies Intern Poster Session(2011)*, Foster City, CA, **best poster award**
- I. Astrovskaia, B. Tork, **S. Mangul**, I. Mandoiu, P. Balfe and A. Zelikovsky, “VISPA: Viral Spectrum Assembling Method”, *Poster at 1st IEEE International Conference on Computational Advances in Bio and medical Sciences (ICCABS 2011)*, Orlando, FL, **best poster award**

Total number of posters is **200** (available upon request)

AWARDS AND FELLOWSHIPS

International Organization for Migration (IOM) travel grant	May 2012, Aug 2017
ECCB 2016 Oxford Nanopore Travel Fellowship, The Hague, Netherlands	Sept 2016
The Jackson Laboratory Travel Scholarship Award, Bar Harbor, ME	Sept 2015
HiTSeq 2015 NSF Travel Fellowship, Dublin, Ireland	July 2015
ISMB 2014 NSF Travel Fellowship, Boston, MA	July 2014
CSHL Biology of Genomes 2014 Travel Fellowship, Cold Spring Harbor, NY	May 2014
PSB 2014 NIH Travel Fellowship, The Big Island of Hawaii	Jan 2014
ICCABS 2013 NSF Travel Fellowship, New Orleans, LA	July 2013
RECOMB 2013 NSF Travel Grant, Beijing, China	Apr 2013
ACM-BCB 2012 Travel Grant, Orlando, FL	Oct 2012
ECCB 2012 Travel Fellowship, SFETBR, Basel, Switzerland	Sept 2012
ISMB 2012 NSF Travel Fellowship, Long Beach, CA	July 2012
RECOMB 2012 NSF Travel Grant, Barcelona, Spain	Apr 2012
ICCABS 2011, 2012, 2013 NSF Travel Fellowship	Feb 2012
ISBRA 2011 NSF Travel Fellowship, Changsha, China	May 2011
Georgia State University Scholarship, Georgia State University, Atlanta	Jul 2008 – Jul 2009
Travel Fellowship, Institute of Mathematics, Romanian Academy	Jul 2007
Fellowship, CERMCS, Moldovan Research and Development Association	Sep 2006 - Jun 2007

SOFTWARE SKILLS **Languages:** Python, Unix shell scripts, C/C++, Pascal, Assembler, Prolog, HTML
Operating Systems: Unix/Linux/Ubuntu, Mac OS, Windows

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