Paula Restrep





Education

BA | Biological Sciences

George Washington University | 2017

- Concentration in Bioinformatics
- Cum Laude
- GPA: 3.51/4.0

Skills

Computing

Programming Languages Python • R • Bash Nextflow • Matlab/Octave **Operating Systems** Linux • Mac • Windows **HPC Platforms** Slurm • LSF • SGE • AWS IDEs & Reproducible Research Jupyter • RStudio • R Shiny Vim • Docker • Singularity

Bioinformatics

Data Types Whole Exome Sequencing (WES) RNA-sea Repositories & Databases TCGA • GEO • GitHub Bioconductor Sequence Alignment BWA • STAR • Bowtie SNV and CNV calling GATK • Samtools VarScan2 • CNVkit • XHMM Differential Gene Expression limma/voom • DEseg2 • Cufflinks **Immunogenomics** MixCR • NetMHC • Optitype

Laboratory

PCR • qPCR • Western Blot Mammalian Cell Culture SDS-PAGE

General

Software **LATEX** • Photoshop • Illustrator Languages English (Native) • Spanish (Fluent)

Experience

Icahn School of Medicine | Associate Researcher I (Bioinformatics)

Department of Genetics & Genomics Sciences

Lab of Dr. Bojan Losic | May 2018 - Present

- Conducted research in multiple disease systems, including inflammatory bowel disease (IBD), glioblastoma, and hepatocellular carcinoma.
- Integrated multi-omics data, including RNA-seq, whole-exome sequencing (WES). and RRBS methylation profiling to characterize intra-tumoral heterogeneity and its relationship to the tumor micro-environment.
- Built WES data processing pipelines for internal use using Nextflow.
- Collaborated on multiple projects with other departments internally, with clinicians, and with external biotech industry partners.
- Managed data storage and organization for a large multi-omics dataset in collaboration with biotech industry partners using ad-hoc scripts.
- Drafted and prepared manuscripts for submission to peer-reviewed journals.
- Presented research findings at internal department seminars and externally at conference poster sessions.

George Washington University | Undergraduate Research Assistant

Department of Pharmacology & Physiology

Lab of Dr. Anelia Horvath | Aug 2015 - May 2017

- Integrated WES and RNA-seq data from TCGA to characterize the gene expression profiles of tumor suppressor and oncogenes in cancer.
- Processed WES and RNA-seg data using standard pipelines for alignment, QC, and variant calling.
- Wrote and implemented ad-hoc filtering and processing scripts using Python.
- Implemented the usage of citation management software to streamline manuscript preparation.
- Contributed to manuscript preparation and data analysis for three peer-reviewed publications.
- Trained nine new lab members in using relevant pipelines, software, and analysis.

George Washington University | Intern

Department of Medicine, Microbiology, Immunology & Tropical Medicine Lab of Dr. Mudit Tyagi | May 2015 - Aug 2015

- Investigated protein expression in cell lines affected by HIV using western blot during a summer internship.
- Documented experiments in a laboratory notebook.
- Maintained cell lines using aseptic technique, mixed buffer solutions, and assisted with routine laboratory duties.
- Followed proper safety protocols for operating in a biosafety-level 2 environment.



Teaching

GWU | Teaching Assistant BIOC 6240: Next Generation Sequencing

- Spring 2016
- Spring 2017

Awards

Jun 2020 Scholars in Training (AACR) May 2016 Dean's List (GWU) Dec 2016 Dean's List (GWU)

Coursework

Bioinformatics (Grad. Level) Next Generation Sequencing (Grad. Level) Neural Circuits & Behavior Developmental Neurobiology Biochemistry

References

Available upon request.

Publications

- Restrepo P, Bubie A, Craig A, Labgaa I, Schwartz M, Thung S, Stolovitzky G, Losic B, Villanueva A. Intra-tumoral epigenetic heterogeneity signatures and aberrant molecular clocks in hepatocellular carcinoma. Manuscript in Preparation. 2020 Aug.
- Słowiński P, Li M, Restrepo P, Alomran N, Spurr LF, Miller C, Tsaneva-Atanasova K, Horvath A. GeTallele: a method for analysis of DNA and RNA allele frequency distributions. Frontiers in Bioengineering and Biotechnology. 2020 Aug 4. Accepted for Publication. Preprint available on BioRxiv. doi:10.1101/491209.
- von Felden J, Garcia-Lezana T, Dogra N, Kozlova E, Eren Ahsen M, Craig A J, Gifford S, Wunsch B, Smith J T, Kim S, Long J, Chen X, Labgaa I, Haber P K, Olsen R, Han D, Restrepo P, D'Avola D, Hernandez-Meza G, Allette K, Sebra R, Saberi B, Tabrizian P, Asgharpour A, Dieterich D, Llovet J M, Cordon-Cardo C, Tewari A, Schwartz M, Stolovitzky G, Losic B, Villanueva A. Unannotated small RNA clusters in extracellular vesicles detect early stage liver cancer. BioRxiv. 2020 May 02. doi:10.1101/2020.04.29.066183.
- Losic B, Craig AJ, Villacorta-Martin C, Martins-Filho SN, Akers N, Chen X, Ahsen ME, von Felden J, Labgaa I, D'Avola D, Allette K, Lira SA, Furtado GC, Garcia-Lezana T, Restrepo P, Stueck A, Ward SC, Fiel MI, Hiotis SP, Gunasekaran G, Sia D, Schadt EE, Sebra R, Schwartz M, Llovet JM, Thung S, Stolovitzky G, Villanueva A. Heterogeneous immune and tumor clonal evolution patterns in liver cancer. Nature Communications. 2020 Jan 15. doi:10.1038/s41467-019-14050-z. PubMed PMID: 31941899.
- Restrepo P, Yong R, Laface I, Tsankova N, Nael K, Akturk G, Sebra R, Gnjatic S, Hormigo A, Losic B. Tumoral and immune heterogeneity in PD-1 responsive glioblastoma: a case study. Cold Spring Harbor Molecular Case Studies. 2020 Jan 6. doi: 10.1101/mcs.a004762. PubMed PMID: 31907277.
- Spurr L, Li M, Alomran N, Zhang Q, Restrepo P, Movassagh M, Trenkov C, Tunnessen N, Apanasovich T, Crandall KA, Edwards N, Horvath A. Systematic pancancer analysis of somatic allele frequency. Scientific Reports. 2018 May 16. doi: 10.1038/s41598-018-25462-0. PubMed PMID: 29769535.
- Restrepo P, Movassagh M, Alomran N, Miller C, Li M, Trenkov C, Manchev Y, Bahl S, Warnken S, Spurr L, Apanasovich T, Crandall K, Edwards N, Horvath A. Overexpressed somatic alleles are enriched in functional elements in Breast Cancer. Scientific Reports. 2017 Aug 15. doi: 10.1038/s41598-017-08416-w. PubMed PMID: 28811643.
- Movassagh M, Alomran N, Mudvari P, Dede M, Dede C, Kowsari K, Restrepo P, Cauley E, Bahl S, Li M, Waterhouse W, Tsaneva-Atanasova K, Edwards N, Horvath A. RNA2DNAlign: nucleotide resolution allele asymmetries through quantitative assessment of RNA and DNA paired sequencing data. Nucleic Acids Research. 2016 Dec 15. doi: 10.1093/nar/gkw757. PubMed PMID: 27576531.

Posters

- Bubie A, Restrepo P, Craig A, Labgaa I, Schwartz M, Thung S, Stolovitzky G, Losic B, Villanueva A. Regional DNA methylation profiling reveals novel epigenetic intratumoral heterogeneity signatures and aberrant molecular clocks in hepatocellular carcinoma. Poster Presentation. Abstract nr 1507. American Association for Cancer Research Annual Meeting. 2020. Virtual Format.
- Restrepo P, Yong R, Laface I, Tsankova N, Gnjatic S, Hormigo A, Losic B. Mapping tumoral and immune heterogeneity in PD-1 responsive glioblastoma. Poster Presentation. Abstract nr 2528. American Association for Cancer Research Annual Meeting, 2019. Atlanta, GA.
- Restrepo P, Yong R, Laface I, Tsankova N, Gnjatic S, Hormigo A, Losic B. Mapping tumoral and immune heterogeneity in PD-1 responsive glioblastoma. Poster Presentation. Abstract nr B088. Fourth CRI-CIMT-EATI-AACR International Cancer Immunotherapy Conference: Translating Science into Survival. 2018. New York, NY.

