# JASVINDER AHUJA

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# PROFESSIONAL SUMMARY

Results-driven data expert with over 10 years of experience in leading research projects, conducting data analysis, and presenting findings to diverse audiences. Proficient in Linux based environments, R, Python, Excel, and SQL.

# **EDUCATION**

#### **Purdue University - West Lafayette**

February 2024 - August 2024

Certification, Business Analysis

- BABOK
- Microsoft Excel
- SOL
- PowerBI
- Tableau

# **Cleveland State University**

January 2006 - December 2014

GPA: 3.83

PhD, Cell & Molecular Biology

#### PROFESSIONAL EXPERIENCE

# **Oregon Health and Science University**

Portland, OR, USA

Research Assistant Professor

May 2022 - February 2024

- Improved identification of infertility-causing mutations by using Population Sampling Probabilities (PSAP) modeling R, Python and high performance computing (HPC, similar to AWS) for data analysis and storage, involving DNA sequencing from over 1500 patients.
- Secured NIH funding (\$70k) for functional analysis of causal mutations by presenting findings to National Institutes of Health.
- Enhanced research collaboration by co-managing two postdoctoral fellows and co-coordinating research projects involving 20 medical centers globally, ensuring effective DNA sequencing and analysis.

#### National Institutes of Health Bethesda, MD, USA

Research Fellow

February 2015 - May 2022

- Created a 1% heterozygosity in a 6kb DNA stretch for a homologous recombination study by designing variants using Gibson assembly.
- Phased SNPs in DNA sequences by developing and running custom scripts in R, Python, and bash on Biowulf cluster using slurm and snakemake.
- Improved DNA recombination understanding by publishing a new DNA repair model in Molecular Cell 2021, contributing to gamete formation research.

#### **Cleveland State University**

Cleveland, OH, USA

Graduate Assistant

- January 2006 December 2014
- Published a groundbreaking discovery of a proteasome mutant affecting DNA recombination in top STEM journal Science 2017, contributing to the understanding of genetic mechanisms.
- Enhanced research efficiency by developing plugins for ImageJ and using Excel-VBA and R for data analysis, facilitating more accurate and streamlined data processing.
- Advanced knowledge in gamete formation by creating mutant yeast strains and evaluating protein requirements through targeted mutations, recombination, and immunofluorescence microscopy, leading to significant insights in genetic research.
- Improved student research skills by mentoring students in experimental techniques and data analysis, fostering a collaborative and educational research environment.

### **SKILLS**

**Skills:** R, Excel/Numbers/Sheets, Powerpoint, Linux/Unix, Bash, Slurm, Data Analysis, Business Analytics, Project Management, Python, Git, MySQL, Power BI, Tableau, Docker, Statistics, Research

## SELECTED PODIUM PRESENTATIONS

- 2020 "Mechanisms of homologous recombination during meiosis." Department of Reproductive and Development Sciences & Department of Genetics at Oregon National Primate Research Center, Portland, OR.
- 2018 "Fine-structure analysis of meiotic recombinants reveals that divergent mechanisms lead to formation of noncrossovers and crossovers" at Gordon Research Seminar, Colby Sawyer College, New London NH.
- 2018 "Fine-structure analysis of meiotic recombination products" Mid Atlantic Mitosis and Meiosis Meeting, John Hopkins University, Baltimore, MD.

# SELECTED SCIENTIFIC PUBLICATIONS

- **Ahuja, J.S.**, Sandhu, R., Huang L., Klein F., Börner G.V. (2024). Temporal and Functional Relationship between Synaptonemal Complex Morphogenesis and Recombination during Meiosis. *bioRxiv*, 2024.01.11.575218.
- **Ahuja, J.S.,** Harvey C., Wheeler, D.L. and Lichten, M.J. (2021). Repeated strand invasion and extensive branch migration are hallmarks of meiotic recombination. *Mol. Cell.* 81:4258–4270.e4. PMID: 34453891.
- **Ahuja, J.S.**, Sandhu, R., Mainpal, R., Lawson, C., Henley, H., Hunt, P.A., Yanowitz, J.L., Borner, G.V. (2017). Control of meiotic pairing and recombination by chromosomally tethered 26S proteasome. *Science*. 355: 408-11. PMID: 28059715.
- **Ahuja, J.S.,** and Börner, G.V. (2011). Analysis of meiotic recombination intermediates by two-dimensional gel electrophoresis. *Methods Mol Biol.* 745:99-116. PMID: 21660691.

# PROFESSIONAL MEMBERSHIPS

International Institute of Business Analysis (Portland OR, Chapter)