Henry Hollis

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PROFESSIONAL SUMMARY

Biomedical Engineer and Computer Scientist with extensive experience in computational genomics, single-cell transcriptomics, and algorithm development. Expert in applying rigorous software engineering principles to complex biological problems, specifically in neurodegenerative disease and circadian biology. Proven ability to build novel analysis pipelines, visualize high-dimensional data for top-tier publications (*Neuron*, *Nature Neuroscience*, *Frontiers*).

TECHNICAL SKILLS

- **Languages:** R (Advanced), Python, Bash/Shell scripting.
- **Bioinformatics:** snRNA-seq analysis, Seurat, Scanpy, Genomic Data Visualization, Time-series analysis.
- **Data Science:** Machine Learning, Statistical Modeling, High-Performance Computing (HPC), Dimensionality Reduction (PCA, UMAP, t-SNE).
- **Tools:** Git/GitHub, Docker, Adobe Illustrator (Scientific Illustration), CNC/CAD.

PROFESSIONAL EXPERIENCE

Doctoral Researcher *Drexel University* | *2021-2026*

- Designed and implemented custom computational pipelines to analyze single-cell RNA sequencing (snRNA-seq) datasets, identifying key circadian transcriptomic changes in Alzheimer's disease models.
- Processed large-scale genomic datasets, optimizing algorithms for memory efficiency and runtime on high-performance computing clusters.
- Authored and co-authored manuscripts for high-impact journals including *Neuron* and *Nature Neuroscience*; created production-quality graphical abstracts to distill complex methodological concepts into clear visual narratives.
- Collaborated with wet-lab experimentalists to translate biological questions into executable code and statistical tests.

EDUCATION

Ph.D. in Biomedical Engineering *Drexel University, Philadelphia, PA.* | GPA: 4.0 (Expected Grad May 2026)

B.S. in Computer Science, Minor in Mathematics *Wake Forest University, Winston-Salem, NC.* | GPA: 3.96

SELECTED PUBLICATIONS

- **Hollis**, et al. "Reconstructed cell-type-specific rhythms in human brain link Alzheimer's pathology, circadian stress, and ribosomal disruption" *Neuron*, 2025.
- **Hollis**, et al. "Multi-tissue transcriptional changes and core circadian clock disruption following intensive care" *Frontiers*, 2022.
- Sheehan, et al. "A glial circadian gene expression atlas reveals cell-type and disease-specific reprogramming in response to amyloid pathology or aging" *Nat Neuroscience,* 2025.