# The relationship between gene expression correlation and 3D genome organization

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# **Big Question**

Do gene expressions across cells correlate when genes are close to each other along DNA?



	cell1	cell2	cell3	cell4	cell5	cell6	cell7
gene1	59	62	86	70	14	37	93
gene2	60	55	91	67	11	44	94
gene3	26	95	84	78	12	46	89



Measure counts of RNA transcripts of a certain gene in a cell to determine number of times that gene is expressed in that cell

## Example of RNA-seq table

	cell1	cell2				
gene1	92	3				
gene2	76	66				
gene3	78	49				
gene4	27	41				
# of times gone1 has been expressed						

# of times gene1 has been expressed in cell1

#### **Pearson Correlation**

measuring the strength of the linear relationship between two variables



https://en.wikipedia.org/wiki/Pearson\_correlation\_coefficient#/media/File:Correlation\_examples2.svg

#### The data

"Single-cell RNA sequencing of mouse brain and lung vascular and vessel-associated cell types" (GSE98816; Sci Data. 2018 Aug 21;5:180160 He et. al)

scRNA-seq on 19937 genes of 3186 mouse brain cells, which was used to determine 15 cell types



- PC Pericytes v- venous SMC - Smooth muscle cells MG - Microglia OL - Oligodendrocytes FB - Vascular Fibroblast-like cell EC - Endothelial cells
- **AC-Astrocytes**

cap - capillary a - aterial aa - arteriolar 1,2,3 - subtypes



https://www.nature.com/articles/sdata2018160 https://figshare.com/articles/Description of each single-cell samples/6170075/1

#### What we did

Plot each pair of genes as a point on the xyplane

x=DNA base distance between pair of genes (distance between midpoints of both genes)

y=Pearson correlation of expression between the pair of genes across all brain cells

Only consider gene pairs within a single chromosome

No significant pattern found



#### Violin plot of chromosome 1



## Violin plot of chromosome 1 (closer range)



#### What about TADs (Topologically Associated Domains)?

Regions of DNA where loci inside them contact each other frequently compared to loci outside of TADs

Shown in Hi-C as small, bright squares along the diagonal

Smaller than compartments, which are groups of regions of DNA whereby loci in the same compartment contact each other than loci in different compartments



https://advances.sciencemag.org/content/5/4/eaaw1668

#### Gene pairs intra- and inter- TADs

chr1 gene pair dist vs corr intraTAD

intraTAD: gene pairs 0.8 within a single TAD 0.6 gene pair corr (Pearson) 0.4 0.2 0.0 TADs are of retinal neurons from Falk et. al. 250000 500000 1000000 1250000 1500000 1750000 2000000 0 750000 gene pair dist (DNA bases)

#### Gene pairs intra- and inter- TADs

interTAD: gene pairs between two TADs



TADs are of retinal neurons from Falk et. al.

#### Gene pairs intra- and inter- TADs with violin plot



intra-TAD on left side of each violin (light blue)

inter-TAD on right side of each violin (dark blue)

gene pair dist (DNA bases)

#### Gene expression correlation within a single cell type



PC cell type from He et. al.; cell type containing the highest number of cells

#### Gene expression correlation within a single cell type



capilEC cell type from He et. al.; cell type containing the 2nd highest number of cells

## What we found

No significant relationship between distance and correlation of gene pairs

Correlation is not enhanced with TADs or cell type filtering

## Other people's work

- For E. Coli there is a pattern, but it is highly dependent on gene coregulation



https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5395161/

## **Future Work**

In the future we would like to investigate:

- Coregulation (sharing molecules that activate them)
- Enhancers (short regions of DNA that make a gene more likely to be transcribed)/insulators
- Single Cell Assay for Transposase-Accessible Chromatin using sequencing (scATAC-seq)
- compartments/more Hi-C data
- different ways of calculating distance between genes (3D)

# Bibliography

Luecken, Malte D, and Fabian J Theis. "Current Best Practices in Single-Cell RNA-Seq Analysis: a Tutorial." Molecular Systems Biology, John Wiley & Sons, Ltd, 19 June 2019, https://www.embopress.org/doi/10.15252/msb.20188746.

Kruglyak, Semyon, and Haixu Tang. "Regulation of adjacent yeast genes." Trends in Genetics. Cell, www.cell.com/trends/genetics/comments/ S0168-9525(99)01941-1. Accessed 6 Sept. 2019.

Szabo, Quentin, et al. "Principles of Genome Folding into Topologically Associating Domains." Science Advances, American Association for the Advancement of Science, 1 Apr. 2019, https://advances.sciencemag.org/content/5/4/eaaw1668.

van Berkum, Nynke L, et al. "Hi-C: a Method to Study the Three-Dimensional Architecture of Genomes." Journal of Visualized Experiments : JoVE, MyJove Corporation, 6 May 2010, https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3149993/.

## Works Cited

Falk, Martin, et al. "Heterochromatin Drives Compartmentalization of Inverted and Conventional Nuclei." Nature, U.S. National Library of Medicine, 5 June 2019, https://www.ncbi.nlm.nih.gov/pubmed/31168090.

He, Liqun, et al. "Single-Cell RNA Sequencing of Mouse Brain and Lung Vascular and Vessel-Associated Cell Types." Nature News, Nature Publishing Group, 21 Aug. 2018, https://www.nature.com/articles/sdata2018160.

Pannier, Lucia, et al. "Effect of Genomic Distance on Coexpression of Coregulated Genes in E. Coli." PloS One, Public Library of Science, 18 Apr. 2017, https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5395161/.

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