Statistical Methods for Exploring Spatial Arrangement of Myelin Basic Protein in the Human Visual Cortex

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Joint work with Ahad Daudi, Pratheepa Jeganathan and Kathy Murphy
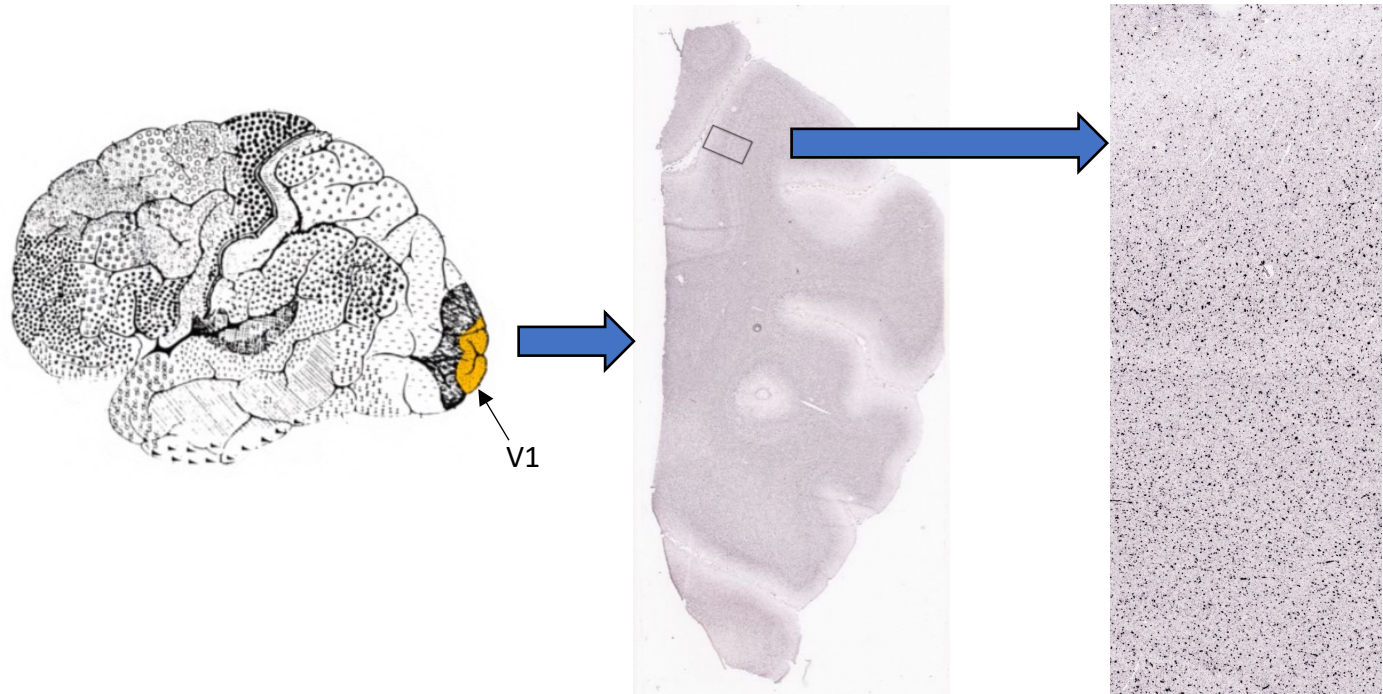
BioC 2022, Lightning Talk

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Introduction

Problem of concern: The **spatial arrangement** of **Myelin basic protein** in the **human primary visual cortex (V1)**.
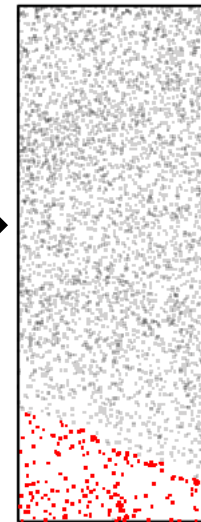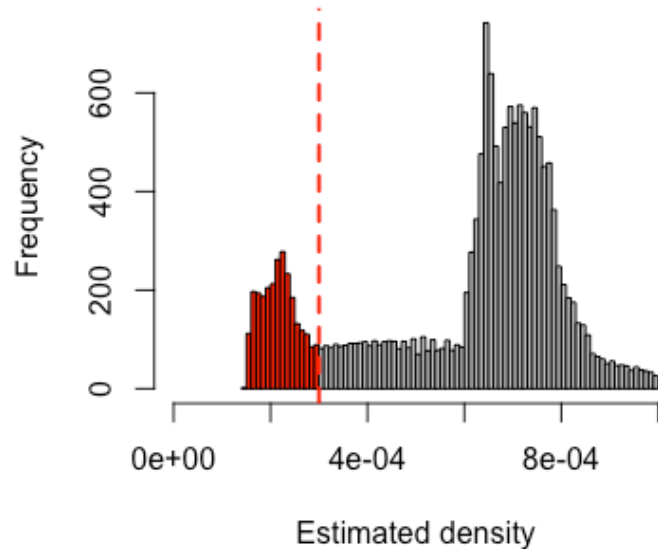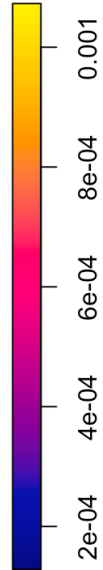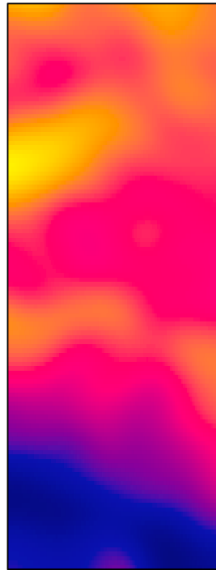

An example of primary visual cortex (V1)

How we get the data

Methods

- Convert the dataframe to a ppp object.

spatstat::ppp or SpatialExperiment

- Kernel density estimation of cells with edge correction.

spatstat::density

- Generate histogram of estimated intensity.
- Vertical line denotes the threshold used to identify layers.
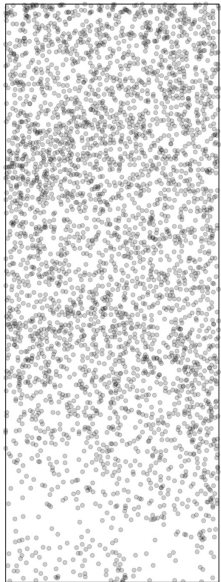
Apply the following methods to the entire point pattern and segmented point pattern:
- Nearest neighbor distance
- Ripley's K function
- Paired correlation function*
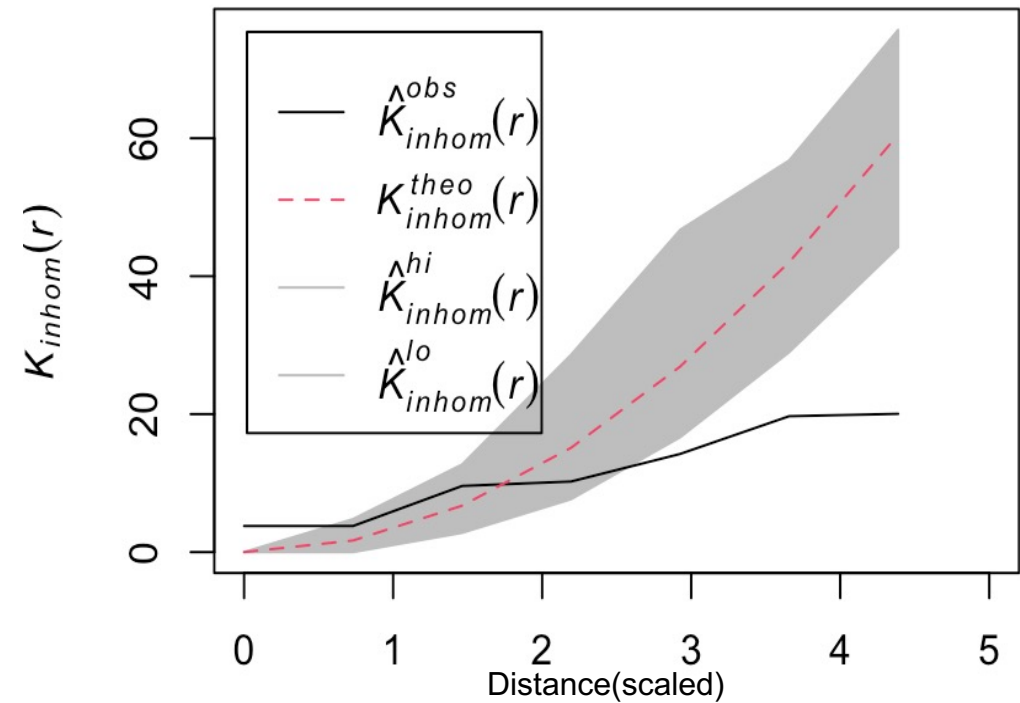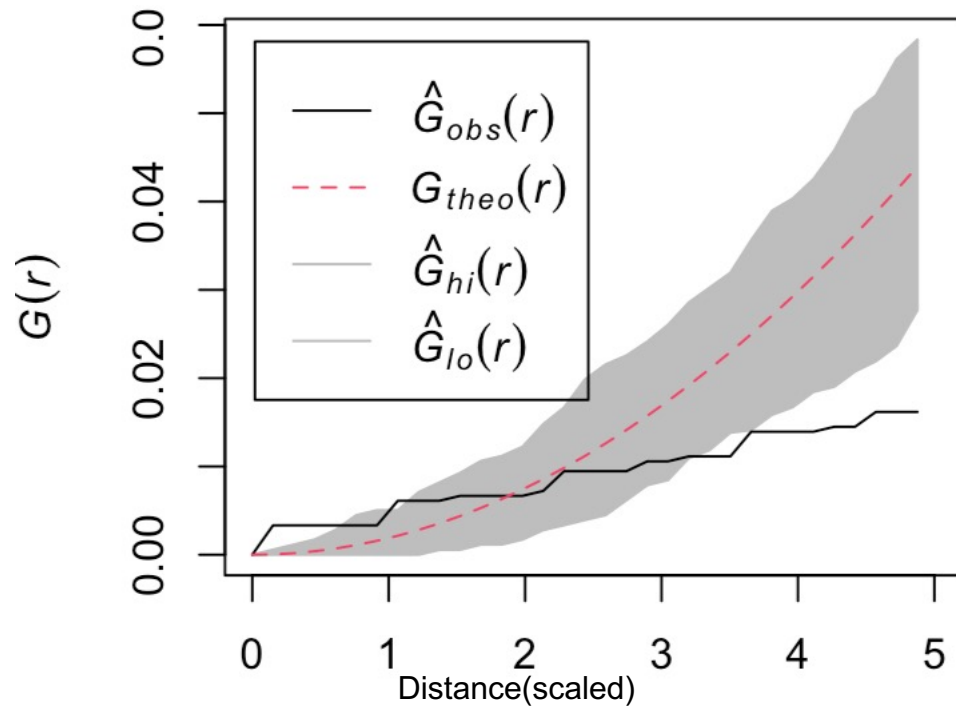- L function*

* Not presented in the slides

Methods

- Identify complete spatial randomness (CSR)

    - Nearest neighbor distance G(r): average number of MBP cells within distance r. To compute this, we use the command spatstat::Gest.

- Compute the intensity of MBP cells

    - Kernel density estimation with edge correction.

- Identify spatial dependence

    -Ripley's K function: $K(r) = \frac{1}{\lambda}$ E[number of additional events] with in distance r and intensity λ.

    -If the point pattern is a complete random pattern, we use spatstat::Kest. If not, we use spatstat::Kinhom.

Results

We plot the observed values along with the theoretical values.

- Black line – Observed G(r) or K(r) function are computed based on the observed point pattern.
- Envelope – the simulation-based envelope is generated under the assumption of homogeneous Poisson process (HPP).
- Red line – the average value of G(r) or K(r) under the assumption of HPP.

If there are clustering trend, we expect excess of small r compared to the envelope. We also have a similar expectation for K(r).
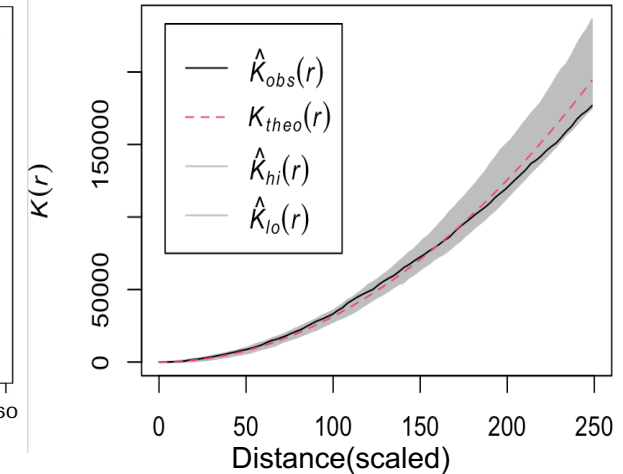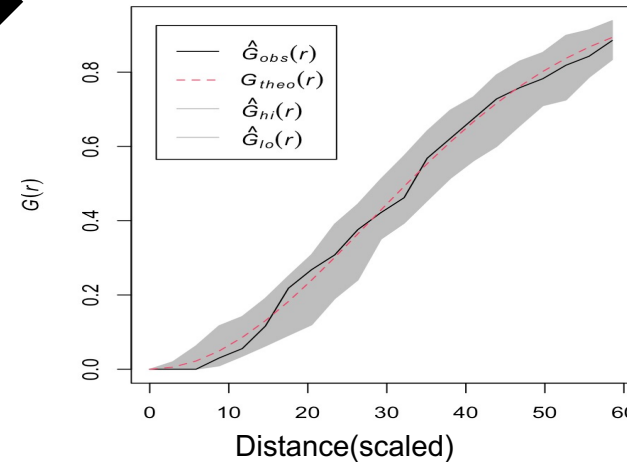
Results & Summary

Point pattern of the entire observation window:
- G function shows that the point pattern is not CSR at some distances.
- K function shows there are spatial dependence at some distances.
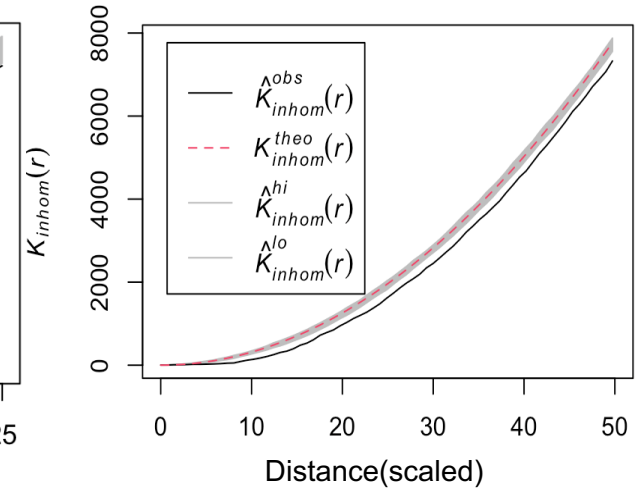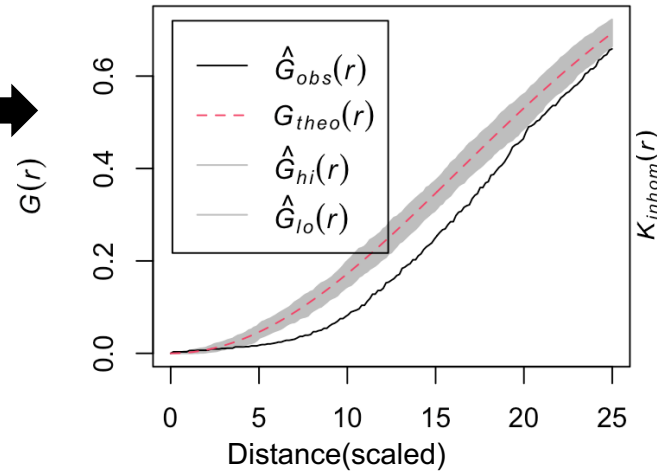
Point pattern of the selected layer:
- G function shows that the selected layer is CSR
- K function shows that there is no spatial dependency.

Summary:
- Some parts of the point pattern are complete spatial randomness (CSR).
  - Thus, we can make **compact window** for other parts. And this would improve the **computational efficiency** for statistical modeling.
- We integrate R/Bioconductor packages to understand spatial arrangement of the primary visual cortex V1.

Acknowledgement