

# Statistical analysis of Biological point patterns

*supervised by*

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Interest in analysing spatial point patterns is rapidly expanding across many fields of science particularly within biology where the development of automation technologies has enabled scientists to capture large datasets at a much greater granularity and lower cost than ever before. The rapid growth in size and complexity of this data has led to a growth in interest in developing spatial statistical techniques tailored for biological applications. The purpose of this project will be to investigate and develop statistical techniques to maximise information extraction from complex spatial point patterns derived from: cell populations derived from (i) neurodegenerative disease or (ii) immune cell function datasets, or (iii) investigating the clustering behaviour (oligomerisation) of fluorescently labelled membrane proteins evaluated using single molecule imaging techniques with implications for the diagnosis and treatment of cancer. Working closely with interdisciplinary collaborators, these project(s) are intended to develop novel spatial statistical to uncover novel biological insights and require high-level skills in mathematics, stochastic processes theory and computer programming.

## REFERENCES

- [1] BADDELEY, A.J. AND TURNER, R., *Spatstat: An R package for analyzing spatial point patterns*, Journal of Statistical Software, 2004.
- [2] DIGGLE, P.J., *Statistical analysis of spatial and spatio-temporal point patterns*, Chapman and Hall/CRC, 2013.