**Polyploidy, regular patterning of genome copies, and alternative control of DNA partitioning in the Lyme disease spirochete**

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**Brief code description.**

This document summarizes the code generated and/or used as part of the study “Polyploidy, regular patterning of genome copies, and alternative control of DNA partitioning in the Lyme disease spirochete” by Constantin N. Takacs et al. and uploaded to the GitHub code repository at (<https://github.com/JacobsWagnerLab/published>). The description provided here is intended to be a cursory description of the code we provide, rather than an exhaustive usage guide.

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| Code | Description |
| loadimseries.m | Loads a folder of microscopy images into the MATLAB workspace |
| loadIMstack.m | Loads a stack of microscopy images into the MATLAB workspace |
| Modified\_Find\_Irregular\_Spots.m | Identifies fluorescent spots cellist from input fluorescence images |
| VisualizeSpotDetection.m | Visualizes the spots identifies using the code above |
| add\_spots\_to\_cellList.m | Identifies fluorescent spots using Modified\_Find\_Irregular\_Spots and associates them with the corresponding cells in the cellList |
| export\_to\_table.m | Exports the data from a cellList format to a MATLAB table format |
| extract\_field.m | Extracts the data belonging to specified fields from the cellList |
| calculate\_distance\_ratio.m | Performs various spacing analyses of the spots detected in the cells |
| simulate\_distance\_ratio.m | For each cell, it redistributes the spots randomly along the same length, then performs the same spacing analyses as the code above |