**Morphology Analysis Microglia morphData (FracLac and Skeletonize)**

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| **Characteristic** | **Unit** | **Interpretion** |
| Fractal dimenstion | DB (Box counting) | Cell complexity (higher = complexer) |
| Lacunarity | Mean pixels per box | Cell shape (higher = more heterogenic shape) |
| Span ratio |  | Cell shape (higher = more rod-like/“auseinandergezogen“) |
| Density |  | Cell complexity (lower = complexer); ramification index |
| Roughness |  | Cell complexity(higher = complexer) |
| Cell area | px² (area in pixels oft he cell enclosing the pixelated part of an image) | Cell size |
| Cell perimeter | px (perimeter in pixels oft he cell enclosing the pixelated part of an image) | Cell size and complexity (higher = bigger or more complex) |
| Circularity |  | Cell shape (higher = rounder; 1 = circle) |
| Convex hull area | px² (area in pixels oft he convex hull enclosing the pixelated part of an image) | Cell size |
| Convex hull perimeter | px (perimeter in pixels oft he convex hull enclosing the pixelated part of an image) | Cell size and complexity (higher = bigger or more complex) |
| Convex hull circularity |  | Cell shape (higher = rounder; 1 = circle) |
| Average branch length | µm | Cell shape |
| Maximum branch length | µm | Cell shape |
| Junction | actual junctions = merging neighbor junction voxels (Junction voxels: if they have more than 2 neighbors) | Cell complexity |

Analyze Skeleton documentation: <https://imagej.net/plugins/analyze-skeleton/>

Fraclac documentation: https://imagej.nih.gov/ij/plugins/fraclac/fraclac-manual.pdf