

TIAM+

extending the Tool for Integrative Analysis of Motility
<https://github.com/r-medina/TIAM->

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Features

Helmuth *et al.* paper titled “A novel supervised trajectory segmentation algorithm identifies distinct types of human adenovirus motion in host cells” offers a methodology (features and procedure) for classifying segments of cell tracks. The features for some trajectory part P_j of l_w steps are:

- ▶ Net displacement
- ▶ Straightness
- ▶ Bending
- ▶ Efficiency
- ▶ Asymmetry
- ▶ Point position skewness
- ▶ Point Position kurtosis

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- ▶ Net displacement:

$$p_1 = \|\vec{x}_{j+l_w} - \vec{x}_j\|$$

- ▶ Straightness
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- ▶ Net displacement
- ▶ Straightness:

$$p_2 = \frac{1}{l_w - 1} \sum_{i=j}^{j+l_w-2} \cos \beta_i$$

- ▶ Bending
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$$p_3 = \frac{1}{l_w - 1} \sum_{i=j}^{j+l_w-2} \sin \beta_i$$

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- ▶ Net displacement
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- ▶ Efficiency:

$$p_4 = \frac{\|\vec{x}_{j+l_w} - \vec{x}_j\|^2}{l_w \sum_{i=j}^{j+l_w-1} \vec{s}_i^2}$$

where \vec{s}_i is the “step” from \vec{x}_i to \vec{x}_{i+1}

- ▶ Asymmetry
- ▶ Point position skewness
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- ▶ Net displacement
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- ▶ Efficiency
- ▶ Asymmetry:

$$p_5 = -\log \left(1 - \frac{(\lambda_1 - \lambda_2)^2}{2(\lambda_1 + \lambda_2)^2} \right)$$

where λ_1 and λ_2 are the eigenvalues of R , the 2D radius of gyration tensor of the set of all points in P_j

- ▶ Point position skewness
- ▶ Point Position kurtosis

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- ▶ Asymmetry
- ▶ Point position skewness:

$$p_6 = \frac{\sqrt{l_w + 1} \sum_{i=j}^{j+l_w} (x_i - \langle x_i \rangle)^3}{\left(\sum_{i=j}^{j+l_w} (x_i - \langle x_i \rangle)^2 \right)^{3/2}}$$

- ▶ Point Position kurtosis:

$$p_7 = \frac{\sqrt{l_w + 1} \sum_{i=j}^{j+l_w} (x_i - \langle x_i \rangle)^4}{\left(\sum_{i=j}^{j+l_w} (x_i - \langle x_i \rangle)^2 \right)^2}$$

where x_i is the projection of the points in P_j onto the dominant eigenvector \vec{v} of R : $x_i = \vec{x}_i \cdot \vec{v}$.

Features

Other features we're considering:

- ▶ Mean-squared displacement (MSD):

$$MSD(\Delta t) = \langle \{(x(t + \Delta t)) - (x(t))\}^2 + \{(x(t + \Delta t)) - (x(t))\}^2 \rangle$$

- ▶ Diffusion coefficient: taken from the initial slope of the MSD for a given track segment
- ▶ Feature developed by Simson *et al.* to detect temporary confinement:

$$L = \begin{cases} -\log(\Psi) - 1 & \Psi \leq 0.1 \\ 0 & \Psi > 0.1 \end{cases}$$

where $\log \Psi = 0.2048 - 2.5117Dt/R^2$ and D is the diffusion coefficient, t is some period of time, and R is the maximum distance the particle travelled during that time.

Algorithm

Helmuth *et al.* propose using a support vector machine (SVM) learning model—we intend to do the same.