Have you ever noticed how ink spreads in water? Its area expands proportionally to the amount of time elapsed. This is an example of normal diffusion, but things are anomalous in nature. We can observe patterns of diffusion that are significantly faster (super-diffusion) or slower (sub-diffusion) than ink in water. This is described as anomalous diffusion, and it happens at all scales, from the movement of individual molecules to the migration of entire populations.

**Main methods:**
- Classical statistical analysis
- Machine learning algorithms

Which choice is the best?

**CONDOR is an innovative method that combines machine learning with classical statistics to provide a deeper understanding of the underlying diffusion process [1].**

**REFERENCES**


github.com/sam-labUCL/CONDOR.git

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**LOOK. LEARN. CREATE.**

- High processing speed (up to 80k trajectories/s)
- Great accuracy (up to 91%)
- Robustness to the addition of localisation noise

**CONDOR performance.** (a) Mean accuracy for 1D, 2D, and 3D datasets, each consisting of 10k trajectories. (b) Classification accuracy as a function of the signal to noise ratio, which measures the strength of noise by which the trajectories are corrupted. The dotted lines represent the overall performance as seen in (a) [1].

By processing experimental trajectories, CONDOR can efficiently characterise the subdiffusive dynamics exhibited by biomolecules, such as RNA and membrane receptors [2].

- Understanding biological processes for drug development
- Optimising the design of new materials
- Improving environmental monitoring