

Fast Step Transition and State Identification (STaSI) for Discrete Single-Molecule Data Analysis

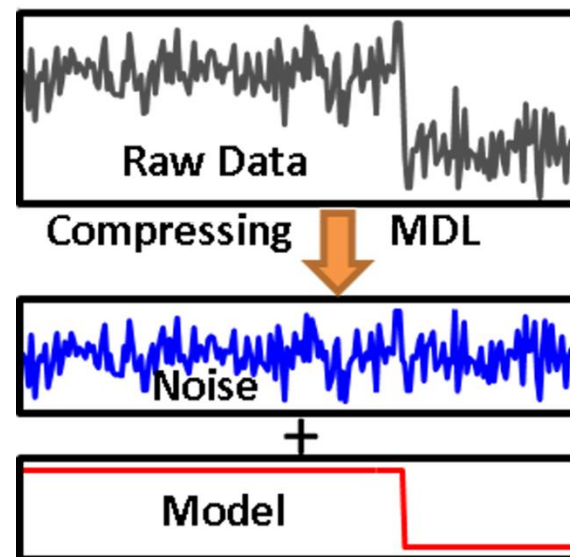
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Jan. 08, 2015





RICE

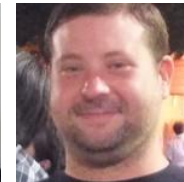
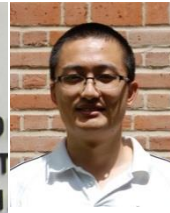
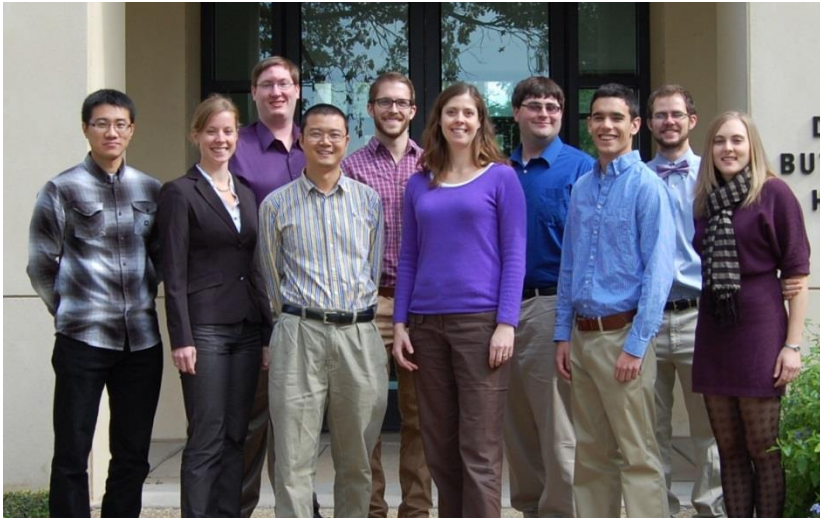
Acknowledgements

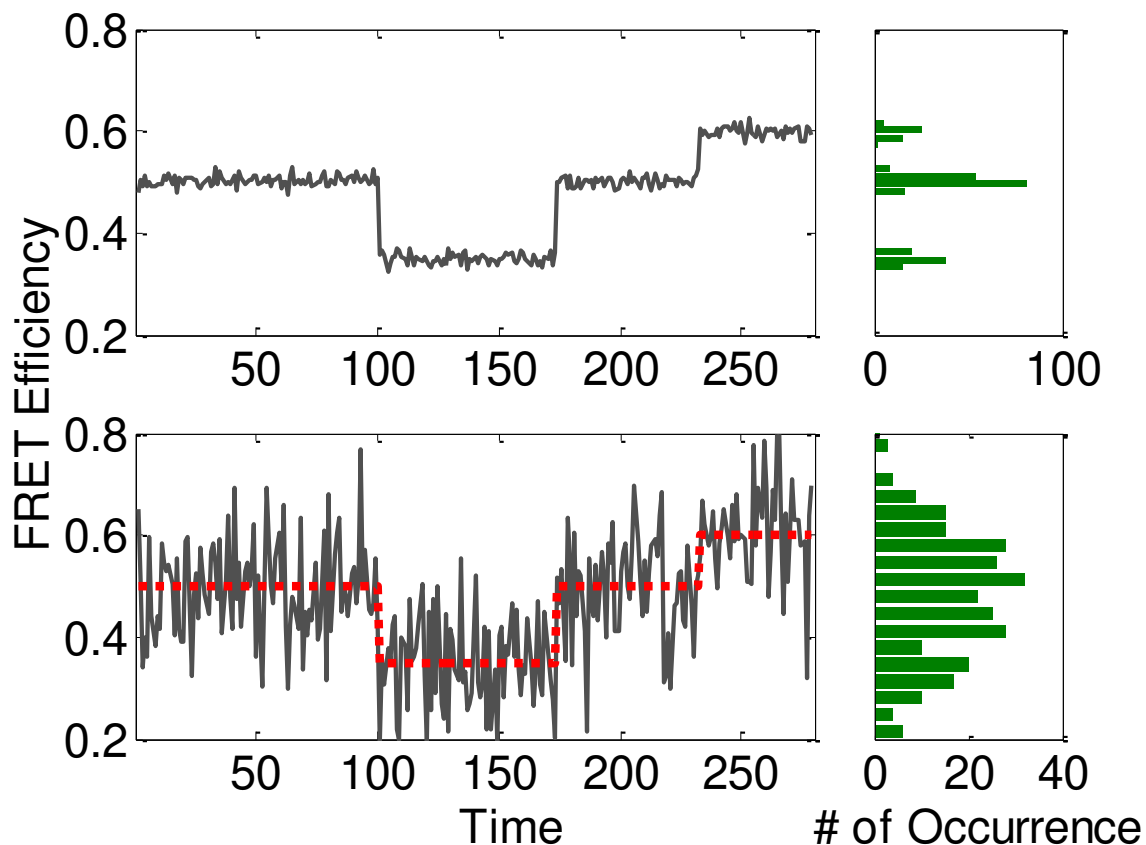
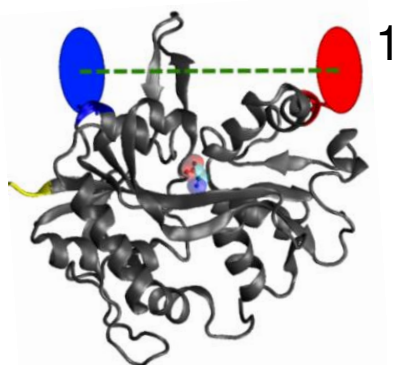
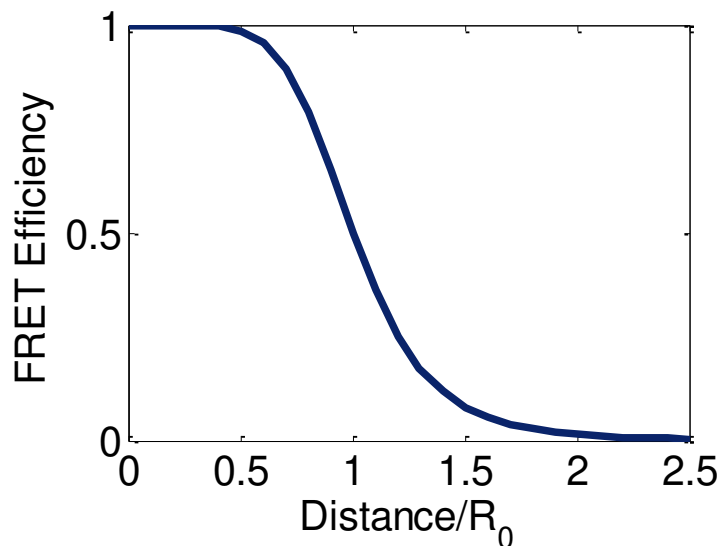


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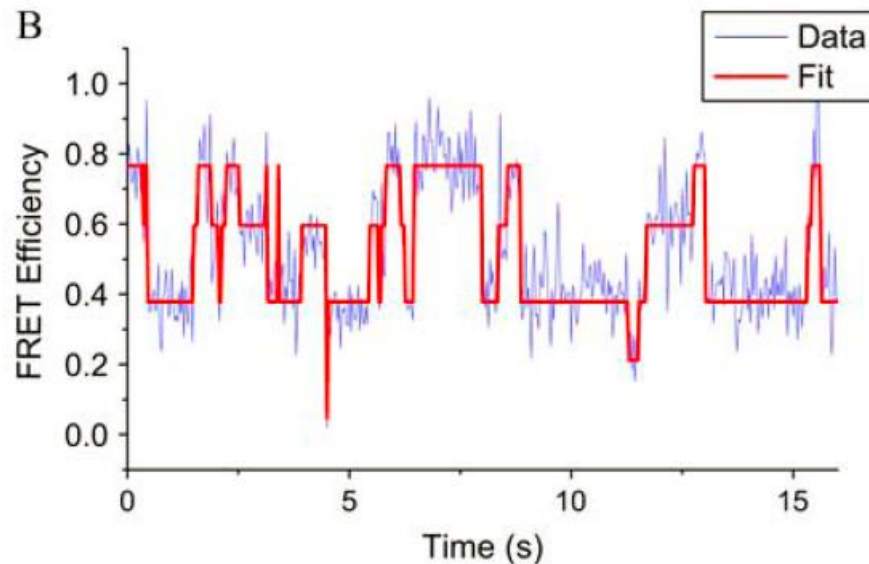
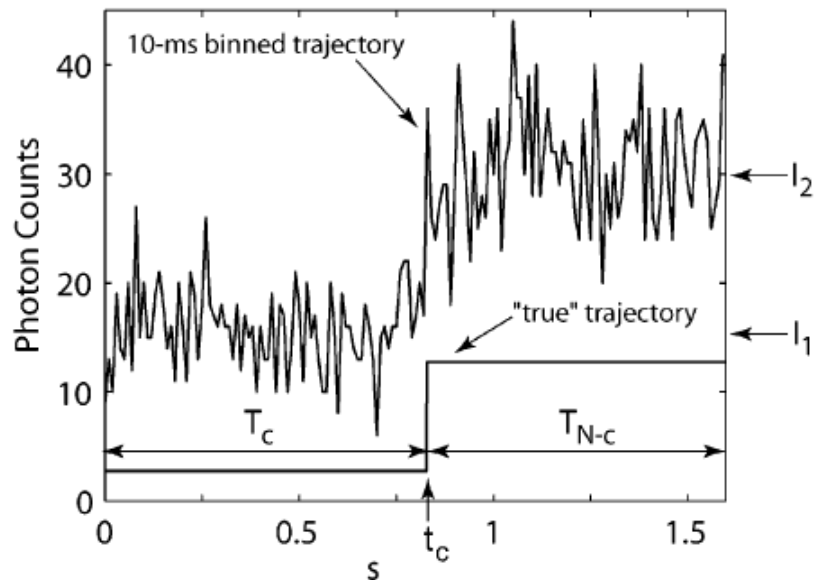


FRET: Förster (fluorescence) resonance energy transfer

1 Cooper, D. et. al. unpublished image

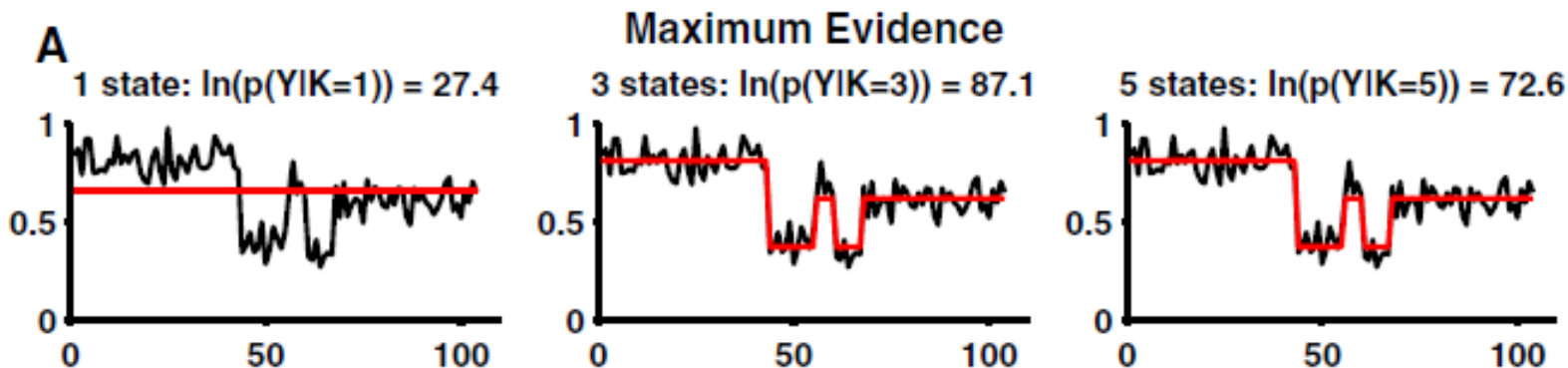


RICE Cutting Edge Methods



Watkins and Yang, *J. Phys. Chem. B* 2005

McKinney, Joo and Ha, *Biophys. J.* 2006



Bronson, et. al. *Biophys. J.* 2009

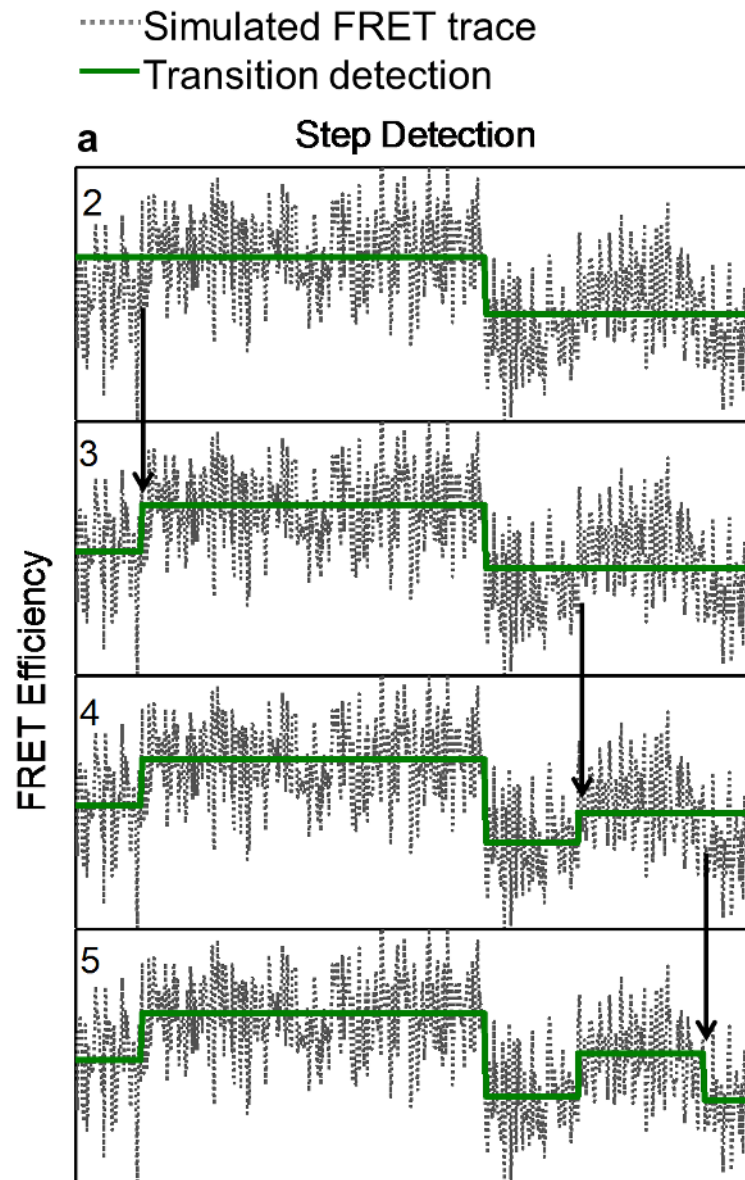


- Targeting binned data
- 1) Fitting of different number of states
 - Student's t test
- 2) Determine the optimum number of states
 - Minimum Description Length Principle (MDL)



Step 1: Step Detection using Student's t -test:

$$R(t_i) = \frac{|I_2(t_{i+1}, t_N) - I_1(t_1, t_i)|}{\sigma \sqrt{\frac{1}{i} + \frac{1}{N-i}}}$$



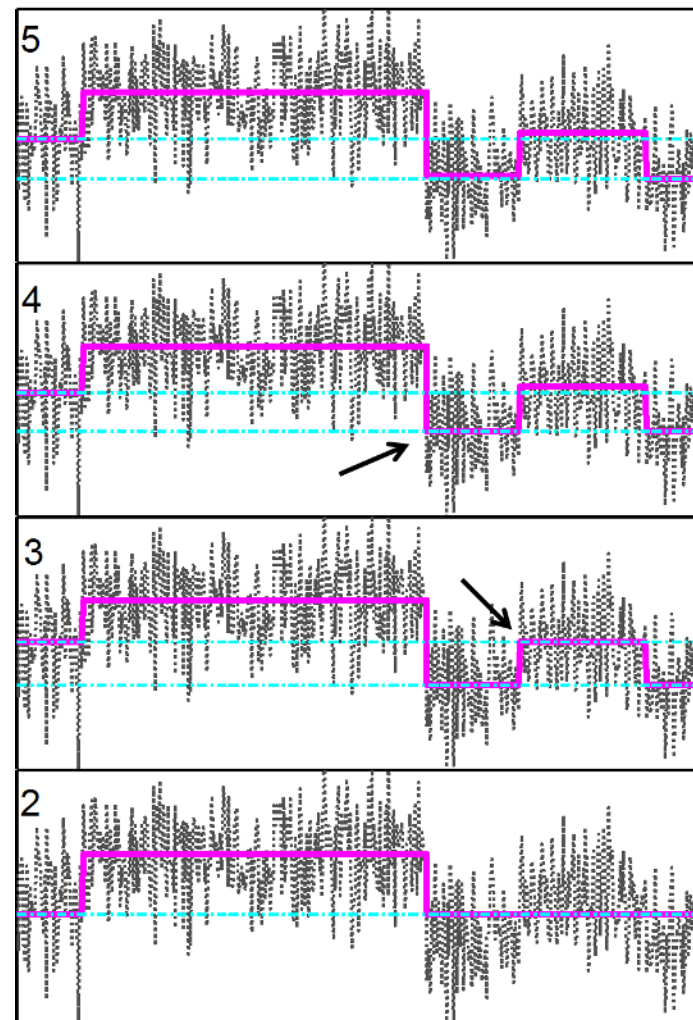


Step 2: Group similar states using a greedy algorithm

$$M(i, j) \propto (m_i + m_j) * I_{i,j}^2 - (m_i * I_i^2 + m_j * I_j^2)$$

— Grouped states
- - - Indication of unequal/equal states

b State Identification





Step 3: Determine the Optimum Number of States

$$\text{MDL} = F + G$$

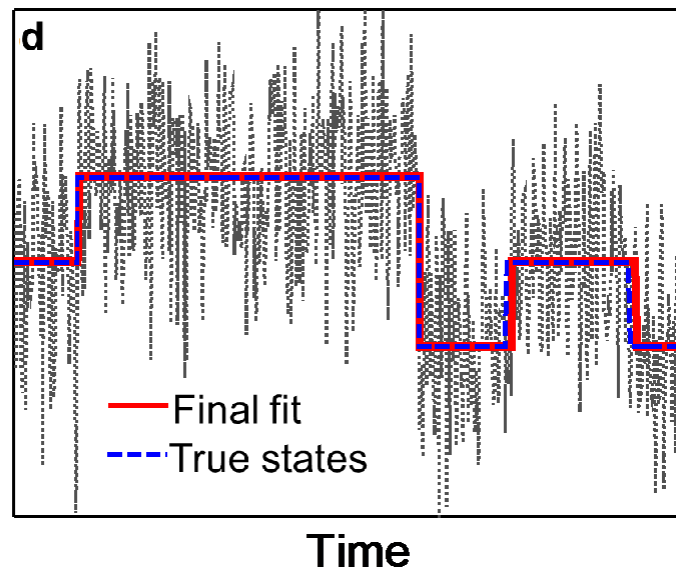
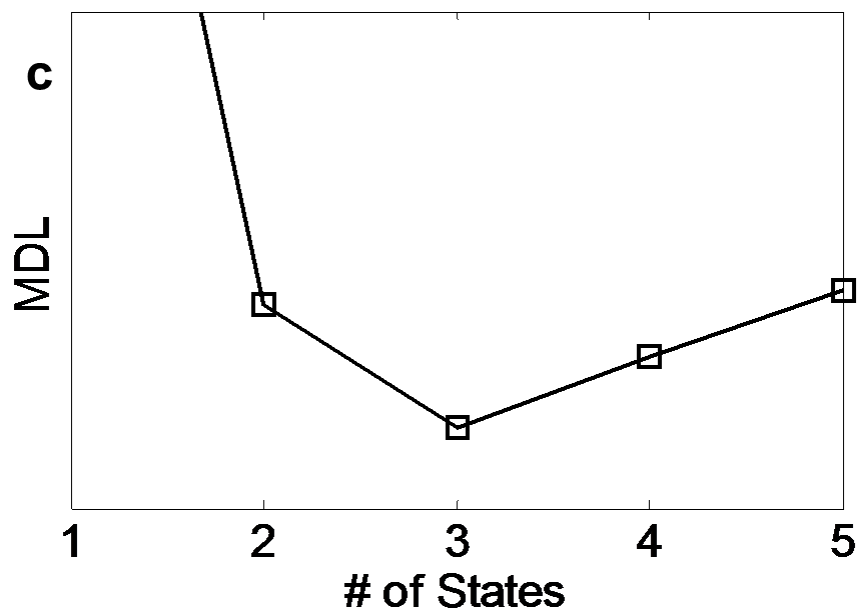
$$F = \frac{\sum_{i=1}^N |y(t_i) - y_{fit}(t_i)|}{2\sigma}$$

$$G = \frac{k}{2} \ln \frac{1}{2\pi} + k \ln \frac{V}{\sigma} + \frac{N_{\text{tp}}}{2} \ln N + \frac{1}{2} \left(\sum_{i=1}^k \ln n_i + \sum_{j=1}^{N_{\text{tp}}} \ln \frac{T_j^2}{\sigma^2} \right)$$

of states

of data points in i^{th} state

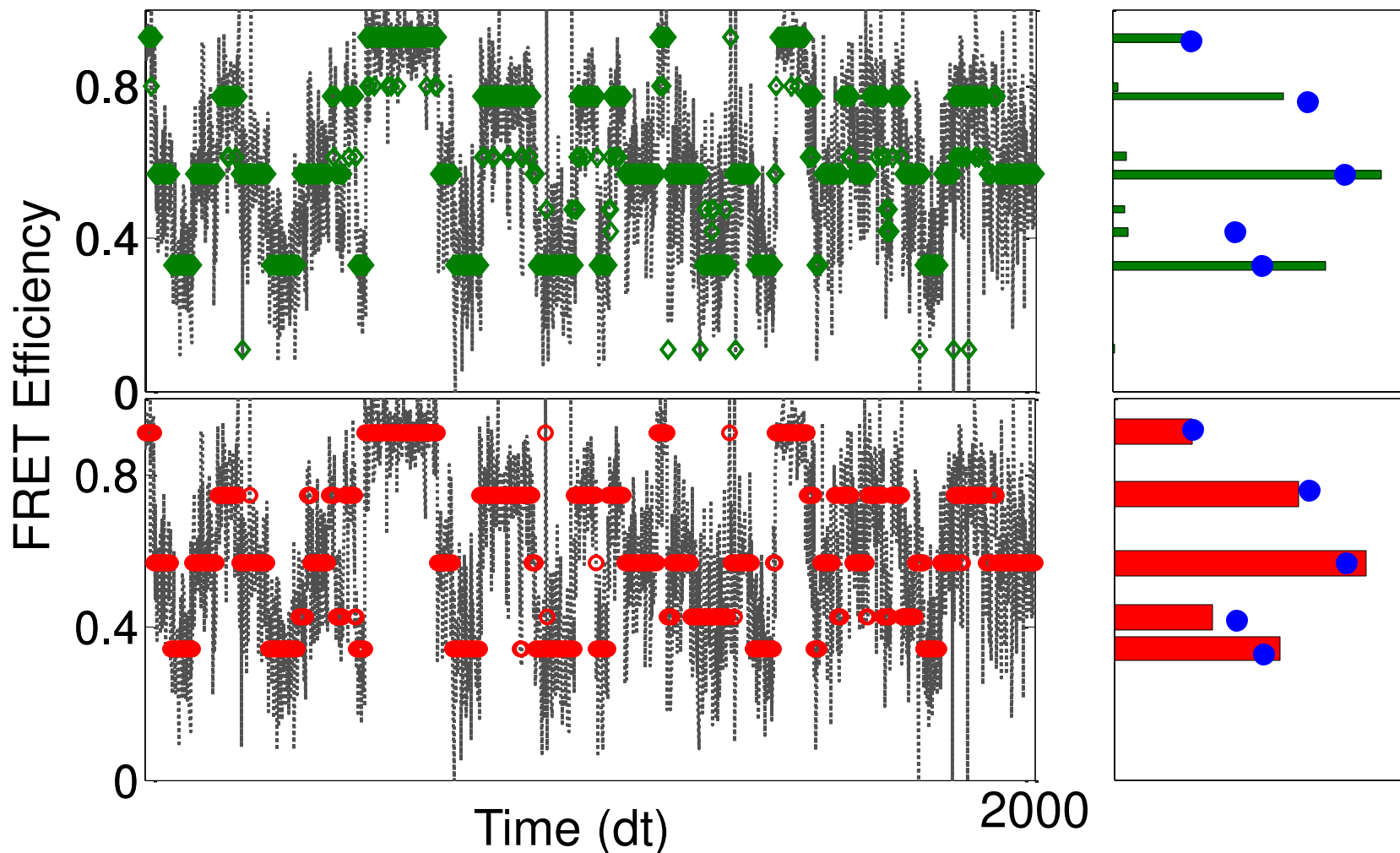
transitions





RICE Performance: More Accurate

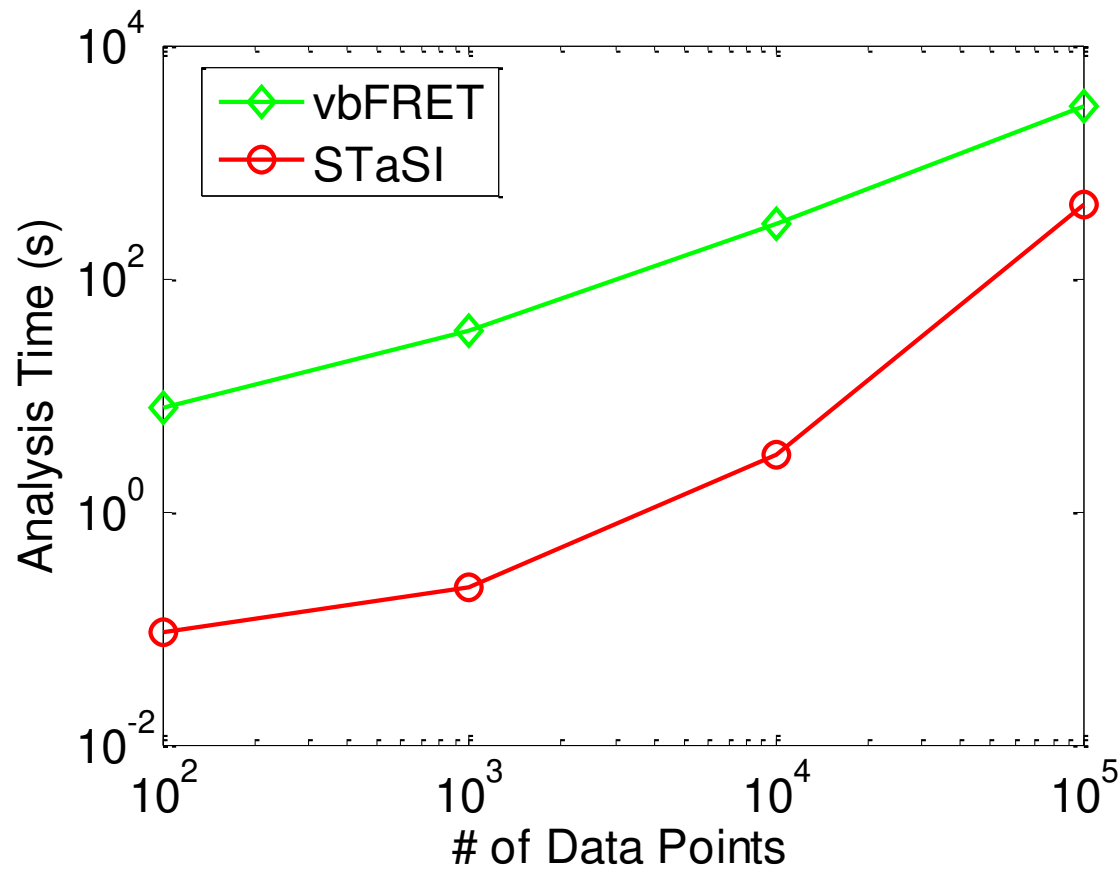
Gray: Simulated FRET trace Red: StaSI fit
Green: vbFRET fit¹ Blue: True states



¹ Bronson, J. E., et. al. *Biophys. J.* **2009**, 97, 3196-3205.

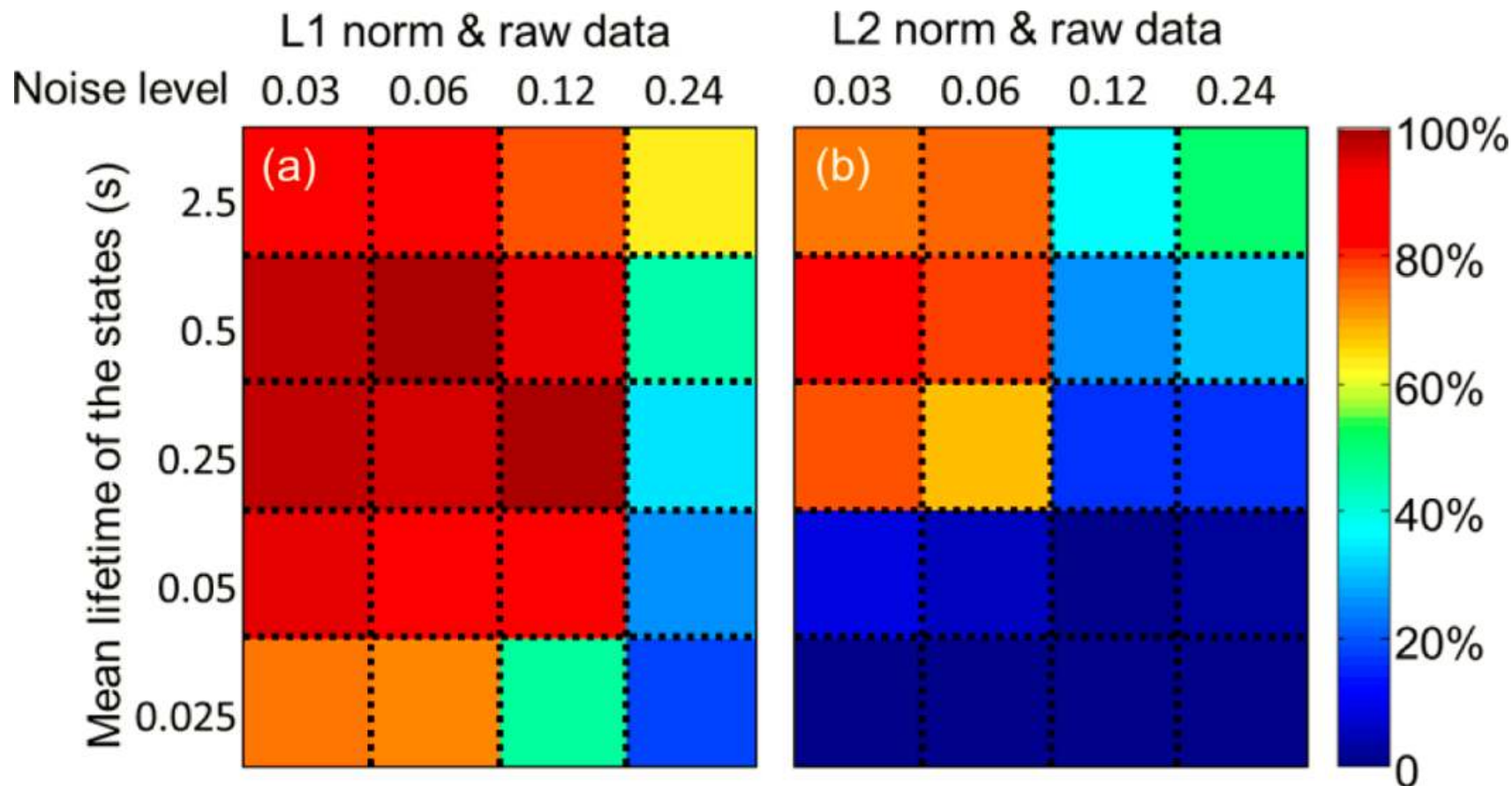


RICE Performance: Faster in Computation





RICE The Importance of L1 norm

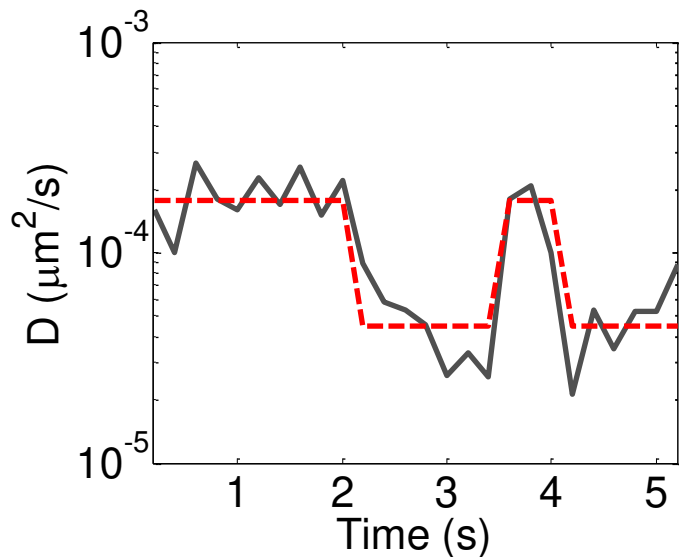


$$F = \frac{\sum_{i=1}^N |y(t_i) - y_{fit}(t_i)|}{2\sigma}$$

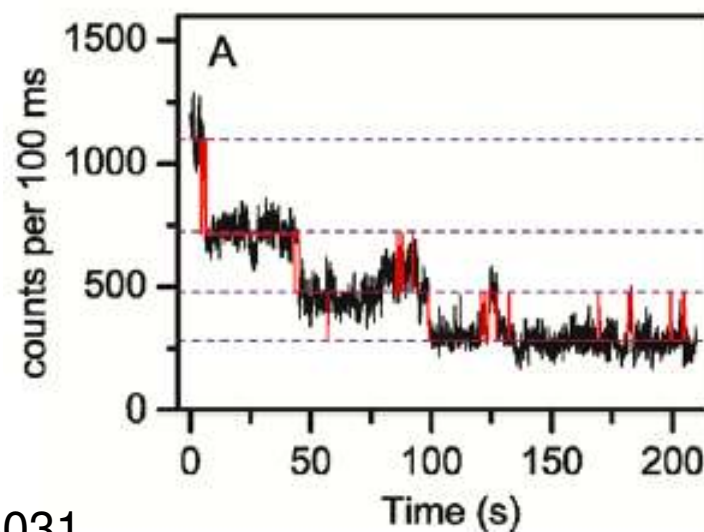
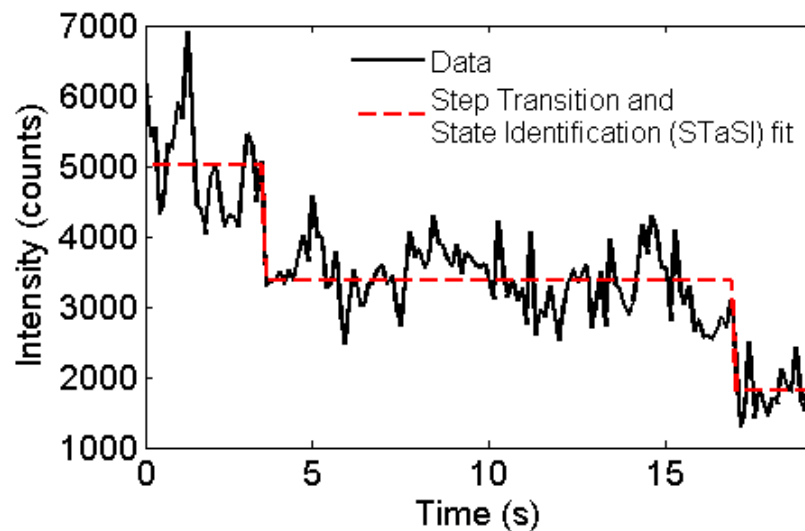
$$F = \frac{\sum_{i=1}^N (y(t_i) - y_{fit}(t_i))^2}{2\sigma^2}$$



Instantaneous diffusion coefficient



Photobleaching steps





RICE The Program with GUI

Untitled 1

FRET Efficiency

Data Points

Relative Population

Run StaSI

Status
Done analysis.

View Results

x axis controller

Left Position Range

Use 5 States Save

MDL value

of States

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- STaSI provides comprehensive, objective analysis of multiple traces requiring few user inputs about the underlying physical models, and is faster and more precise in determining the number of states than established and cutting-edge methods for single-molecule data analysis.
- This method improves the state determination for noisy data or data with fast dynamics, which potentially increases the temporal resolution in single-molecule measurements.
- We plan to extend this method to data with variance change or frequency change.
- Our program (in MATLAB) can be downloaded at:
<http://lrg.rice.edu/Content.aspx?id=96>

