

ESTIMATIONTOOL AND FANDPLIMITTOOL – USER-FRIENDLY SOFTWARE PACKAGES FOR SINGLE MOLECULE LOCALIZATION/RESOLUTION AND ACCURACY CALCULATIONS

Anish V. Abraham*, Sripad Ram, Jerry Chao*, E. Sally Ward**, Raimund J. Ober***

*** Dept. Electrical Engineering, University of Texas at Dallas, Richardson, TX, USA**

**** Dept. of Immunology, University of Texas Southwestern Medical Center, Dallas, TX, USA**

The 2D/3D localization and resolution of single molecules from their images has the potential to provide much biological insight. However, they are complex and challenging tasks involving fitting various model profiles to single molecule images using various parameter estimation algorithms. We developed the EstimationTool (1) to facilitate this process. Through a user-friendly graphical user interface, the tool allows a user to select from a variety of localization/resolution tasks, select from a variety of image models (Gaussian, Airy, Born-Wolf), noise models (Poisson, Gaussian), and estimation algorithms (maximum likelihood, least squares), and customize every aspect of the associated calculations. The accuracy of results from the various localization/resolution tasks varies based on the estimation algorithm, noise model, and image profile used. Therefore it is important to know the best possible accuracy with which either the location of single molecule or the distance between closely-spaced single molecules can be estimated. Various localization/resolution measures have been developed for this purpose (2,3,4,5). The FandPLimitTool (Fundamental and Practical Limit Tool) is a software package that calculates these localization/resolution measures for various estimation scenarios (6). Together, the EstimationTool and FandPLimitTool provide significant assistance in the quantitative analysis of single molecule data.

1. <http://www4.utsouthwestern.edu/wardlab/EstimationTool>
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6. <http://www4.utsouthwestern.edu/wardlab/FandPLimitTool>