

ChiSurf is a software package for the analysis of complex fluorescence data acquired in time-resolved single-molecule and ensemble fluorescence experiments. The main feature of ChiSurf is the joint (global) analysis of multiple datasets.

### History

The original of ChiSurf was to estimate errors of model parameters of fluorescence intensity decays in Förster-resonance energy transfer (FRET) experiments for FRET-driven structural models of protein and other biological macromolecules. It started as a collection of python scripts. With time more features were added, e.g. the analysis of correlation curves, correlation of time-tagged-time resolved (TTTR) data. A graphical user interface makes these scripts and tools available for users without programming experience.

Overall, ChiSurf is highly experimental and its core is still heavily refactored. Consequently, features, which worked in old versions, may be not supported in newer versions, unless users explicitly demand these functions.

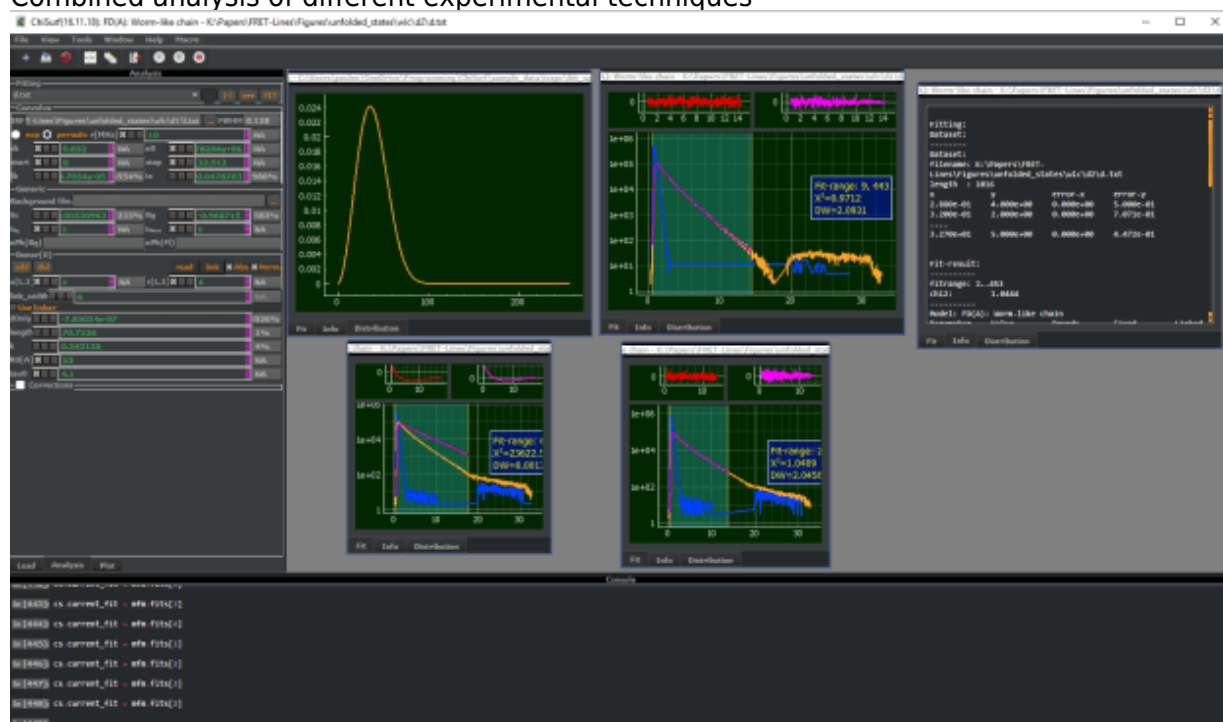
### Features

#### General features

Scripting interface and open API

Interactive analysis of multiple datasets

Combined analysis of different experimental techniques



#### Global analysis

Analysis of multiple data sets by joint model function freely defined by the user  
Freely definable models for FCS analysis & adaptable models for fluorescence decays analysis

#### Fluorescence decay analysis

Global analysis of multiple fluorescence decays

Generation of fluorescence decay histograms based on TTTR data

Analysis of time-resolved anisotropy decays

Analysis of FRET quenched fluorescence decays by physical model functions<sup>1</sup>

#### Fluorescence correlation spectroscopy

Analysis of FCS curves

Correlation of TTTR-data by efficient correlation algorithms<sup>2</sup>

#### Simulation of fluorescence observables

Kappa2 distributions based on residual anisotropies<sup>3</sup>

Simulation of fluorescence quenching in protein by aromatic amino acids<sup>1</sup>

Simulation of FRET rate constant distributions based on accessible volumes<sup>4</sup>

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Name \*

Email \*

**Github**

As part of the effort for open software for fluorescence analysis, ChiSurf is also available on github

<https://github.com/Fluorescence-Tools/ChiSurf>

**References**

1. Peulen T, Opanasyuk O, Seidel C. Combining Graphical and Analytical Methods with Molecular Simulations To Analyze Time-Resolved FRET Measurements of Labeled Macromolecules Accurately. *J Phys Chem B*. 2017;121(35):8211-8241. [PubMed]
2. Wahl M, Gregor I, Patting M, Enderlein J. Fast calculation of fluorescence correlation data with asynchronous time-correlated single-photon counting. *Opt Express*. 2003;11(26):3583-3591. [PubMed]
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4. Kalinin S, Peulen T, Sindbert S, et al. A toolkit and benchmark study for FRET-restrained high-precision structural modeling. *Nat Methods*. 2012;9(12):1218-1225. [PubMed]