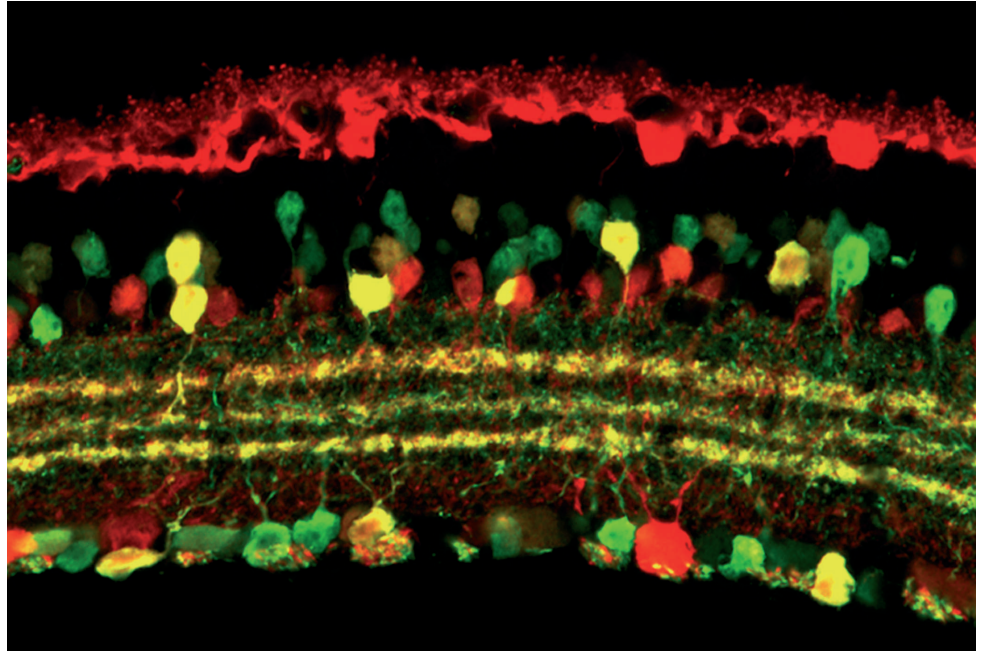




FITMASTER

Software for data review, analysis and fitting

FITMASTER is the ideal software for analysis of electrophysiological data.



If you believe your job is to make new discoveries...

... discover FITMASTER:

The software FITMASTER is a tremendous step forward in the development of HEKA's analysis software. FITMASTER contains all advantages of its predecessor PULSEFIT...

- data review
- analysis and fitting of data traces
- fit of analysis results
- export of data and fit results

... but is even further advanced by virtue of...

- more fit functions
- merging results from different experiments
- analysis of train-type data
- support of PATCHMASTER's data structure
- clipboard support
- convenient graph scaling

HEKA

HEKA provides the finest instruments today to achieve the needed progress of tomorrow...

FITMASTER features analysis and fitting routines for electrophysiological data. Analysis can be performed on the levels of sweeps/traces and series. Besides standard fit functions such as Polynomials, Exponentials, Gaussians, and Boltzmanns, tailored functions to fit e.g. whole-cell current traces according to Hodgkin&Huxley gating formalism, current-voltage relationships and dose-response curves allow publication-proof analysis of your data. Don't forget: FITMASTER is the only electrophysiological data analysis program featuring the Simplex fitting algorithm to guarantee the highest speed and performance.

FITMASTER, the second member of the PATCHMASTER software family, was designed to fully support the extended PATCHMASTER data structure. It directly makes available the analysis functions you already know from HEKA's PULSEFIT software.

Furthermore, FITMASTER includes many new features allowing analysis of the more complex data recorded or pre-analyzed by PATCHMASTER. New features, such as the work buffer concept, make analysis with FITMASTER even more powerful.

Fitting

Available fit functions

| Functions | TraceFit | SeriesFit |
|-----------------|----------|-----------|
| OnlineAnalysis | ● | |
| Polynomial | ● | ● |
| Exponential | ● | ● |
| 1-Exponential | ● | ● |
| Hodgkin-Huxley | ● | |
| Gaussian | ● | ● |
| RiseTime | ● | |
| Measure | ● | |
| Boltzmann | | ● |
| Exp(x-x0)^n | | ● |
| Dose-Response | | ● |
| Current-Voltage | | ● |

The functions can be displayed, providing information about the underlying math and the status of the fit parameters, i.e. whether a parameter is constant or variable. The variable parameters are identified according to whether they are linear or non-linear.

Simplex fit

TraceFit and SeriesFit use Simplex fitting algorithm to guarantee high speed and performance. The settings for the simplex fit routine can be set separately for TraceFit and SeriesFit.

Fit status

The status of the fitting procedure is displayed: "fitting", "converged", "max. iterations", "break".

Start values

The start values for the fit functions can be specified, stored and loaded later on to guarantee identical initial conditions for different data traces.

Manual fitting

A fit function can be calculated and drawn to the data trace corresponding to parameters manually entered by the user.

TraceFit: Versatile tools for analysis of electrophysiological data

Analysis Control:

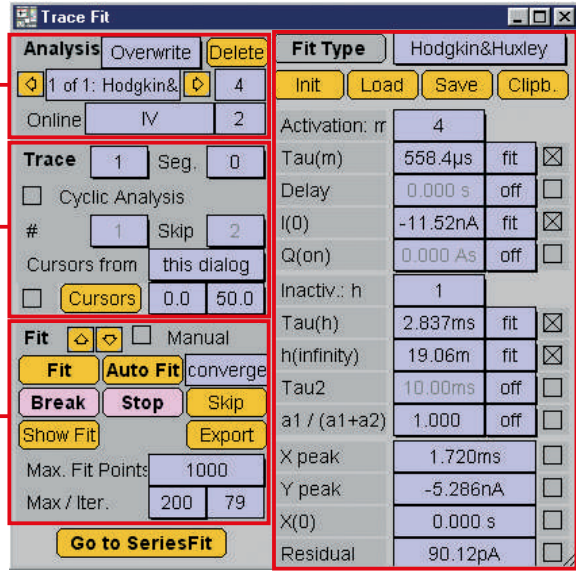
Shows the analysis under study and indicates the number of parameters analyzed.

Trace Controls:

Trace and segment number can be specified for the analysis. Cyclic Analysis allows to be performed multiple analyses in a trace, e.g. to analyze responses to tetanus stimulation. Cursors can be defined here or retrieved from an Online Analysis function.

TraceFit Controls:

Buttons for the control of fits to raw data traces. Auto Fit performs a fit on all sweeps of a series.



TraceFit Function:

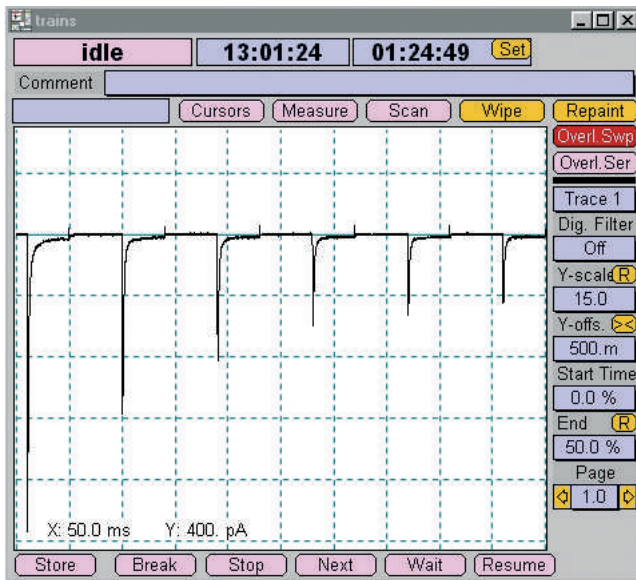
A fit function can be selected and the parameters to be stored can be marked. All fit functions can be displayed and constant, linear and non-linear parameters can easily be distinguished by color.

$$t = x$$

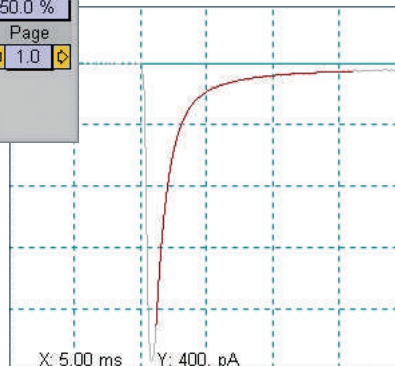
$$m(t) = 1 - \exp(-t/\tau_{aM})$$

$$h(t) = h_{inf} + (1 - h_{inf}) * \exp(-t/\tau_{aH})$$

$$I(t) = I(0) m^4 h^1$$



The use-dependent inactivation of sodium channels is analyzed. The Cyclic Analysis feature allows multiple responses in a data trace to be automatically analyzed.



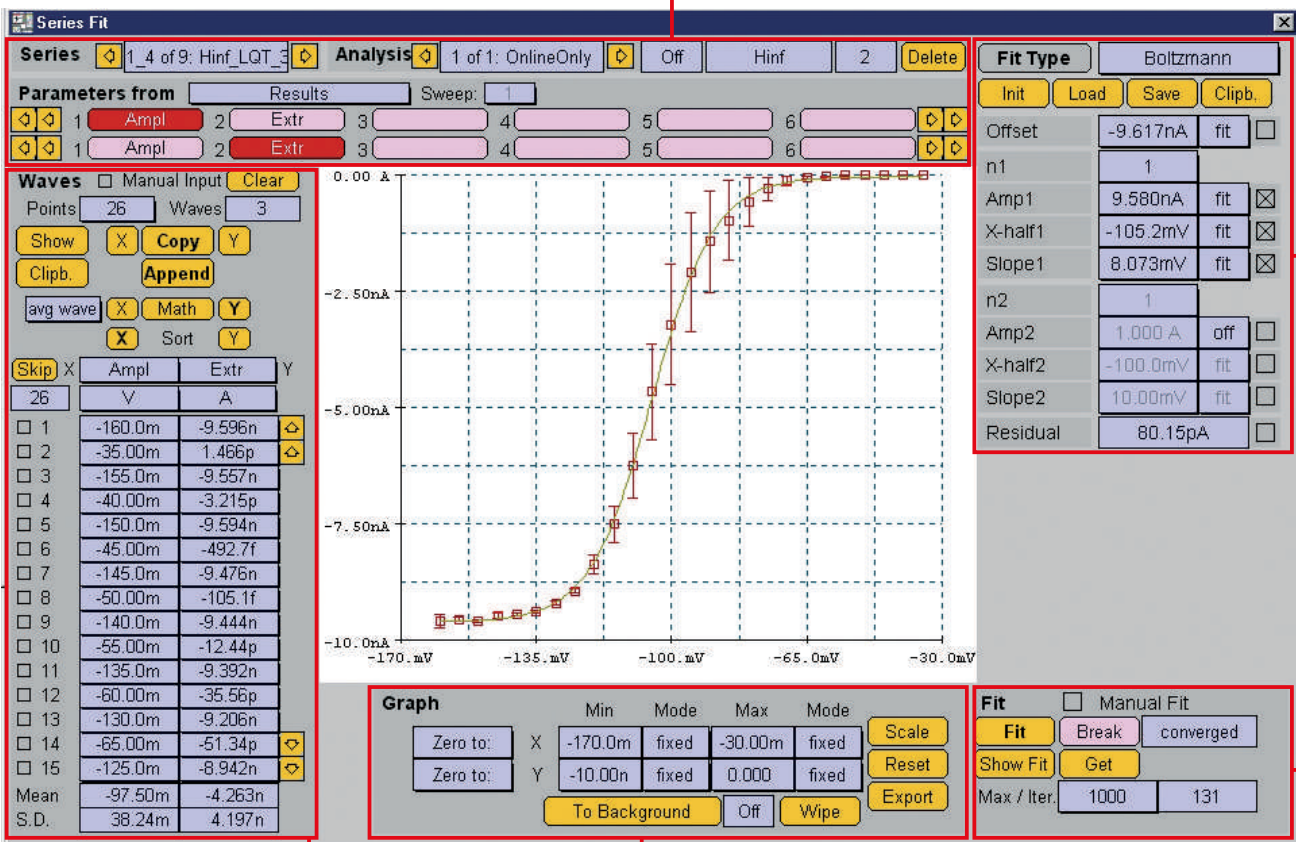
The decay of an individual sodium current is analyzed. For fitting of the double-exponential decay of the ionic current, the display is automatically zoomed to the region of interest. The theoretical curve is superimposed upon the raw data.

Data and Parameter Selection:

The series and the analyses for processing in SeriesFit can be selected. A pair of X and Y parameters determined by TraceFit can then be specified for the analysis.

SeriesFit Function:

A fit function can be selected and the parameters to be exported can be marked. By pressing Fit Type the fit function is displayed. Initial starting parameters can be stored, loaded or set to default values.



Waves Control:

Results of the TraceFit can be added to the work buffer. The content of the work buffer can be displayed in the SeriesFit graph. A spreadsheet shows the individual data entries as well as the mean value and the standard deviation. Single data points can be edited. The sort function allows sorting the buffer content with respect to the X or Y wave. Multiple waves, for example, can be averaged in the work buffer and the mean values with error bars can be displayed in the SeriesFit graph.

Graph Control:

Data presentation in the SeriesFit graph can be adjusted. Auto and fixed scaling can be specified for X and Y axis separately. Data display can be offset and normalized easily. Multiple background traces can be stored and superimposed upon the data. Data and fits including errors and fit parameters can be exported.

SeriesFit Control:

Control buttons for SeriesFit. Here a Boltzmann function fitted to the average of three analyses and superimposed upon the data. A fit previously stored to the analysis file can be retrieved and displayed.

TraceFit

Complex analysis functions

Even complex mathematical expressions can be analyzed with the Online Analysis and then processed with SeriesFit in FITMASTER. Online methods created with PATCHMASTER can be used in FITMASTER.

Multiple analyses

TraceFit supports the analysis and the storage of results from multiple functions for a given series. A set of results for a given series, for example, can consist of parameters from different analysis and fit functions or from results retrieved from different segments of a trace.

Zoom for fit

When executing data fits in TraceFit, data sections of interest can be zoomed automatically to provide an optimal view necessary to decide upon the quality of the fit.

Cyclic analysis

Performs multiple analyses on a single data trace. Useful to analyze responses to tetanus stimulation or other cyclic high speed stimulation.

SeriesFit

Mathematical preprocessing

Results from single or multiple analyses can be compiled in a work buffer before being processed by SeriesFit. This way, data originating from different series can be merged (appended) for later analysis.

Work buffer math functions

In addition to appending SweepFit results to the analysis work buffer, FITMASTER also allows data with identical X-references to be processed. One can form e.g. the average of multiple results. Such averaged data are then shown with or without error bars and a fit function can be fit to the mean data.

Math functions allows some basic mathematical functions average, "+", "-", "*", "/" to be performed between data sets.

In addition, the content of the work buffer can be processed with the functions "invers", "square", "sqrt", "ln", "exp", "+ const", "- const", "* const", "/ const".

Work buffer statistics

The "mean" and "standard deviation" of the entire work buffer content are shown at the bottom of the columns at any time.

Data sorting

Data in the work buffer can be sorted according to their X- or Y-values.

Skipped data points

Data points from the work buffer can be omitted from analysis. Results from non-converged fits in TraceFit are automatically marked as skipped.

Graphing in SeriesFit

The SeriesFit graph can be scaled and modified in many ways such as changing the colors, tics, scaling of the axes etc. In addition, the axis range can now be defined as "fixed" or "auto" for minimum and maximum as well as X- and Y-axis separately. The scale range in the "auto" mode can be based either on all data points or on the active, i.e. non-skipped, data points only. The data in the graph can be offset or normalized easily.

Mouse actions on the SeriesFit graph

By clicking of individual data points in the SeriesFit graph, the number and value is shown in the notebook. Also toggling of the skip status can be performed by a mouse click.

Background trace

Multiple background traces can be stored and overlaid to the SeriesFit graph.

Compatibility

Runs on Windows 98 / NT4.0 / 2000 / XP (requires a parallel printer port on Windows computers) and on Mac OS 9 and Mac OS X (requires a USB port on Macintosh computers).

FITMASTER can read sweep data recorded with PATCHMASTER and PULSE or generated with PULSETOOLS or PULSESIM.

Export

Data export

Data and fits of the TraceFit and SeriesFit can be exported into ASCII and IgorPro format. The export mode can be configured to customize output.

Clipboard support

Fit parameters in TraceFit as well as in SeriesFit can be sent to the clipboard with a single mouse click and transferred to other programs easily.

Related Products

PATCHMASTER

Multi-channel stimulation/acquisition and analysis software package for Windows and Mac OS.

PATCHMASTER PRO

Multi-channel stimulation/acquisition and analysis software package for Windows and Mac OS with support of a set of Good Lab Practice (GLP) standards for data acquisition and handling, as established by the Food and Drug Administration (FDA) (21CFR Part 11).

PULSETOOLS

Software for data reorganization, editing and averaging. Amplitude histograms and noise analysis.

PULSESIM

Modeling and simulation of data based on kinetic schemes or discrete Markov models.



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