Kinetics Release Notes
Updated May 2024

Kinetics 1.9.2.4463

Release May 2024
- Features
- Updates
- Known Issues
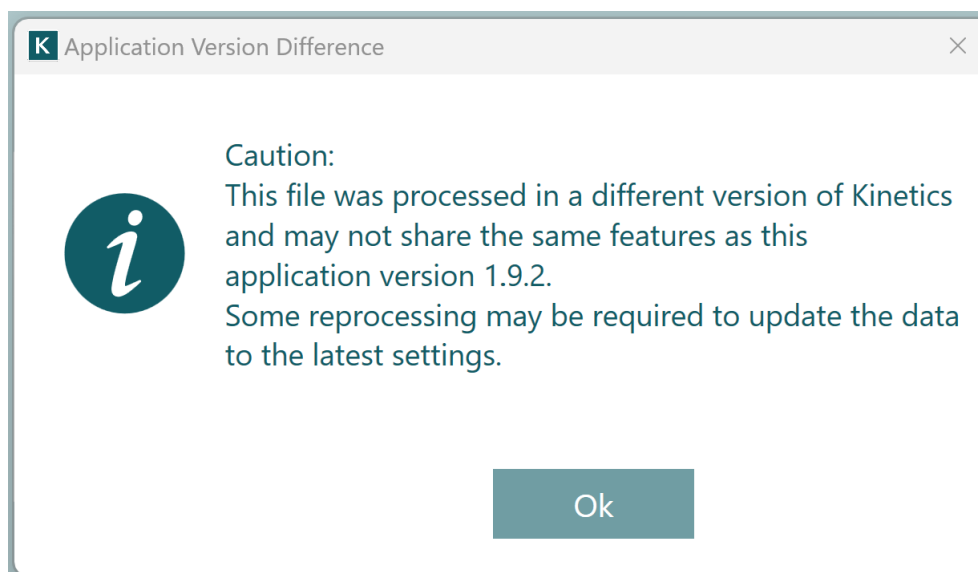
Changes Since Last Release

Features

- **Misc**
  - Updates made to application installer to recognize existing installed Microsoft C++ redistributables and simplify installation dialog
  - Kinetics 1.9.2.4463 will be the last version to support the .lsadata file format

- **File Opening and Saving**
  - If files saved in previous versions are opened, caution message will appear about recommended best practices when working with the file in this latest version

- **Data Tab**
  - Reassignment of Analytes in right-click menu is restricted based on original assignment (Analyte or Immob) to avoid errors

- **Processing Tabs**
  - ROI map view now uses experimental coordinates indicating the actual placement of ROIs on the chip during the run. Note that for previously processed files the ROI map will revert to a default layout.
  - ROI map is now draggable and zoom in/zoom out can be done by CTRL+ mouse wheel

- **Data Fitting**
  - Fitting progress dialog now included when fitting data on the Kinetics>Kinetic Analysis tab

  - Default ka fitting uses range of starting values to avoid fitting minima which impact accuracy of ka fits
  - Users have option of instead checking *ka* box on Kinetics tab and assigning a specific ka starting value

  - Show KD Units is now unchecked by default

- **Analysis Tab**
  - No new features

- **Report Point Tab**
  - No new features

- **Data Export**
  - Headers are no longer merged in the Excel export
  - Analyte and Ligand Report Point tables are now separate tabs in Excel export
  - With Show KD Units now unchecked by default, no units are included in the export tables

Updates

- **Misc**
  - No updates

- **File Opening and Saving**
  - No updates

- **Data Tab**
  - Duplicate prints now correctly separated into discrete Link Groups
  - Correction of bug allowing space to be appended at end of Ligand names
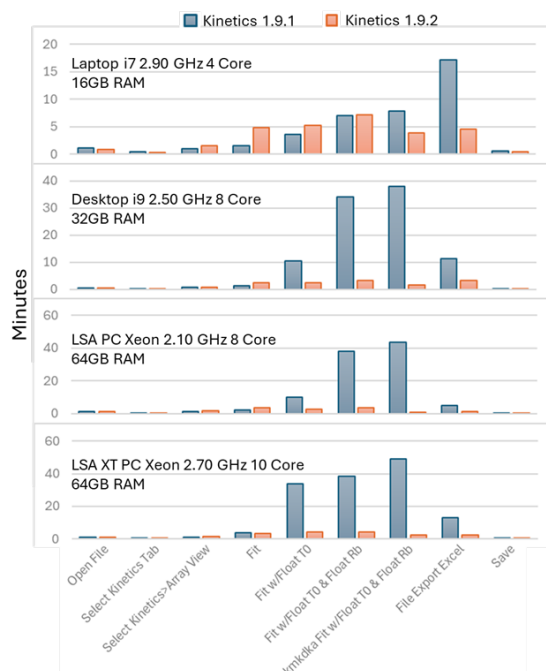 - Carryover of ligand names from previous experiments in block 1 resolved

- **Processing Tabs**
  - Corrections made to custom and global referencing options to ensure displayed referencing assignments are applied appropriately

- **Data Fitting**
  - T0 is now functional when analyzing previously analyzed files without requiring deselecting, fitting, then reselecting. Carterra still recommends refitting processed files when opened in the latest builds to ensure most recent improvements are applied to the data.

- Fitting speed performance improvements implemented which reduce fitting steps by up to an order of magnitude. See chart below for examples of performance when fitting a 16-link group file on various PC types in Kinetics 1.9.1 vs. 1.9.2

- Flagging of data in the Steady State tab only highlights and no longer removes data from the view

- **Analysis Tab**
  - Issues with data not fully displaying on Isoaffinity chart have been resolved
  - Errors when sorting on the Affinity tab have been resolved

- **Report Tab**
  - No updates

Known Issues

- Report point export tables for Immobilization are missing Bay information
- Data flagged as < 50% Rmax, kd below limit, and/or km below limit is not treated as Flagged in the Analysis tabs
- Characters or numbers other than numbers 1 through 432 added to the Global Reference in the Analyte and Ligand Processing tabs will cause an error to appear
- When Normalization is applied in Steady State, chart autoscaling may not apply correctly and therefore scales should manually defined
- In previously processed files, the ROI map will open with a default layout that is not consistent with the physical layout on the chip. Referencing relationships are correct, however.
- When running Capture Kinetics without specifying prints, the data file will open with default names of Ligand 1, Ligand 2, etc., and the ligand names will need to be manually added to the file.

Kinetics 1.9.1.4215
Release October 2023

Changes Since Last Release
- Features
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Features

- Allow k_d fitting for multichannel (immob) data
- Data displayed during multichannel rinsing phase
- Chart export now acounts for screen scaling
- Ability to correct sensorgram bulk shift
- Display data within analyte injection cycle
- Kinetic fitting routine code improvements
- Kinetics and Steady Stage pages, Array View tabs: make "Show ROI Position" and "Show Ligand Name" clicked on by default
  Update Settings > Table Options > Display ROI to be Checked by Default
- Gear menu options to hide Ligand Name and ROI from Array View
- Add Global Referencing to Analyte Processing Page
- K_D header row moved in File>Excel Export to simplify table processing

Updates

- Link Groups not correctly delineating
- Tiles in File>Export do not follow sorted order in application
- High residuals in some off-rate fits
- An unstable error appears when opening certain saved .kitx files
- Incorrect sorting option by ROI ID in the Kinetic Analysis, Global Analysis tables
- Analysis > Stats page: Axis data is clipped
- Incorrect behavior of "ka" gates on the Analysis > Iso-Affinity page
- The X and Y axis label size settings don't apply to the chart on the Analysis > Stats page
- The chart text size settings don't apply to the chart on the Analysis > Scatter Plot page
- The Inactive ligands are displayed in the "Analytes" tab on the Analysis > Stats page
- Application isn't updated dynamically after using the "Data Filter" option
- Experiments are not displayed on the charts on the Analysis pages when the experiment assigning to the Default group from the
  Inactive group on the Steady State page
- Sort order changed after experiments are assigned to the Inactive / Complex / Excluded Group in the Kinetic Analysis table
- "Copy All Data to Clipboard" Error on Kinetics > Array View • Scatter plot pasted values dont match plot
- Data page: Font sizes do not change
- SQLite Export missing ResSd value from fitting results
- Cannot Copy/Paste into Analyte Processing > Referencing > Assignments Table
- Steady State > Global Analysis Table Missing "ROI" Column
- Quant Page - Report "[Concentration Value] <,> [Max/Min Allowable Concentration]" instead of ND
- After Fitting on the Steady State Page Some Ligands with ND values are not colored as Inactive

Known Issues

- Fitting times increase as more fit variables/options are selected

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