

Maurice – ProteinSimple

cIEF & CE-SDS

INTRODUCTION

The Lumetics LINK™ software platform scans network locations for new measurement data files, copies data directly to a centralized database, and provides a powerful user interface for rapid multi-measurement multi-technique data aggregation, visualization, analysis, and reporting. LINK employs a client/server-based architecture where the LINK server hardware is provided by the end user and resides on the end user's network. The LINK client is a portable web-based application that may be placed on any computer with network connectivity to the LINK server. For successful import, the LINK webserver requires read access to the folders where user data resides.

Maurice innovates the conventional capillary electrophoresis technology to automate protein profiling either by size or charge. iCE™ platforms give you reproducible, quantitative analysis of identity, purity, and heterogeneity profiles for your therapeutic proteins. Maurice platforms also automate size separations for you, so you'll get robust and quantitative analysis for your monoclonal antibodies too.

DETAILS

LINK will import data from two sources:

- A peaks.txt file, with optional associated raw data (Fluorescence or Absorbance vs pI) contained in a CDF file found in the same folder as the peaks.txt file. All injections found in the peaks.txt must have at least two markers present to import raw data from the CDF file, as they are required to calculate the x-axis pI values from the position (pixels) data in the CDF file.
- A PDF report (raw data is currently not available for measurements imported from PDF report)

The Maurice peaks TXT data file must meet the following criteria to be imported:

- it must be exactly named "peaks.txt".
- it must contain at least a column called "Injection", and a column called "Peak"

The Maurice TXT data file example is as follows:

	Injection	Injection Name	Sample	Location	Method	Peak	Name	Position	pI	Height	Area	%Total	%Area	Width	S/N	Baseline	Resolution
1	1	SS Sample A	B1	System Suitability	1	Mkr	3.38	327.1	3.38	8398.72	104675.991	0.0567	377.9	212.65			
2	1	SS Sample A	B1	System Suitability	2		862.1	5.968	8612.35	99788.4	25.94	0.0527	387.5	87.22	27.88		
3	1	SS Sample A	B1	System Suitability	3		924.8	6.271	12637.78	180957.464	47.04	0.0651	568.7	78.21	3.03		
4	1	SS Sample A	B1	System Suitability	4		1696.8	10.008	12724.55	103927.299	27.02	0.0371	572.6	72.06	43.03		
5	1	SS Sample A	B1	System Suitability	5	Mkr	10.17	1730.3	10.17	12149.25	108592.432	0.0406	546.7	73.24	2.45		
6	2	Blank	Blank	C1 method 1	1	Mkr	6.14	381.3	6.14	609.87	19392.041	0.0655	29	32.89			
7	2	Blank	Blank	C1 method 1	2	Mkr	9.50	1911.2	9.5	1207.07	11825.666	0.0202	57.3	31.37	46.1		
8	3	Sample B	Sample B	D1 method 1	1	Mkr	6.14	405.5	6.14	696.79	10503.612	0.031	29.6	77.75			
9	3	Sample B	Sample B	D1 method 1	2		1013.2	7.466	219.52	2626.817	1.2	0.0246	9.3	103.56	28.17		

A unique measurement is defined by the following criteria in the peaks.txt file

- Sample
- Injection Name
- Location (e.g. well plate position)
- peaks.txt "Last Modified" date (assigned to Analysis Date in LINK)

Acidic and Basic Species Calculations

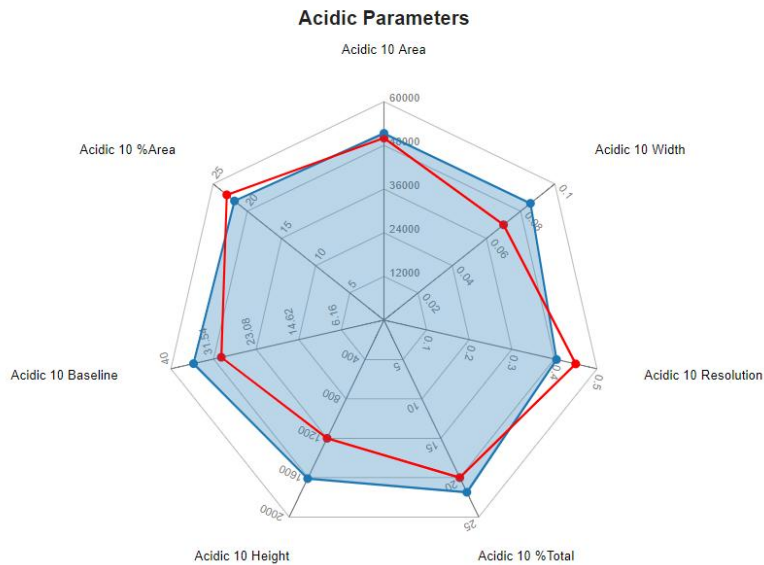
When importing Maurice data from a peaks.txt file, the LINK software will automatically calculate additional values around the Main Peak (defined by the max peak height) for a given measurement, called the Acidic Species and Basic Species parameters. This is done for the following parameters found in the peaks.txt table: Position, pI, Height, Area, %Total, %Area, Width, S/N, Baseline, and Resolution.

When calculating Acidic Species and Basic Peak parameters, where multiple peaks (excluding markers) are present in each, the Area, % Total, and % Area will be summed. All other peak parameters will be averaged. Note that for peaks.txt files where there is no values for the %Area column and/or the %Total column, these values are calculated dynamically by dividing the Acidic/Basic peak area column by the overall sum of the Area columns for all peaks (or within peaks covered in the optional pl range), giving identical values to both the %Total and %Area columns. If not, all peaks are desired to be included in this calculation, there is an Import Method page available to optionally specify a pl start and end range for the Acidic/Basic Species parameter calculations.

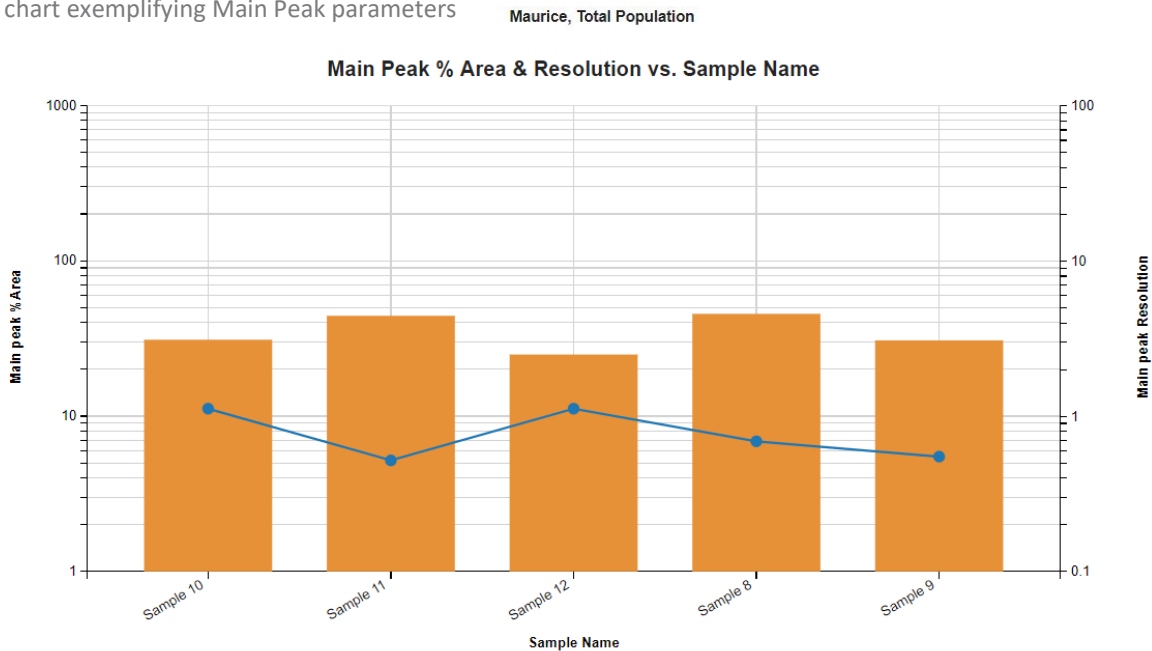
EXAMPLES

Included below are example dashboards from Maurice measurement files:

1. Radar Chart representing multiple acidic 10 parameters



2. Column chart exemplifying Main Peak parameters



3. Tabular Summary examples

Measurement Summary Table – Instrument Settings

LINK Record ID #	Sample Name	Analysis Date	Cartridge Type	Run Completed	Run Started	Tray Temperature	Sample Load Duration
17	Sample 8	2017-02-22 15:32:00	ciEF	Wed 8:32 PM Feb 22, 2017 GMT	Wed 4:15 PM Feb 22, 2017 GMT	4°C	55.0 Seconds
18	Sample 9	2017-02-22 15:32:00	ciEF	Wed 8:32 PM Feb 22, 2017 GMT	Wed 4:15 PM Feb 22, 2017 GMT	4°C	55.0 Seconds
19	Sample 10	2017-02-22 15:32:00	ciEF	Wed 8:32 PM Feb 22, 2017 GMT	Wed 4:15 PM Feb 22, 2017 GMT	4°C	55.0 Seconds
20	Sample 11	2017-02-22 15:32:00	ciEF	Wed 8:32 PM Feb 22, 2017 GMT	Wed 4:15 PM Feb 22, 2017 GMT	4°C	55.0 Seconds
21	Sample 12	2017-02-22 15:32:00	ciEF	Wed 8:32 PM Feb 22, 2017 GMT	Wed 4:15 PM Feb 22, 2017 GMT	4°C	55.0 Seconds

Measurement Summary Table – Measurement Results

LINK Record ID #	Sample Name	Main peak %Total - AVG	Main peak %Area - AVG	Main peak Resolution - AVG	Main peak Baseline - AVG	Main peak Width - AVG	Main peak pl - AVG	Main peak Position - AVG
17	Sample 8	45.50	45.50	0.69	17.50	0.11	8.37	1320
18	Sample 9	30.70	30.70	0.55	-42.90	0.08	8.37	1334
19	Sample 10	31.00	31.00	1.12	-54.70	0.08	8.37	1328
20	Sample 11	44.00	44.20	0.52	27.30	0.11	8.36	1317
21	Sample 12	24.90	24.90	1.12	-25.50	0.07	8.36	1320

CONTACT LUMETICS

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