Glossary of terminology

The full glossary can be downloaded as a separate document on the MatrixExplorer Documentation site.

Screen-related metrics

Metric name	Explanation
BARCODE	Barcode of the assay plate
DRUGSET_ID	ID of the drug set used for the assay plate (Drug set describes the individual plate layout & drug composition)
cmatrix	Identifier for a combination matrix within a drug set
well_treatments	Combination of drug set library tags

Cell line-related metrics

Metric name	Explanation
CL	Cell line identifier used in the curve fit
CELL_LINE_NAME	Name of the cell line
MASTER_CELL_ID	Sanger database master ID
COSMIC_ID	COSMIC database identifier
SIDM	Sanger ID Model (Cell Model Passports identifier)
TISSUE	Sanger tissue classification
CANCER_TYPE	Sanger cancer type classification

Library drug-related metrics

The two drugs used in the matrices are called “lib1” and “lib2”, with lib1 being the first drug listed in the combination. All metrics below are available for both drugs.

Metric name	Explanation
lib1	Drug set library tag identifier
lib1_ID	Sanger database identifier of drug
lib1_name	Drug name
lib1_conc	Highest screened concentration (in µM)
lib1_RMSE	RMSE: root mean square error Describes how far the data points are from the single agent curve fit
lib1_MaxE	Fitted inhibition value at the highest used concentration
lib1_IC50_ln	Natural log of IC50
lib1_IC50_uM	IC50 in µM
lib1_target	Protein target(s)
lib1_pathway	Pathway of protein target(s)
lib1_owner	Sanger database drug owner

Combination response-related metrics

Metric name	Explanation
matrix_size	Number of wells treated with the combination e.g. 49 for a 7x7 matrix
combo_MaxE	Maximum inhibitory effect of the combination within the matrix Based on the 2nd highest data point in the matrix
Delta_MaxE_lib1	*combo_MaxE - lib1_MaxE*
Delta_MaxE_lib2	*combo_MaxE - lib2_MaxE*
Delta_combo_MaxE_day1	*combo_MaxE - day1_inhibition_scale*

Synergy-related metrics

All metrics below have been derived for two synergy reference models: Bliss excess and HSA excess. The used placeholder "X" thereby stands either for "Bliss" or for "HSA".

Metric name	**Explanation**
X_synergistic_wells	Number of wells with a response in excess of that expected by the synergy reference model
X_matrix	Mean excess effect over X across the matrix Calculated by *sum all wells* / *number of wells*
X_matrix_SO	Mean excess effect over X across the matrix (synergistic wells only) Calculated by *sum synergistic wells* / *number of synergistic wells*
X_window_size	Local sub-matrix size in one dimension e.g. "3" = 3x3 matrix
X_window	Mean excess effect over X across the window Calculated by *sum all wells* / *number of wells*
X_window_dose1	Locator of upper right corner of window (library 1) D1-D7 with D1 being the highest screened concentration
X_window_dose2	Locator of upper right corner of window (library 2) D1-D7 with D1 being the highest screened concentration
X_window_SO_size	Local synergy only sub-matrix size in one dimension e.g. "3" = 3x3 matrix
X_window_SO	Mean excess effect over X across the window (synergistic wells only) Calculated by *sum synergistic wells* / *number of synergistic wells*
X_window_SO_dose1	Locator of upper right corner of synergy only window (library 1) D1-D7 with D1 being the highest screened concentration
X_window_SO_dose2	Locator of upper right corner of synergy only window (library 2) D1-D7 with D1 being the highest screened concentration

Day1-related metrics

Metric name	**Explanation**
day1_intensity_mean	Mean observed luminescent intensity of Day1 plate
day1_intensity_sd	Standard deviation of observed luminescent intensities across Day1 plate
day1_viability_mean	Mean viability of Day1 plate, scale: 0-1 with 1 = full viability Calculated with respect to Day4 controls
day1_viability_sd	Standard deviation of Day1 plate viabilities
day1_inhibition_scale	Mean viability of Day1 plate converted to inhibition scale, scale: 0-1 with 1 = full inhibition *1 - day1_viability_mean*
growth_rate	$log_2((NC) / day1\_intensity\_mean)$ Where NC is the mean intensity of negative controls for the Day4 plate
doubling_time	Doubling time in hours $72 * log_2(2) / (log_2(NC) - log_2(day1\_intensity\_mean))$