Score Signatures
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Summary: This module is used to predict the activation of oncogenic pathways in each sample of a gene expression data set. The data should have been generated on an Affymetrix U133A (U133Av2) array and then preprocessed with both RMA and MAS5, generating two variants of the data. Both variants should be provided to the module.

Empirically, it was previously determined that some the pathways work best on RMA preprocessed data, and others on MAS5. Thus, if only an RMA data set is provided, the module will only generate predictions for the pathways that have been validated on RMA.

For more information on the pathways, see:
Gatza *et al*. "A pathway-based classification of human breast cancer." *Proc Natl Acad Sci USA*. 107(15):6994-9, 2010.

Parameters: rma_expression_file, mas5_expression_file
These are the gene expression data sets to be analyzed. One has been preprocessed with RMA, and the other with MAS5. At least one of these files need to be provided. These files can be in PCL, GCT, and some other formats.

Parameter: which_signatures
This determines which signatures to run. By default, this module predicts the activity of all the signatures in the Duke Signature databases. However, you can also select the signatures individually by setting this to *I choose myself*. That will reveal the entire set of signatures in database, and let you select them individually.

Parameter (hidden)**:** sig_*<name of signature>*
By default, this parameter is hidden from the user. However, if you elected to choose the signature individually (see *which_signatures*), then this parameter lets you select whether this signature is run. The possible values are:

yes (default parameters)	Run with default parameters.
yes (custom parameters)	Choose the parameters yourself.
no	Do not run this signature.

If *yes (custom parameters)* is chosen, then the interface will reveal addition controls to select the values for individual parameters.

Parameter (hidden)**:** sig_*<name_of_signature>*_num_genes,
sig_*<name_of_signature>*_num_metagenes,
sig_*<name_of_signature>*_apply_quantile_normalization,
sig_*<name_of_signature>*_apply_shiftscale_normalization
By default, these parameters are hidden from the user, and then activated when the user chooses to use their own parameters (see above). The meanings of these parameters are

described in the documentation for the CreateSignature module. The default recommended values are from the Duke Signature Database.

For help, please email: jeffrey.chang@duke.edu.