

## ER-flow Application Description Template

<b>Application Name:</b> Double Cross Validation with Penalized Logistic Regression
<b>Application domain:</b> <a href="#">Metabolomics</a> , <a href="#">Proteomics</a> , <a href="#">BioStatistics</a>
<b>Brief description of application</b> Penalized logistic regression is a method to build a model by using available data, which is a common step in biomarker discovery research. Double cross validation is a strategy used to check if a model built using part of the data can correctly predict the value of the rest of the data. This is repeated for a large number of permutations to make sure the model is not biased.  data: input data format: data in tab-delimited text output data format: Tab-delimited text sample data and documentation: <a href="http://www.bioinformaticslaboratory.nl/twiki/bin/view/EBioScience/LRDCUserDoc">http://www.bioinformaticslaboratory.nl/twiki/bin/view/EBioScience/LRDCUserDoc</a> Publication: Kloet, F.M. et al. <a href="#">Discovery of early-stage biomarkers for diabetic kidney disease using ms-based metabolomics (FinnDiane study)</a> , <i>Metabolomics</i> , vol. 8, no. 1, pp. 109-119,
<b>Execution environment</b> DCI: (computing, data, VO, etc) grid middleware: glite workflow system: WS-PGRADE
<b>Execution characteristics</b> data size (per unit, typical number of units): input: ~10MB to ~100MB output: ~10MB to ~100MB processing time (per unit): ~5 – 30 hours memory usage: tbd disk usage: same as output
<b>Target users</b> Biomedical researchers that have data from which they want to extract a model. This applies to various types of datasets. number of users: 5+ users user type: end-user
<b>Usage scenario for workflow in the ER-FLOW</b>  This is a very general step in bio-statistics, which will be made available to end-users as an application in the AMC gateway. The workflow can also be retrieved by other users from the SHIWA repository (requires gUSE 3.5.8 or higher).
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