
Software Ontology (SWO) version 81

[http://bioportal.bioontology.org/ontologies/42036](http://bioportal.bioontology.org/ontologies/42036)

description: The Software Ontology (SWO) has the scope of describing types of software used in Bioinformatics. The SWO covers areas such as the software type, the manufacturer of the software, the input and output data types and the uses (i.e. objectives) the software can be put to. The SWO intends to use BFO as an upper level ontology and subclasses types from the Ontology of Biomedical Investigations. Contact James Malone for info: [malone@ebi.ac.uk](mailto:malone@ebi.ac.uk)

**SWO 1st level class hierarchy**

- ![Diagram of SWO 1st level class hierarchy]

**SWO 2nd level class hierarchy**

- ![Diagram of SWO 2nd level class hierarchy]

**SWO 3rd level --detailed full class hierarchy**

- ![Diagram of SWO 3rd level class hierarchy]
**comments:** We cannot get the meaning of classes hierarchy by check the protégé view. Thus we get the snapshot of http://bioportal.bioontology.org/visualize/42036, which gives us the visualization of this ontology.

![Snapshot of the ontology](image)

**first two levels:**

- information
  - algorithm
  - data
  - data file format
  - objective specification
  - programming language
  - software
  - version number
- material entity
  - organization

**full-details:**
information
algorithm
- Bayesian Model
- M-estimation regression
- Markov Chain Monte Carlo
- 2-sample pooled t-test
- ACME
- AMDIS
- ANCOVA
- ANOVA
- ARACNE algorithm
- associative T method
- average log expression across arrays (ALE)
- avgNRRs
- AWS algorithm
- BaldiLongT
- Base-Pair-Distance Kernel
- BCRANK
- BGL
- Binning clustering method
- Bootstrap
- Category analysis
- CBS
- CBS algorithm
- chi-square
- CLR algorithm
- clustering algorithm
- CMA
- Complex Estimation Algorithm
- Concordance
- Continuous Wavelet Transform (CWT)-based peak detection alg
- COSMO
- CRLMM algorithm
- DFW
- Discriminant Fuzzy Pattern Algorithm
- Dynamic programming algorithm
- Empirical Bayes rule
- Expectation-Maximization (EM) algorithm
- F test
- f-test
- FACS (fluorescence-activated cell sorter)
- FARMS
- FC
- FDR
- Firth's bias reduction procedure
- Fischer's Exact Test
- Fixed effect model
- FoxDimmiCT
- Gamma Gamma Model
- Gamma-Gamma hierarchical model
- GASSCO method
- Gaussian locally weighted regression
- gene array analysis algorithm
- Gene Recommender algorithm
- Gene-Set Enrichment Analysis
- Global test
- HaarSeg algorithm
- Hardy-Weinberg equilibrium
- Heterogeneous Error Model (HEM)
- hexagon binning algorithm
- Hidden Markov Model
- Hidden Variable Dynamic Modelling (HVDM)
- hierarchical clustering
- Hierarchical Ordered Partitioning and Collapsing Hybrid (HOPH)
- Hubert's gamma
- hypergeometric enrichment
- Hypergeometric probability
- iterative Bayesian Model Averaging (BMA)
- iterative local regression and model selection
- Iteratively ReWeighted Least Squares
- Jaccard's index
- k-cores
- k-means
- k-nearest neighbour classification
- KLD
- Kolmogorov Smirnov rank-sum based algorithm
- Langmuir isotherm
- Laplace mixture model
- Library Search Algorithm
- likelihood method
- Linear modelling
- local-pooled-error
- Locally Moderated Weighted-t (LMW) method
- Loess algorithm
- Logic regression
- Logit-t algorithm
- Lognormal Normal Model
- Lognormal Normal with Modified Variance Model
- Mahalanobis distance
- MASS
- MCR algorithm
- Median Average Difference Algorithm
- MI
- Misclassification-Penalized Posteriors (MIPP)
- Mixed model equations
- MMD
- modified version of the GLAD algorithm (Gain and Loss Analysis)
- mnet algorithm
- multinomial probit regression with Gaussian Process priors
- Multiple testing
- Multivariate correlation estimator
- multivariate t mixture models
- Needleman-Wunsch
- negative binomial distribution
- Nested Effects Models
- neural networks models
- non-linear functional regression model
- Nonlinear Estimation by Iterative Partial Least Squares
- PCMG
- Pearson correlation estimator
- PLIER (Probe Logarithmic Error Intensity Estimate) method
- PLM
- position weight matrix (PWM)
- Power Law Global Error Model (PLGEM) analysis method
- PPC algorithm
- Presence-Absence calls with Negative Probesets (PANP)
- Probe level locally moderated weighted median t (PLWm)
- propagation of uncertainty in microarray analysis
- quantile normalization
- quantile regression techniques
- R Interface to boost graph library algorithm (RBGL)
- Radial basis function
- Random effects model
- rank product non-parametric method
- rank-invariant set normalization
- Recursive Feature Elimination (RFE)
- Regression model
- RMA
- RMA+
- RMA++
- Robust likelihood-based survival modeling
- S-Scor algorithm
- SAM
- SBML model
- Semantic Similarity Measures
- Serial Analysis of Gene Expression (SAGE)
- Signaling Pathway Impact Analysis (SPIA) algorithm
- sim method
- Similarity score
- Smith-Waterman
- SNP-RMA algorithm
- statistical tests
- SVDImpute algorithm
- t-test
- Theodore Ts'o's two-stage measurement error model
- variance-stabilizing transformation (VST) algorithm
- Wilcoxon
- Wilcoxon

data
- 'AP-MS data'
- 'BED file'
- 'binart object'
- 'HTML report'
- 'MAQC data'
- ALL/AML data set
- annotation data packages
- chamber slide format
- CHF files
- clustered data set
- covdesc file
- csv data set
- design files
- digital gene expression (DGE) datasets
- FACS data
- gene expression dataset
- gene list
- GEO Matrix Series files
- GEO_data type
- graphs
- heatmaps
- ILLUOMA data
- images
- KGML files
- LC-MS data
- log file
- meta data
- microarray data
- mutual information matrix (MIM)
- OMICS data
- pair files
- pedigree data files
- plots
- qPCR data
- R data frame
- SBML file
- SBMLR file
- text data set

data file format
- data
- java file
- raw files
- rma format
ARR
BPMAP
CDF
cdt
CEL
cls
dkf
FASTA
FCS
gct
gff_format
gmt format
gpr format
gtr
gxml_format
jpeg
Ima
logiFS dataset
MAGE-ML files
MAGE-TAB
mas5 format
newick
pdf
png
ps
rda
rinf
SDF format
sproc
sqlite
TIFF image
XbacCQV and Xba regions
XML

objective specification

programming language
MATLAB
R language
software
- 50-50 MANOVA
- Acuity
- Affymetrix Software
- Agilent Technologies Software
- AIDA
- Applied Biosystems 1700 Expression Array System Software
- ArrayGauge
- ArrayNorm
- ArrayVision
- arrayWoRx
- AtlasImage
- BasReader 3.01
- Beadstudio
- BioConductor Software
- BLAST
- BlueFuse
- BRB-ArrayTools
- BZScan
- CARMAweb
- ChipReader 3.1
- ChipSkipper
- CodeLink Expression Analysis Software
- CodeLink Expression Scanning Software
- Cyber-T
- dChip
- GACK
- GEMTools 2.4
- GenePix
- GeneData Expressionist Analyst v4.05
- GeneTec Analyser
- GLEAMS software
- GMS
- GridGrinder
- ICS-501 (version 2.3) Image Capture System
- ImaGene
- ImageQuant
- ImageReader
- Initial microarray data processing/data filtering/local normal
- MAGE-TAB inputting software
- MATLAB
- MAVI Pro
- Optiquant
- Pathways 2.01 software
- QuantArray scanner software
- R software
- RMAExpress
- Rosetta Resolver