

NXG Logic Solutions for DNA Microarrays

Solutions

Data Pre-processing

Select from a variety of transformations, dimension reduction methods, fast wavelet transforms, and superresolution ROOT MUSIC analysis.

Machine Learning

Perform knowledge discovery, class discovery, and class prediction, based on machine learning and computational intelligence approaches. Text mining can also be performed for document and concept clustering.

Simulation and Monte Carlo Analysis

NXG Logic technologies provide data fitting and simulation capabilities for more than 20 probability distributions, and Monte Carlo uncertainty analysis.

NXG Logic Advantages

- Time savings
- Transpose-free results
- Manifold learning, knowledge discovery
- Machine learning
- Upgradability

Customers

- Students/interns
- Researchers
- Clinicians
- Faculty
- Engineers
- Data analysts
- Healthcare economists
- Risk managers

Research Fields

- Applied computer science
- Chemistry/chemoinformatics
- Molecular biology/genomics
- Drug design/manufacturing
- Clinical trials
- Bioinformatics
- Medical informatics
- Quality assurance & health outcomes



Analyzing DNA microarray data involves pre-processing input data, identifying novel clusters of features (genes) and objects (animals, subjects, etc.), as well as identifying differentially expressed and co-regulatory genes. These analyses form a complex challenge and require a strong set of skills among analysts, but it also requires a wide variety of computational algorithms.

Gaining new insights in genomics and establishing new leads for future research requires data filtering, collapsing, transformation, and application of discriminative and generative models. In addition, the analyst must be able to rapidly condense the results into a format for publication or presentation which is straightforward and understandable. Achieve these goals with NXG Logic.

NXG Logic provides a highly developed set of algorithms based on decades of computational expertise which enables analysts to rapidly tackle their hypothesis- and data-driven tasks. NXG Logic also offers advanced machine learning and computational intelligence tools to solve complex analyses. Genomic science data analysts benefit from the following NXG Logic solutions:

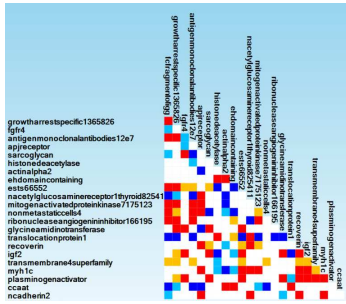
Time-savings. NXG Logic solutions are designed from the bottom-up to shorten and accelerate the time to discovery. Results from each step are typically saved, eliminating the time required for clamping data to the next algorithm. Many graphs are also automatically generated in order to accelerate interpretation.

Transpose-free results. Stop wasting time transposing results from summary statistics and numerous hypothesis tests into user-reader-audience-friendly tables for dissemination, publication, or presentation. NXG Logic summary statistics and hypothesis testing algorithms automatically evaluate numerous tests of assumptions and determine the appropriate tests to be applied. Relevant graphics are also automatically generated.

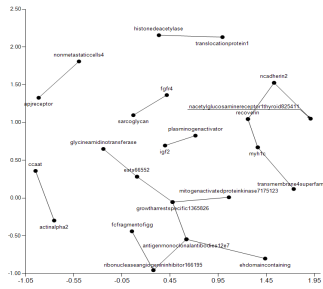
Manifold learning and knowledge discovery. Most analysts directly input data into hypothesis testing, without sufficiently analyzing the data to determine whether certain patterns exist independent of the experimental group or treatment assignments. NXG Logic users can rapidly transform data, reduce dimensions, perform knowledge and class discovery with cluster validity analysis to identify whether a rich cluster structure of the data exists.

Machine learning. NXG Logic algorithms are comprised of a multitude of machine learning techniques, which can offer numerous perspectives on the results obtained. Computational intelligence and swarm intelligence algorithms are also employed to tackle a variety of numerical challenges.

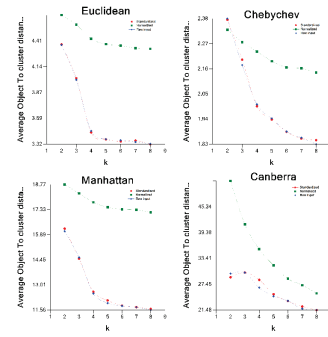
Upgradability. NXG Logic offers several collections of toolkit availability, ranging from the Standard version, Professional version, to the Enterprise version.



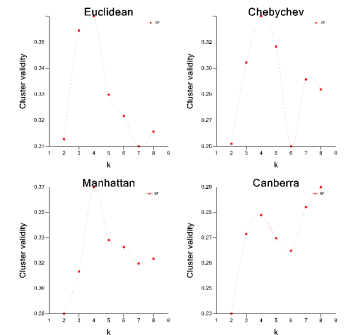
Pearson & Spearman correlation



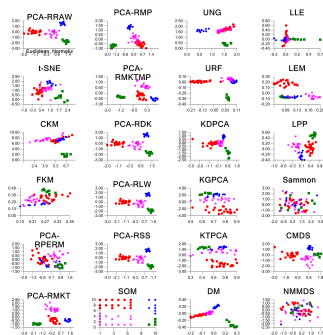
Force plots



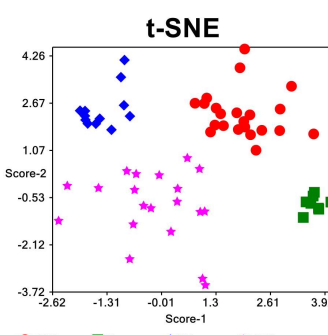
Cluster validity (CV)



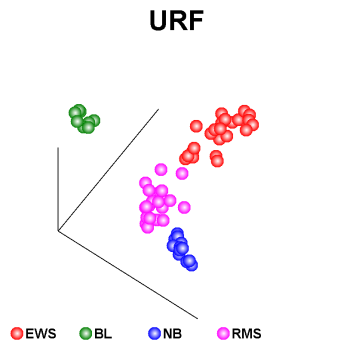
Cluster validity (scores)



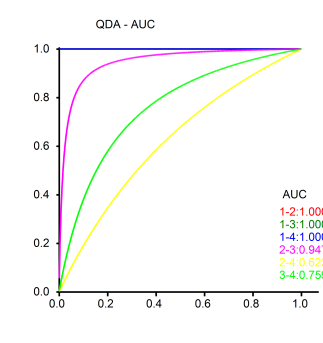
Dimension reduction, class discovery



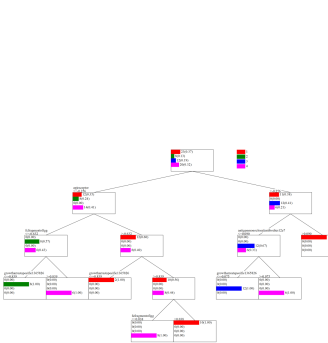
Stochastic neighbor embedding



Class discovery (random forests)



Class prediction (QDA,AUC)



Class prediction (decision trees)

Knowledge discovery and text mining. NXG Logic's technology empowers analysts to transform and transpose data, perform feature selection via cross-validation, dimension reduction with linear and non-linear manifold learning, cluster validity to determine the optimal number of clusters within a dataset, and assess association and generate force plots. NXG Logic's technology also includes text mining via stemming/stopping and N-gram analysis in order to cluster documents, sentences, abstracts, product reviews, and user comments. Extraction of concept clusters also includes graphic output to identify the key words (and documents) which are driving each concept.

Statistical analysis. Analysts can also perform 2- and k -sample hypothesis testing, multiple linear regression, multivariate regression, polytomous (multi-class) logistic regression, Poisson regression, Cox proportional hazards regression, Kaplan-Meier analysis. Regression diagnostics are available for most of the regression models.

Dimension reduction and class discovery. NXG Logic has also developed numerous dimension reduction algorithms based on linear methods and non-linear manifold learning. Examples include correlation-based PCA (CPCA), kernel distance-based PCA (KDPCA), kernel Gaussian radial basis function PCA (KGPCA), kernel Tanimoto distance-based PCA (KTRPCA), diffusion maps (DM), localized linear embeddings (LLE), Laplacian eigenmaps (LEM), and locally preserved projections (LPP). Identification of novel clusters in data can be determined by using NXG Logic's suite of class discovery tools, including crisp K-means cluster (CKM), fuzzy-K-means cluster (FKM), self-organizing maps (SOM), unsupervised neural gas (UNG), unsupervised artificial neural networks (UANN), Gaussian mixture models (GMM), unsupervised random forests (URF), Sammon mapping (Sammon), classic multidimensional scaling (CMDS), non-metric multidimensional scaling (NMMDS), and hierarchical cluster analysis (HCA).

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Class prediction, cross validation, performance. NXG Logic's class prediction techniques include linear regression (LREG), decision tree classification (DTC), supervised random forests (SRF), K-nearest neighbor (KNN), naive Bayes classifier (NBC), linear discriminant analysis (LDA), quadratic discriminant analysis (QDA), Fisher discriminant analysis (FDA), learning vector quantization (LVQ), polytomous logistic regression (PLOG), gradient ascent support vector machines (SVMGA), least squares support vector machines (SVMLS), artificial neural networks (ANN), kernel regression (KREG), particle swarm optimization, supervised neural gas (SNG), and mixture of experts (MOE). The potential for selection bias can be minimized when performing class prediction by employing several types of cross-validation, such as bootstrap bias, k-fold, and leave one out (LOOCV). The performance of class prediction analysis can be evaluated for sensitivity/specificity, kappa vs. error (classifier diversity), receiver operator characteristic (ROC) curves, ROC area under the curve comparisons for all pairwise 2-class comparisons, as well as average area under the curve (AUC).

Simulation. NXG Logic technology also includes fitting probability distributions to data and simulating quantiles from normal, log-normal, chi-squared, Erlang, gamma, Student's t , F-ratio, Cauchy, Laplace, logistic, beta, betaPERT, Pareto, power, Rayleigh, triangle, stable distributions, and performing Monte Carlo uncertainty analysis based on correlated data. Monte Carlo cost analysis can also be performed using stored run parameters for distributions, correlations, etc.