Announcing…

NCSS 2007

ENVISION. DESIGN. DISCOVER. DESCRIBE.

Windows VISTA Compatible

We are pleased to announce a new edition of our NCSS statistical analysis and graphics software.

This edition adds **several new procedures and features** to NCSS, including **mixed models**, an **enhanced user interface** and the ability to create **macros**, which add programmability and streamline repeated tasks. The graphics capabilities have also been greatly enhanced with the addition of **color selection tools** that allow you to create and choose from **millions of colors** for inclusion in NCSS charts and graphs. All datasets and templates of previous versions of NCSS are fully compatible with NCSS 2007.

New Procedures

- Mixed Models
- Merging Two Databases
- Data Simulator
- Double Dendrograms
- Cochrane-Orcutt Regression
- Nondetects Analysis
- Nondetects Regression
- Circular Data Analysis
- Data Matching
- Data Stratification

New Features

- Simplified Interface
- Macros
- Color Enhancements
- Quick Launch
- Improved Help System

Mixed Models

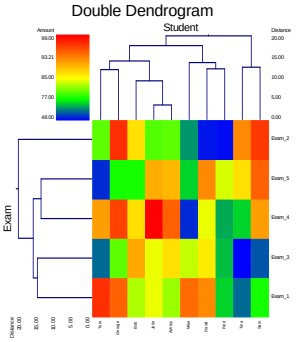
This procedure uses mixed models methods to analyze data from repeated measures studies, split-plot designs, factorial designs, cross-over designs, and designs with covariates, among others. Restricted maximum likelihood and full maximum likelihood techniques are implemented in this procedure.

Merging Two Databases

The Merge procedure is used to merge two databases according to the value of one or more common (index) variables. It may also be used to update one database with the contents of another.

Data Simulator

This procedure allows you to simulate, store, and visualize data from various discrete and continuous distributions, including Beta, Binomial, Cauchy, Constant, Exponential, F, Gamma, Multinomial, Normal, Poisson, T, Tukey's Lambda, Uniform, and Weibull. Mixture distributions may also be simulated. The output includes histograms and numeric summaries of simulated data.



Double Dendrograms

Double dendrograms display clusters for individuals (rows) and variables (columns) in a single graph. A set of eight hierarchical clustering algorithms are available including single linkage, complete linkage, and group average. The procedure outputs lists of the items in each cluster, linkage reports, and a double-dendrogram.

Cochrane-Orcutt Regression

This procedure uses the Cochrane-Orcutt method to adjust for serial correlation when performing multiple regression.

Nondetects Analysis

This procedure computes summary statistics, generates EDF plots, and computes hypothesis tests appropriate for two or more groups for data with nondetects (left-censored) values.

Nondetects Regression

The nondetects regression procedure fits the regression relationship between a positive-valued dependent variable (with, possibly, some nondetected responses) and one or more independent variables.

To Place Your Order:

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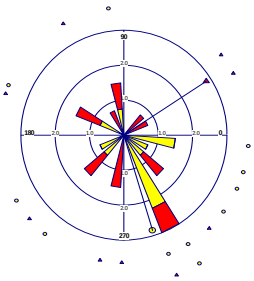
Circular Data Analysis



This procedure computes summary statistics, generates rose plots and circular histograms, computes hypothesis tests appropriate for one, two, and several groups, and computes the circular correlation coefficient for circular data.

Data Matching

This procedure assigns data matches based on one or more numeric variables. Both optimal and greedy matching algorithms are available. The user is able to choose the number of controls to match with each treatment and the distance calculation method.

Data Stratification

This procedure is used to stratify data based on a single numeric variable. The user is able to choose the number of strata to create.

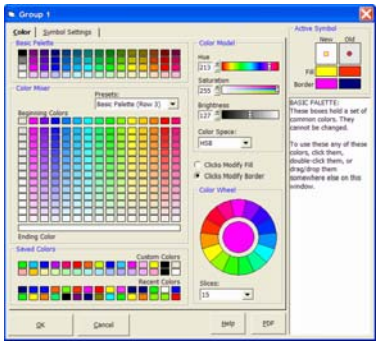
Simplified Interface

The procedure interfaces have been redesigned to make the user input easier to complete. Boxes containing descriptive titles have been added to group similar options together. This allows for easier navigation of the procedure windows and faster identification of input categories.

Macros (Programmability)

NCSS has an interactive (point and click) user interface which makes in easy to learn and use. At times, however, it is necessary to repeat the same steps over and over. When this occurs, a batch system becomes more desirable. This procedure utilizes a batch language that lets you create a macro (script/program) and then run that macro. With the click of a single button, the program will run a series of procedures.

Color Enhancements



The color selection windows let you choose appropriate colors from the 16 million colors that are available on today's monitors. The goal of the color selection window is to provide a tool that will allow you to pick a set of colors that are pleasing to the eye when viewed together, and let the viewer interpret the results quickly and effectively.

Quick Launch

The Quick Launch window contains a button corresponding to each statistical and graphical procedure in the system. The Quick Launch makes it easy to find and launch any procedure from a single screen.

More details at www.ncss.com/ncss.html

NCSS
329 North 1000 East
Kaysville, Utah 84037

Announcing…

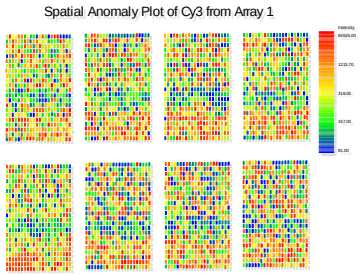
NCSS 2007
GESS 2006

GESS 2006

Gene Expression Statistical System for *Microarrays*

What is GESS?

GESS software is a statistical tool for finding differentially expressed genes from microarray studies. Array files from multiple platforms may be imported, corrected, and normalized using GESS's simple spreadsheet and menu interface. In a systematic, elegant manner, GESS software computes the desired statistical test for each gene, and reports the results with appropriate Bonferroni or false discovery rate adjusted significance. GESS produces scatter plots, dendrograms, and histograms to visualize gene expression results. GESS may also be used for screening or filtering arrays.



GESS Features

Statistical Analyses
Fold-Change Analysis
Paired T-Tests
One-Group T-Tests
Two-Group T-Tests
One-Factor ANOVA
Two-Factor ANOVA
Repeated Measures
GLM ANOVA
Analysis of Covariance
Multiple Regression
Cox Regression
Logistic Regression

Supported Platforms
Affymetrix®
GenePix®
Agilent®
Two-Channel Files
Expression Data Files

Multiple Testing Correction
Bonferroni
False Discovery Rate

Affymetrix® Arrays
RMA Expression Algorithm
Gene List Subsets
Chip Quality Summaries
Background Correction
Quantile Normalization
Comparative Box Plots
Spatial Anomaly Plots

Data Utilities
Save Data to Spreadsheet
File Description
Export to TXT File
Principal Components Analysis
Hierarchical Cluster Analysis

Hierarchical Clustering
Eight Clustering Methods
Three Scaling Methods
Double Dendrograms
Custom Heat Maps

Two-Channel Arrays
Whole Array Box Plots
Print-tip Box Plots
MA Loess Plots
Spatial Anomaly Plots
Spot QC Summaries
Array QC Summaries
Weak Signal Filters
Background Filters
Loess Normalization
Gene List Subsets
Subset Box Plots
Dye-Swap Compatible

More details at www.ncss.com/gess.html

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