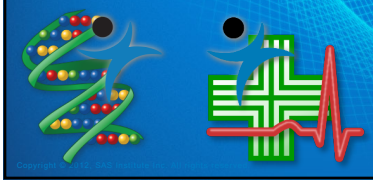
JSM Computer Technology Workshop
31 July 2019

VISUAL INTERACTION, STATISTICAL ANALYSIS AND MACHINE LEARNING TO ADVANCE LIFE SCIENCE RESEARCH WITH JMP SOFTWARE



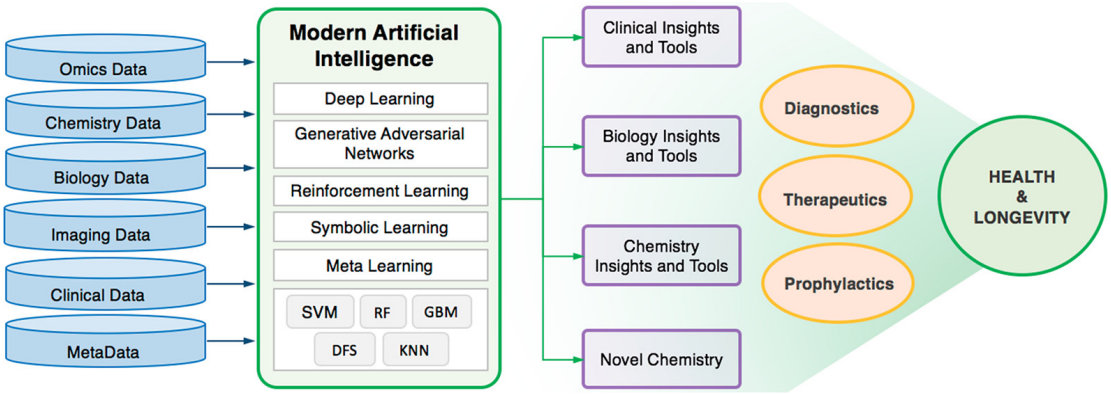
KELCI MICLAUS, PH.D, JMP LIFE SCIENCES
RUTH HUMMEL, PH.D, JMP GLOBAL ACADEMIC

AGENDA

1. Broad Overview
2. Chemoprevention Study Analysis with JMP Products
   - Data Exploration and Cleaning with JMP, JMP Pro, and JMP Genomics
   - Complex Analysis with JMP Genomics
3. Detailed Overview: what else is in these tools?
   - JMP
   - JMP Pro
   - JMP Genomics
   - JMP Public
   - JMP Clinical

POTENTIAL IN DRUG DISCOVERY AND LIFE SCIENCES

Data-rich environment for application of modern machine learning methods



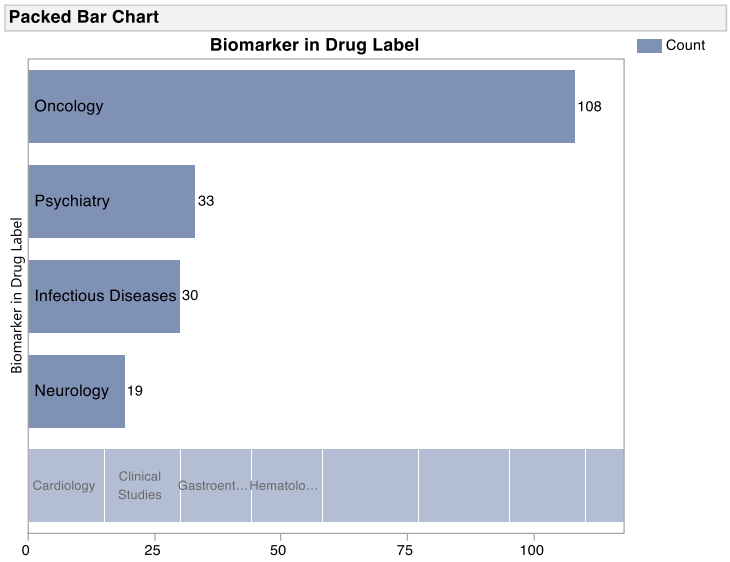
Published in: Alex Zhavoronkov; *Mol. Pharmaceutics* 15, 4311-4313.
DOI: 10.1021/acs.molpharmaceut.8b00930

KEY OPPORTUNITY AREAS

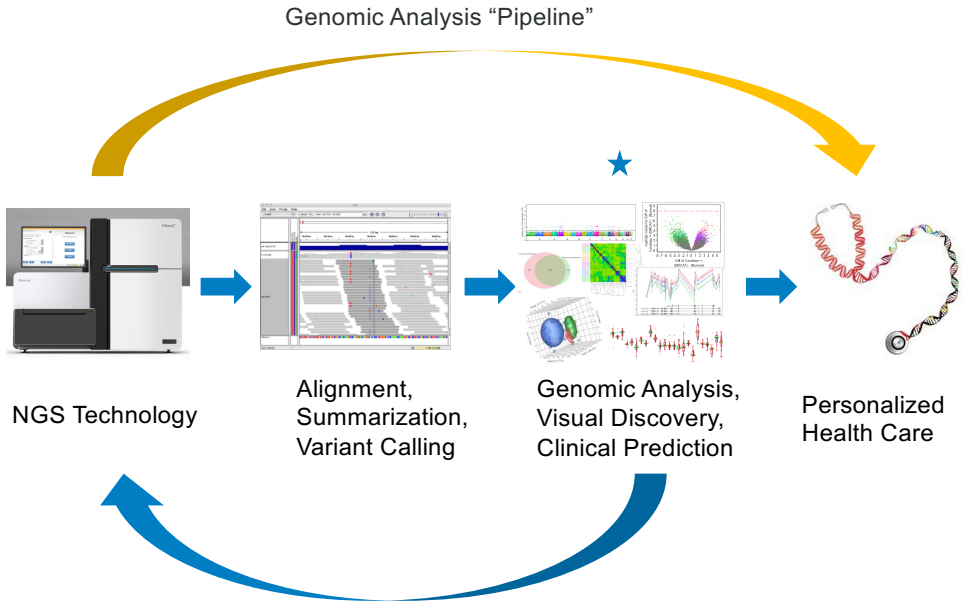
- New Compound and Drug Repurposing
  - Mining on chemical structures to propose new compounds
  - Repurpose drugs on market based on affected biological pathways
- Biomarker Discovery
  - Prognostic and Predictive models using genomic signatures
- Medical Imaging
  - Image classification methods to provide less-subjective assessment
- Toxicity Signals in Clinical Trials
  - Predict potential safety concerns, sub-group analysis
- Clinical Trial Operational Integrity and Quality by Design
  - Modern risk-based assessment for site operational integrity and selection

HIGHLIGHTING SUCCESSES

- Clinical Decision Support Systems
- Chemical Compound Mining
- Biomarker Discovery
  - Prognostic: Determine whether patient should receive treatment
  - Predictive: Patient outcome specific to treatment (Drug label/Companion diagnosti



JMP IN LIFE SCIENCES



JMP Family of Products

Drug Discovery

Discovery	Pre-Clinical	Clinical Trials	Manufactoring	Post Clinical
Biomarker Lead compound	Biological Test	Safety Efficacy	New Drug	Pharmaco- vigilance

JMP Genomics

Omics and genetics for biomarkers

JMP Clinical

Drug safety and efficacy during trials and on the market

JMP/JMP PRO

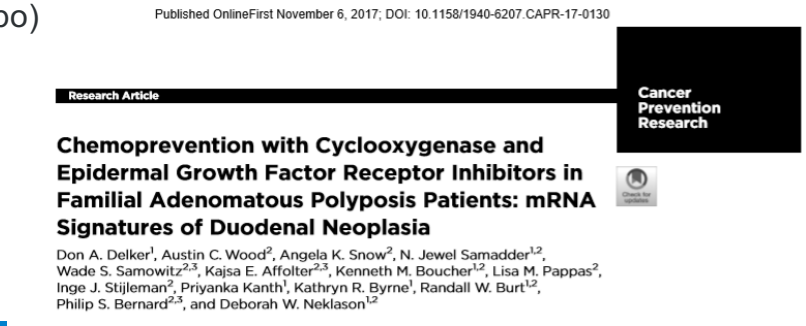
Data cleaning, mining, target identification, formulation development, design of experiment

SAS

EXAMPLE

INCREASINGLY COMPLEX BIOLOGICAL EXPERIMENTS

- Identify biomarkers in differential molecular expression signatures for normal vs. polyp tissues attributable to chemoprevention therapy in FAP
- Molecular expression baseline measurements taken on normal tissue prior to treatment, follow-up mRNA collection on polyp and normal tissue after 6 month treatment (Drug vs Placebo)



Published OnlineFirst November 6, 2017; DOI: 10.1158/1940-6207.CAPR-17-0130

Research Article

Cancer Prevention Research

Chemoprevention with Cyclooxygenase and Epidermal Growth Factor Receptor Inhibitors in Familial Adenomatous Polyposis Patients: mRNA Signatures of Duodenal Neoplasia

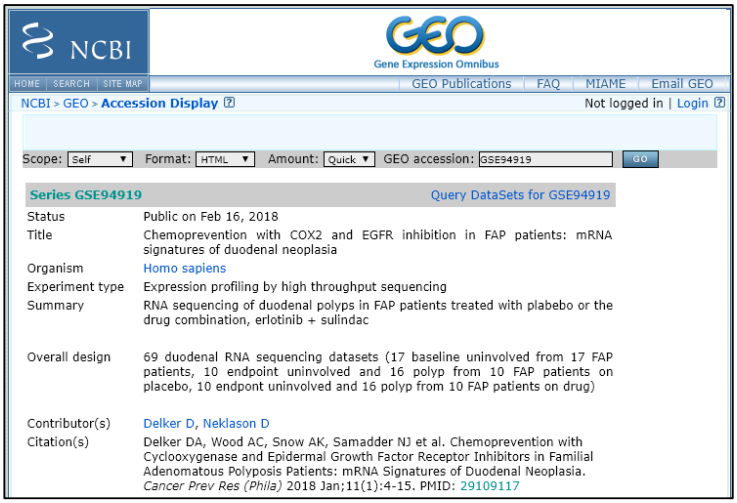
Don A. Delker[1], Austin C. Wood[2], Angela K. Snow[2], N. Jewel Samadder[1,2], Wade S. Samowitz[2,3], Kajsa E. Affolter[2,3], Kenneth M. Boucher[1,2], Lisa M. Pappas[2], Inge J. Stijleman[2], Priyanka Kanth[1], Kathryn R. Byrne[1], Randall W. Burt[1,2], Philip S. Bernard[2,3], and Deborah W. Neklason[1,2]

EXAMPLE

CHEMOPREVENTION STUDY ANALYSIS WITH JMP PRODUCTS

Analysis Outline

- Explore Study Design and Clinical measurements in JMP/JMP PRO
- Complete RNA-seq analysis in JMP Genomics
- Analysis Reporting and Communication with JMP Public



NCBI — Gene Expression Omnibus

HOME | SEARCH | SITE MAP | GEO Publications | FAQ | MIAME | Email GEO

NCBI > GEO > **Accession Display** — Not logged in | Login

Scope: Self | Format: HTML | Amount: Quick | GEO accession: GSE94919 | GO

Series GSE94919 — Query DataSets for GSE94919

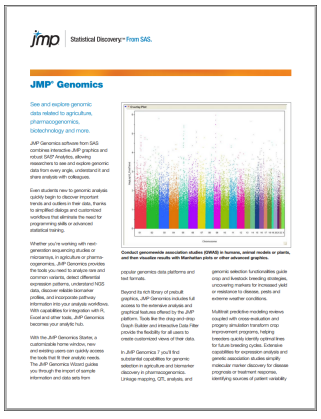
Status	Public on Feb 16, 2018
Title	Chemoprevention with COX2 and EGFR inhibition in FAP patients: mRNA signatures of duodenal neoplasia
Organism	Homo sapiens
Experiment type	Expression profiling by high throughput sequencing
Summary	RNA sequencing of duodenal polyps in FAP patients treated with plabebo or the drug combination, erlotinib + sulindac
Overall design	69 duodenal RNA sequencing datasets (17 baseline uninvolved from 17 FAP patients, 10 endpoint uninvolved and 16 polyp from 10 FAP patients on placebo, 10 endpoint uninvolved and 16 polyp from 10 FAP patients on drug)
Contributor(s)	Delker D, Neklason D
Citation(s)	Delker DA, Wood AC, Snow AK, Samadder NJ et al. Chemoprevention with Cyclooxygenase and Epidermal Growth Factor Receptor Inhibitors in Familial Adenomatous Polyposis Patients: mRNA Signatures of Duodenal Neoplasia. *Cancer Prev Res (Phila)* 2018 Jan;11(1):4-15. PMID: 29109117

https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE94919

JMP FAMILY OF PRODUCTS

SOFTWARE FOR LIFE SCIENTISTS

- JMP*
- JMP Pro
- JMP Genomics*
- JMP Clinical
- JMP Add-Ins
- JMP Live*
- SAS*



jmp | Statistical Discovery™ From SAS.

JMP® Genomics

See and explore genomic data related to agriculture, pharmacogenomics, biotechnology and more.

JMP Genomics software from SAS combines interactive, JMP graphics and robust SAS® Analytics, allowing researchers to see and explore genomic data from every angle, understand it and share analysis with colleagues.

Even students new to genomic analysis quickly begin to discover important trends and outliers in their data, thanks to simplified dialogs and customized workflows that eliminate the need for programming skills or advanced statistical training.

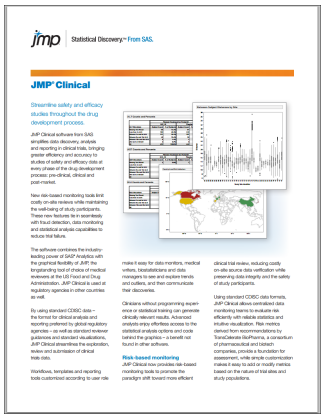
Whether you're working with next-generation sequencing studies or microarrays, SNP, culture or pharmacogenomics, JMP Genomics gives you the flexibility to analyze rare and common variants, detect differential expression patterns, understand NGS data, discover reliable biomarker profiles, and incorporate pathway information into your analysis workflows. With capabilities for integration with R, Excel and other tools, JMP Genomics becomes your analytic hub.

With the JMP Genomics Starter, a customizable home window, new and existing users can quickly access the tools that fit their analytic needs. The JMP Genomics Wizard guides you through the import of sample information and data sets from popular genomics data platforms and text formats.

Beyond the rich library of prebuilt graphics, JMP Genomics includes full access to the extensive analysis and graphical features offered by the JMP® platform. Tools like the drag-and-drop Graph Builder and interactive Data Filter provide the flexibility for all users to create customized views of their data.

In JMP Genomics 7 you'll find substantial capabilities for genomic selection in agriculture and biomarker discovery in pharmacogenomics. Linkage mapping, QTL analysis, and genomic selection functionalities guide crop and livestock breeding strategies, uncovering markers for increased yield or resistance to disease, pests and extreme weather conditions.

Multitrait predictive modeling reviews coupled with cross-evaluation and progeny simulation transform crop improvement programs, helping breeders quickly identify optimal lines for future breeding cycles. Extensive capabilities for expression analysis and genetic association studies simplify molecular marker discovery for disease prognosis or treatment response, identifying sources of patient variability.



jmp | Statistical Discovery™ From SAS.

JMP® Clinical

Streamline safety and efficacy studies throughout the drug development process.

JMP Clinical software from SAS simplifies data discovery, analysis and reporting in clinical trials, bringing greater efficiency and accuracy to studies of safety and efficacy data at every phase of the drug development process: pre-clinical, clinical and post-market.

New risk-based monitoring tools limit costly on-site reviews while maintaining the well-being of study participants. These new features tie in seamlessly with fraud detection, data monitoring and statistical analysis capabilities to reduce that failure.

The software combines the industry-leading power of SAS® Analytics with the graphical flexibility of JMP, the longstanding tool of choice of medical reviewers at the US Food and Drug Administration. JMP Clinical is used at regulatory agencies in other countries as well.

By using standard CDISC data – the format for clinical analysis and reporting preferred by global regulatory agencies – as well as standard reviewer guidances and standard visualizations, JMP Clinical streamlines the exploration, review and submission of clinical trials data.

Workflows, templates and reporting tools customized according to user role make it easy for data monitors, medical writers, biostatisticians and data managers to see and explore trends and outliers, and then communicate their discoveries.

Clinicians without programming experience or statistical training can generate clinically relevant results. Advanced analysts enjoy effortless access to the statistical analysis options and code behind the graphics – a benefit not found in other software.

Risk-based monitoring

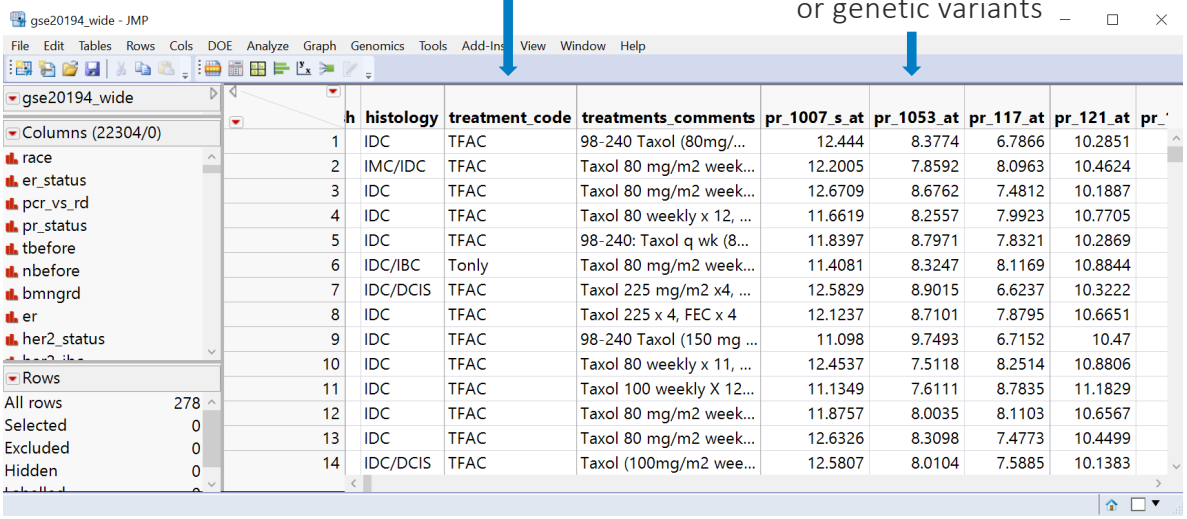
JMP Clinical now provides risk-based monitoring tools to promote the paradigm shift toward more efficient clinical trial review, reducing costly on-site source data verification while preserving data integrity and the safety of study participants.

Using standard CDISC data formats, JMP Clinical allows centralized data monitoring teams to evaluate risk efficiently with reliable statistics and intuitive visualization. Risk metrics derived from recommendations by TransCelerate BioPharma, a consortium of pharmaceutical and biotech companies, provide a foundation for assessment, while simple customization makes it easy to add or modify metrics based on the nature of trial sites and study populations.

JMP DATA TABLES

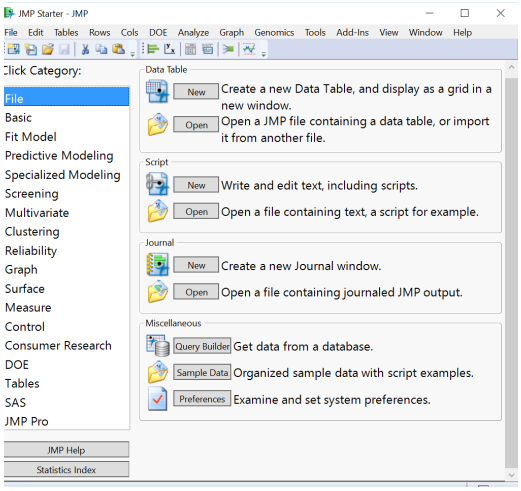
Experimental Factors

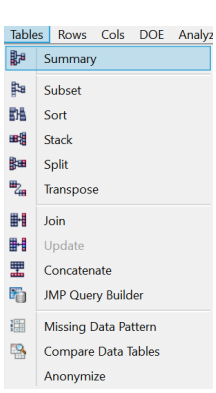
Expression levels, or genetic variants

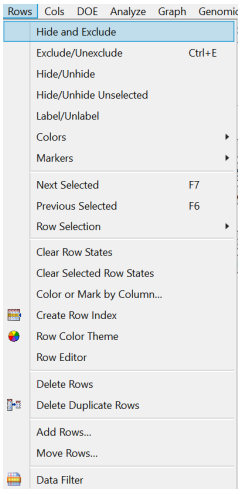


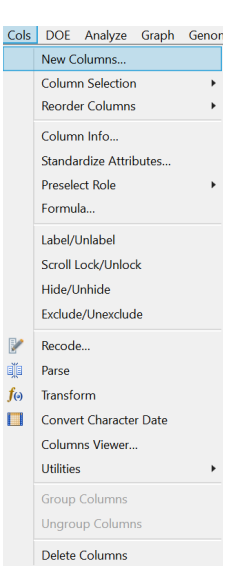
	h	histology	treatment_code	treatments_comments	pr_1007_s_at	pr_1053_at	pr_117_at	pr_121_at	pr_
1		IDC	TFAC	98-240 Taxol (80mg/...	12.444	8.3774	6.7866	10.2851	
2		IMC/IDC	TFAC	Taxol 80 mg/m2 week...	12.2005	7.8592	8.0963	10.4624	
3		IDC	TFAC	Taxol 80 mg/m2 week...	12.6709	8.6762	7.4812	10.1887	
4		IDC	TFAC	Taxol 80 weekly x 12, ...	11.6619	8.2557	7.9923	10.7705	
5		IDC	TFAC	98-240: Taxol q wk (8...	11.8397	8.7971	7.8321	10.2869	
6		IDC/IBC	Tonly	Taxol 80 mg/m2 week...	11.4081	8.3247	8.1169	10.8844	
7		IDC/DCIS	TFAC	Taxol 225 mg/m2 x4, ...	12.5829	8.9015	6.6237	10.3222	
8		IDC	TFAC	Taxol 225 x 4, FEC x 4	12.1237	8.7101	7.8795	10.6651	
9		IDC	TFAC	98-240 Taxol (150 mg ...	11.098	9.7493	6.7152	10.47	
10		IDC	TFAC	Taxol 80 weekly x 11, ...	12.4537	7.5118	8.2514	10.8806	
11		IDC	TFAC	Taxol 100 weekly X 12...	11.1349	7.6111	8.7835	11.1829	
12		IDC	TFAC	Taxol 80 mg/m2 week...	11.8757	8.0035	8.1103	10.6567	
13		IDC	TFAC	Taxol 80 mg/m2 week...	12.6326	8.3098	7.4773	10.4499	
14		IDC/DCIS	TFAC	Taxol (100mg/m2 wee...	12.5807	8.0104	7.5885	10.1383	

JMP (AND JMP PRO)



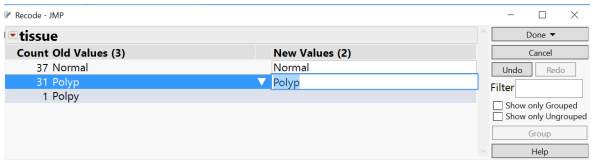


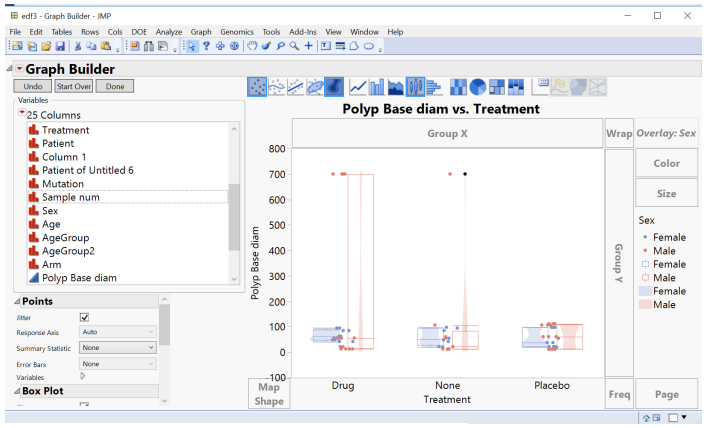




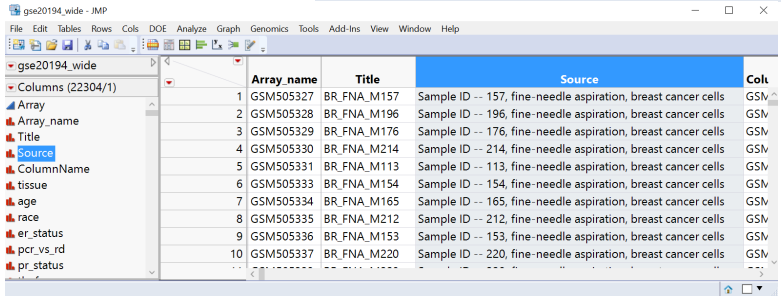
Lots of point-and-click tools for data cleaning (and much more)

JMP (AND JMP PRO)

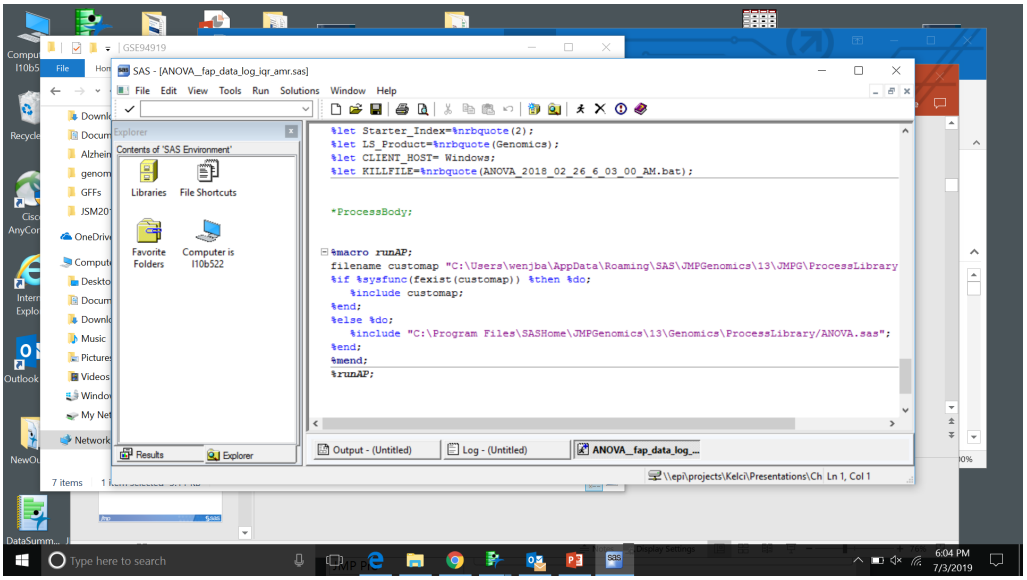




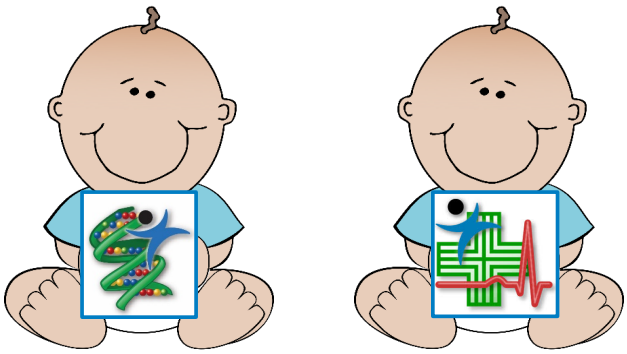
- Easily recode data,
- Parse information, e.g., pull out components from "Title" or "Source" columns
- Create new graphs by drag-and-drop



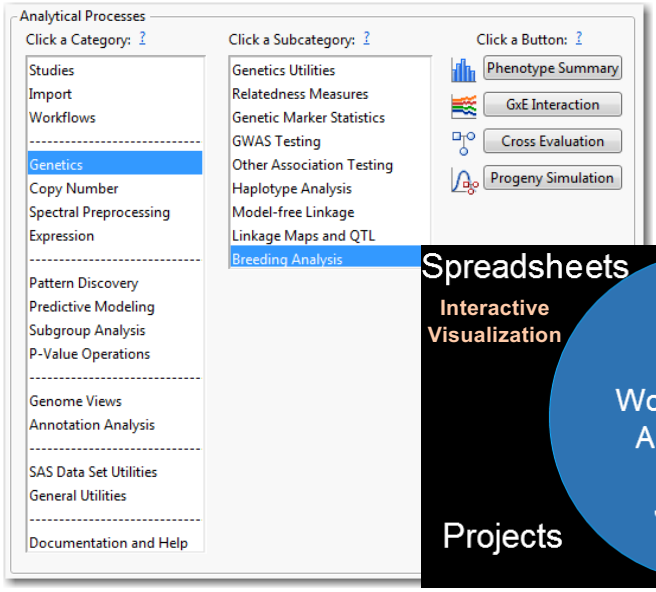
SAS

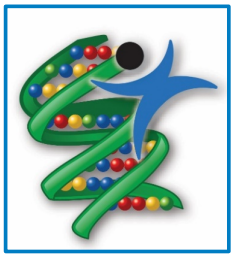


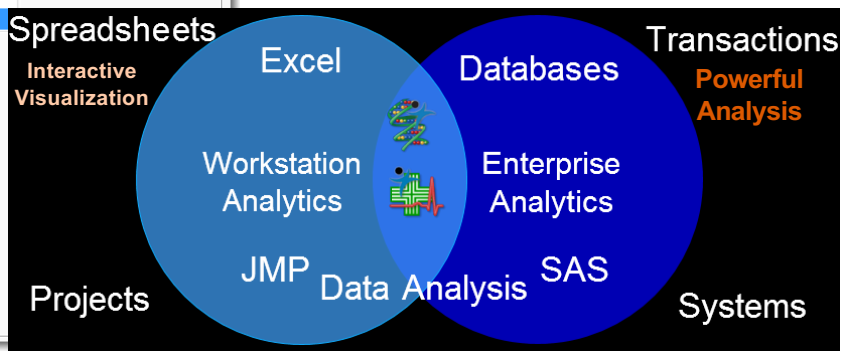
WHEN TWO SOFTWARE PACKAGES LOVE EACH OTHER VERY MUCH…



JMP GENOMICS

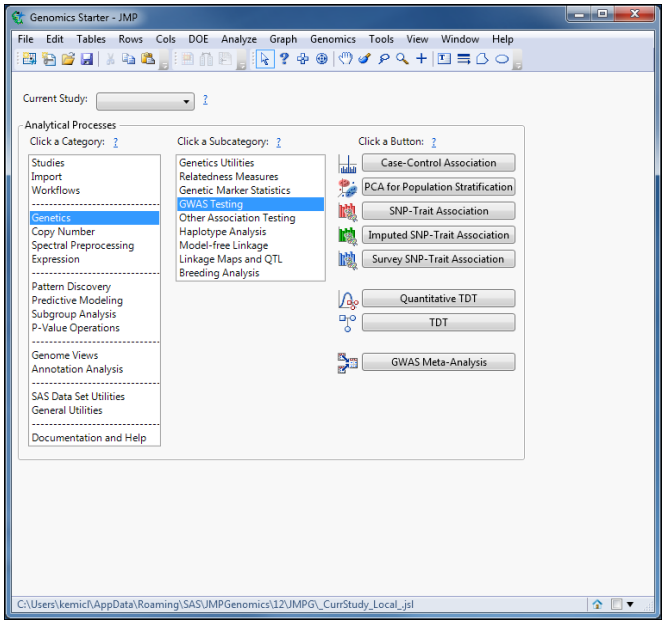






JMP GENOMICS OVERVIEW

- Over 200 customized genomic analysis reports
- Several pre-defined workflows to string together analyses
- Recent development focus:
  - NGS data import/QC/analysis
  - Genetic diversity and relatedness
  - Linkage Mapping and QTL
  - Multi-trait predictive modeling
  - Cross evaluation for plant breeding
  - DNA Methylation
  - Virtual Twins



UNIQUENESS OF JMP GENOMICS

- Broad and Deep Library of Statistical Methods
- Interactive graphics and tables
- *Point-and-Click GUI and programming/scripting*

JMP GENOMICS: BROAD SCOPE, DEEP FEATURES

- Genome-Wide Association Studies (GWAS)
- Linkage Mapping, QTL, and Plant Breeding Analysis
- Complex Analysis for Expression, Metabolomics, Proteomics
- Next-generation Sequencing
- Pattern Discovery, Predictive Modeling and Cross Validation
- Integrated Clinical and Genomic data

Core Capabilities of JMP® Genomics

JMP Genomics lets you visualize and explore large genomic data sets and share analyses with colleagues.

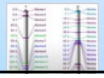
Genomic Selection for Crop Improvement

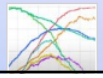

Pharmacogenomics


Expression


Statistical Genetics


Next-Gen Sequencing

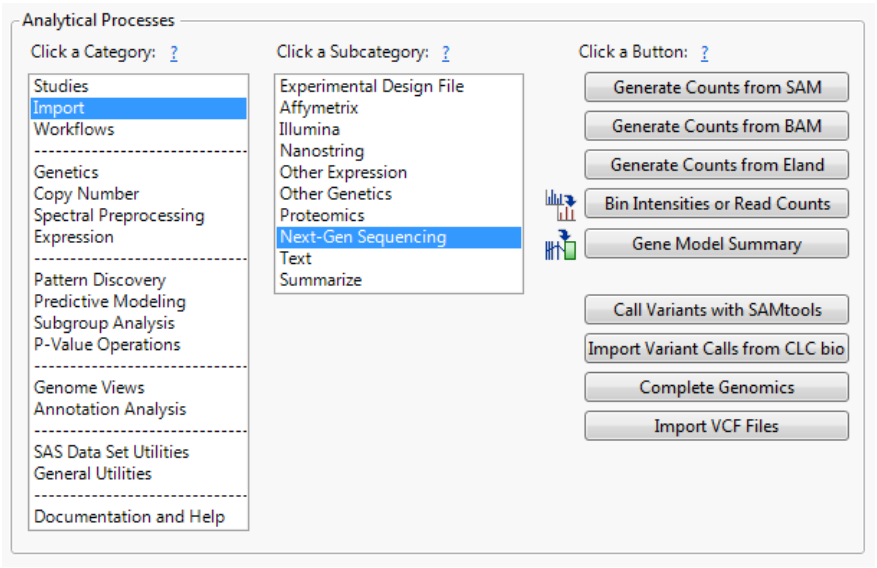

Linkage Mapping


Predictive Modeling

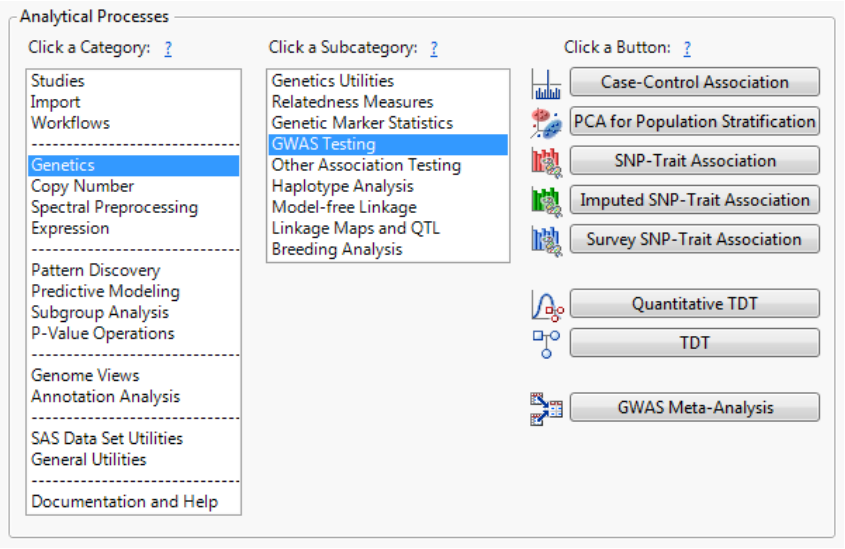
LIBRARY OF STATISTICAL METHODS

JMP GENOMICS

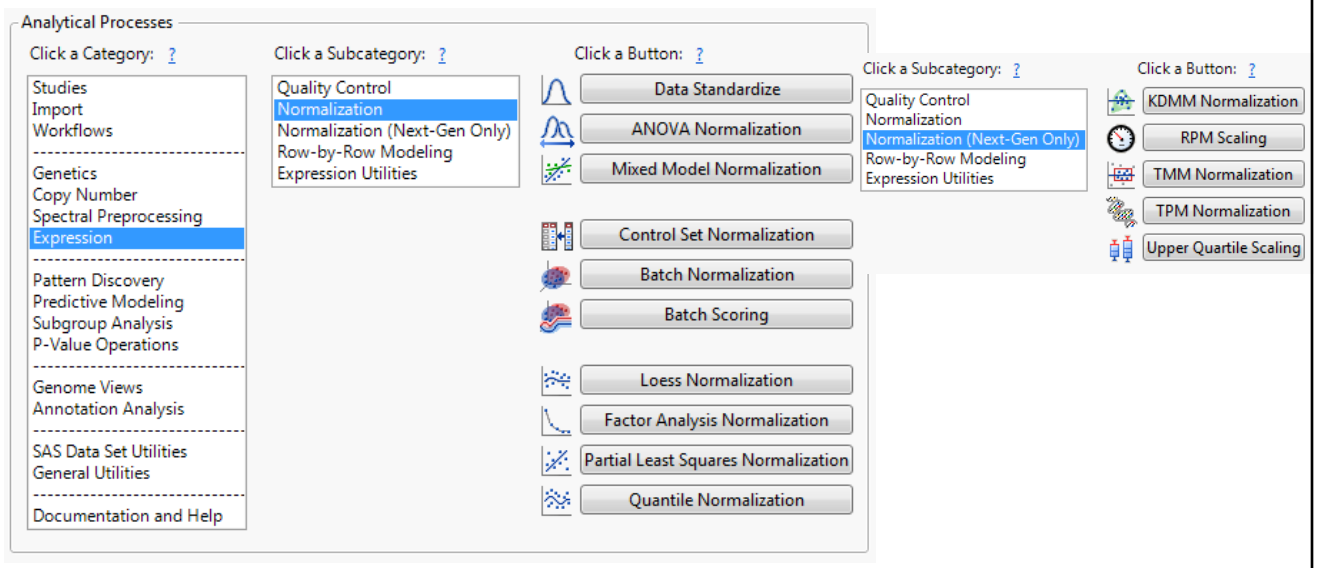
Import Engines



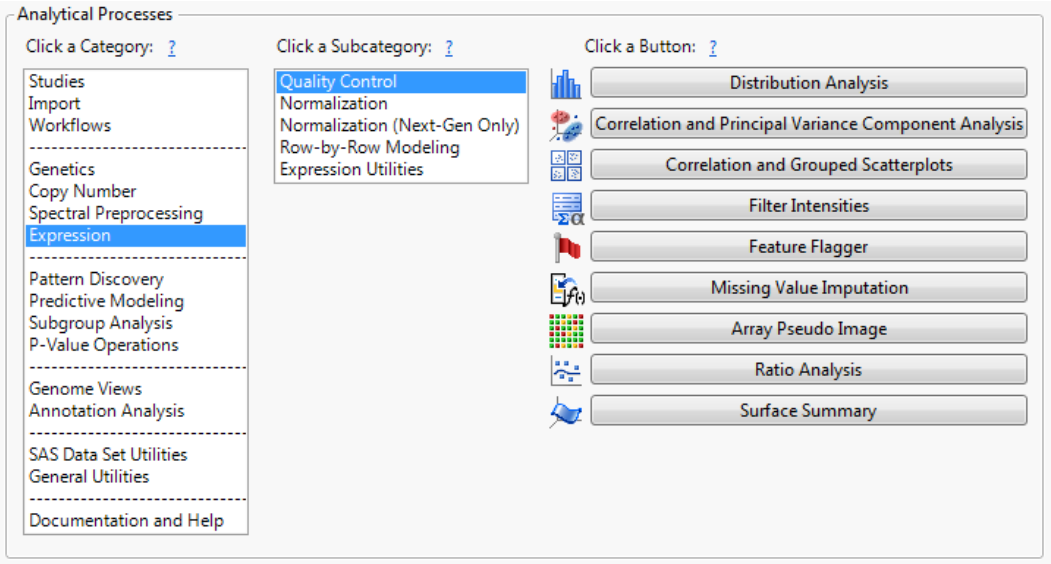
DNA Variant Analysis



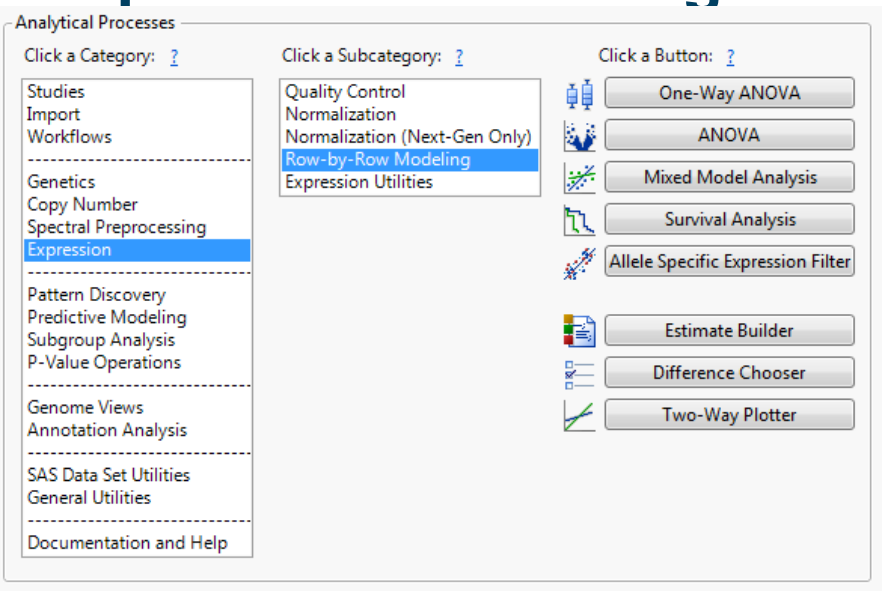
Gene Expression: Normalization



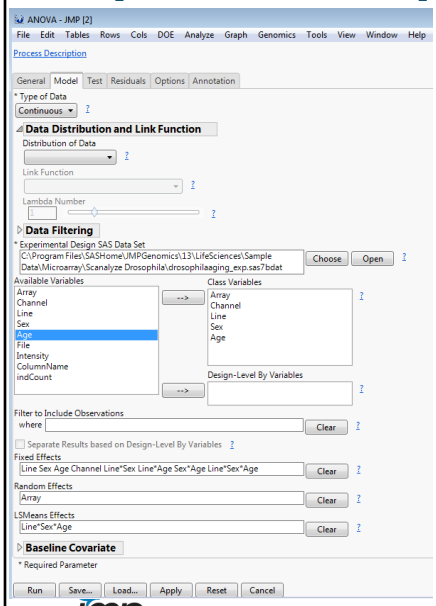
Gene Expression: Quality Control

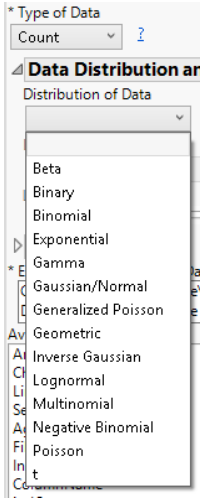


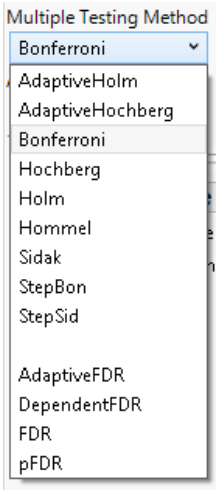
Gene Expression: Modeling

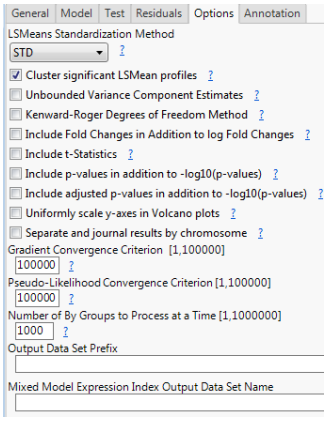


Simple to Complex Modeling Options

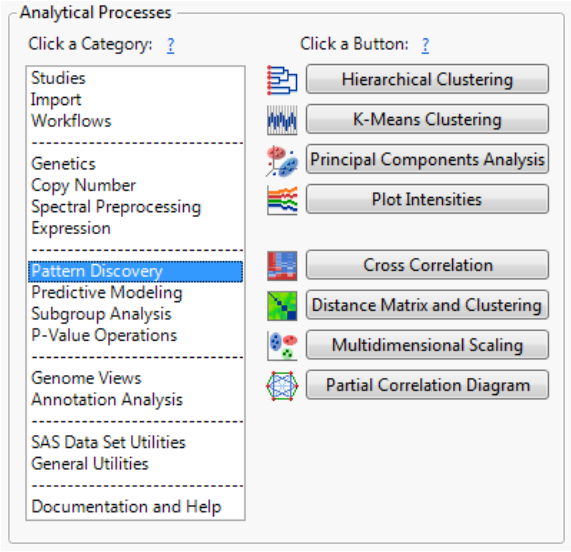




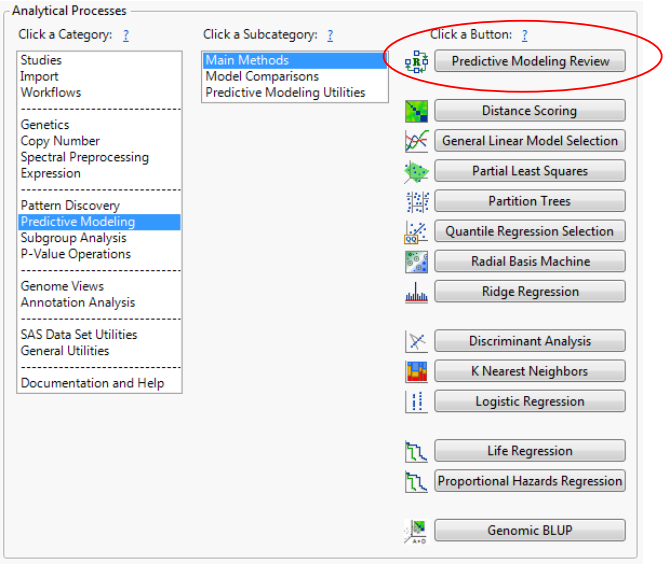




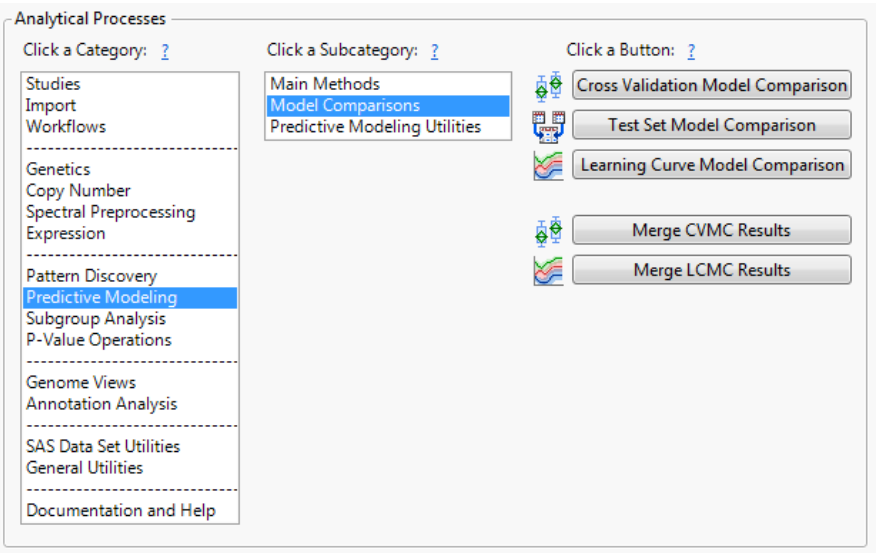
Exploratory Pattern Discovery

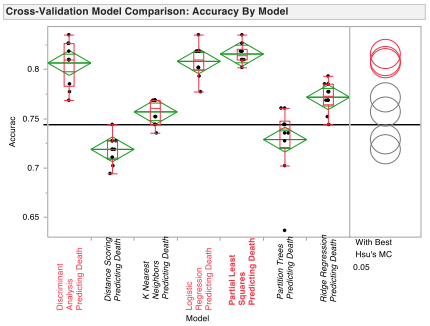


Predictive Modeling Methods

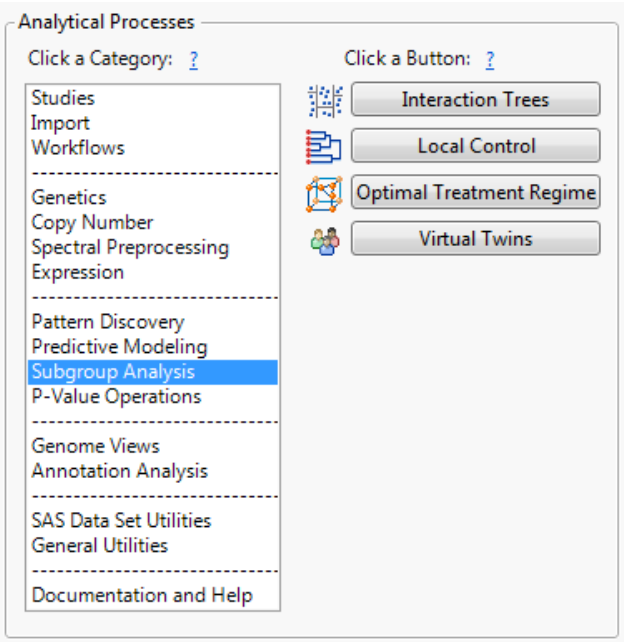


Model Assessment and Comparison





Subgroup Analysis

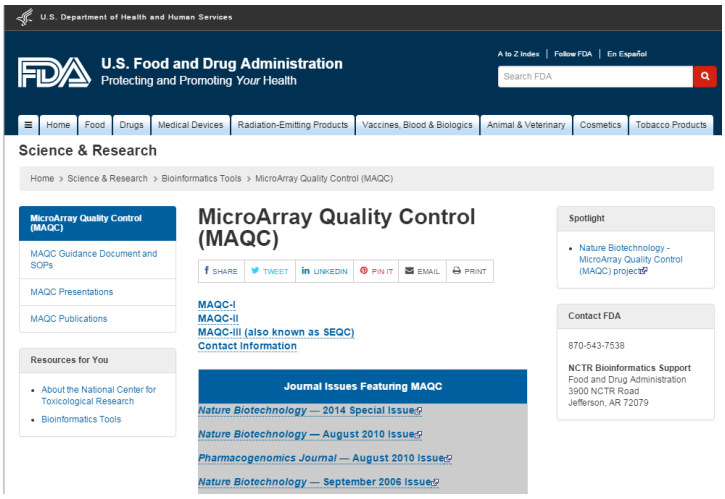


HIGHLIGHTING EXAMPLES

SEQC CONSORTIUM MAQC SOCIETY

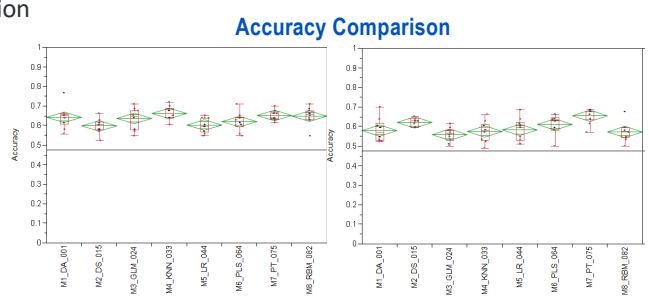
TECHNICAL PERFORMANCE OF NGS TECHNOLOGIES

- Assess predictive performance and reproducibility of microarray and NGS technology for pharmacogenomics and toxicogenomics
- Over 100 researchers across more than 12 dozen institutions



SEQC CONSORTIUM | NEUROBLASTOMA DATA PREDICTION

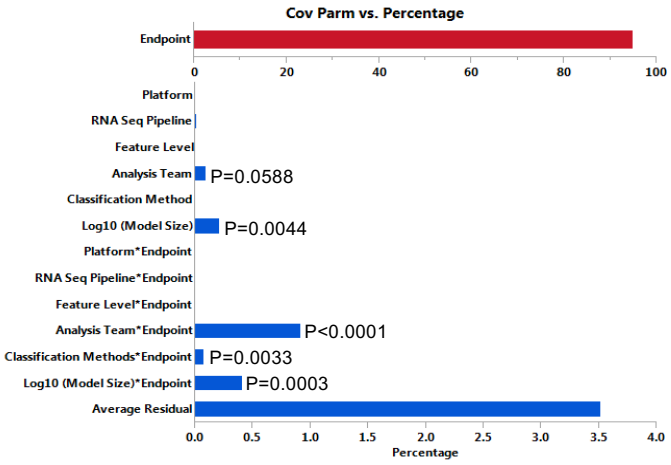
- NB_Microarray (Gene level intensities: 43291 predictors)
- NB_NGS_MAVG (Gene level counts : RNA-seq, 60778 predictors)
- Neuroblastoma survival endpoints (OS_HR 86 samples)
- Eight classification methods for prediction
  - Discriminant analysis
  - Distance Scoring
  - K-Nearest Neighbor
  - GLM Selection
  - Logistic Regression
  - Partial Least Squares
  - Partition Tree
  - Radial Basis Machine
- 5-fold Cross-Validation
  - AUC
  - Accuracy
  - RMSE



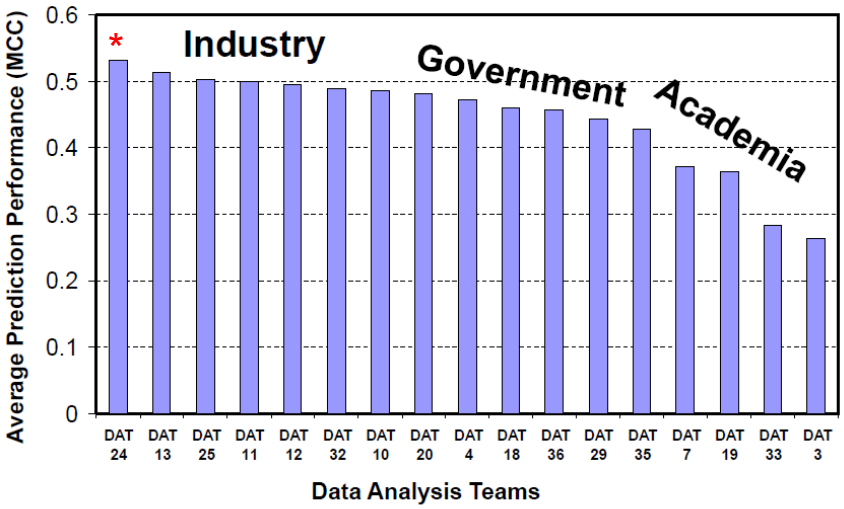
NB_Microarray NB_NGS_MAVG

SEQC CONSORTIUM | PREDICTIVE PERFORMANCE OF TECHNOLOGIES

- Factors contributing to variability in predictive performance of gene-level data on neuroblastoma survival endpoints
- **Analysis, predictive methodology, and model size key contributors**



Proficiency in Prediction (Guess what software was the red star…)



Shi L (石乐明) et al. *Nat Biotechnol.* 2010. **NPG Focus on MAQC-II :** www.nature.com/focus/maqc2/

DISCOVERY AND PREDICTION

HOSPITAL BIOMARKER UTILITY TO PREDICT SEPSIS SURVIVAL

Science Translational Medicine Integrating Medicine and Science

RESEARCH ARTICLE

SEPSIS

An Integrated Clinico-Metabolomic Model Improves Prediction of Death in Sepsis

Raymond J. Langley,[1,2*] Ephraim L. Tsalik,[3,4*] Jennifer C. van Velkinburgh,[1*] Seth W. Glickman,[5,6] Brandon J. Rice,[1] Chunping Wang,[7] Bo Chen,[7] Lawrence Carin,[7] Arturo Suarez,[8] Robert P. Mohney,[9] Debra H. Freeman,[5] Mu Wang,[10] Jinsam You,[10] Jacob Wulff,[9] J. Will Thompson,[4] M. Arthur Moseley,[4] Stephanie Reisinger,[11] Brian T. Edmonds,[12] Brian Grinnell,[12] David R. Nelson,[12] Darrell L. Dinwiddie,[1,13,14] Neil A. Miller,[1,13] Carol J. Saunders,[13] Sarah S. Soden,[13] Angela J. Rogers,[15,16] Lee Gazourian,[15] Laura E. Fredenburgh,[15] Anthony F. Massaro,[15] Rebecca M. Baron,[15] Augustine M. K. Choi,[15] G. Ralph Corey,[5] Geoffrey S. Ginsburg,[5] Charles B. Cairns,[6] Ronny M. Otero,[8] Vance G. Fowler Jr.,[5] Emanuel P. Rivers,[8] Christopher W. Woods,[3,4,5] Stephen F. Kingsmore[1,13†]

Sepsis is a common cause of death, but outcomes in individual patients are difficult to predict. Elucidating the molecular processes that differ between sepsis patients who survive and those who die may permit more appropriate treatments to be deployed. We examined the clinical features and the plasma metabolome and proteome of patients with and without community-acquired sepsis, upon their arrival at hospital emergency departments and 24 hours later. The metabolomes and proteomes of patients at hospital admittance who would ultimately die differed markedly from those of patients who would survive. The different profiles of proteins and metabolites clustered into the following groups: fatty acid transport and β-oxidation, gluconeogenesis, and the citric acid cycle. They differed consistently among several sets of patients, and diverged more as death approached. In contrast, the metabolomes and proteomes of surviving patients with mild sepsis did not differ from survivors with severe sepsis or septic shock. An algorithm derived from clinical features together with measurements of five metabolites predicted patient survival. This algorithm may help to guide the treatment of individual patients with sepsis.

Sci Transl Med 24 July 2013:
Vol. 5, Issue 195, p. 195ra95
Sci. Transl. Med. DOI: 10.1126/scitranslmed.3005893

SEPSIS SURVIVAL

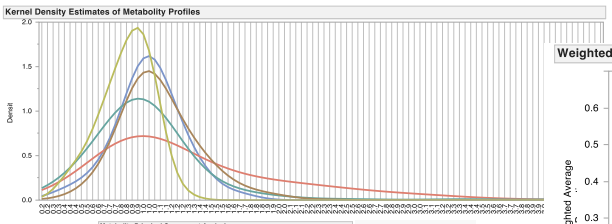
Analysis outline

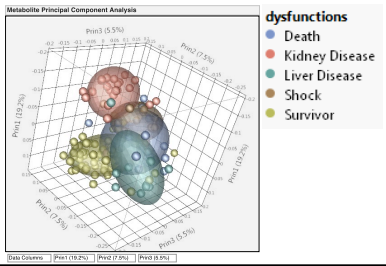
- Background and Goal
  - Sepsis outcome combination of demographics, clinical signs, and biomarkers.
  - Develop clinical + biomarker panel to predict sepsis survival
- Study
  - 1,152 suspected sepsis cases enrolled in ER hospitals.
  - Clinical measures and blood (plasma metabolites and proteins) collected at admittance and 24 hours
  - 31 Sepsis Non-survivors, 89 Sepsis Survivors, 29 SIRS criteria non-sepsis
- Analyses
  - Kernel Density distributions
  - PCVA to explain metabolite variability across clinical measures
  - ANOVA
    - Sepsis Non-survivors Vs. Survivors
    - SIRS Vs. Sepsis Survivors
- Predictive Modeling and Cross-validation
  - External validation data sets

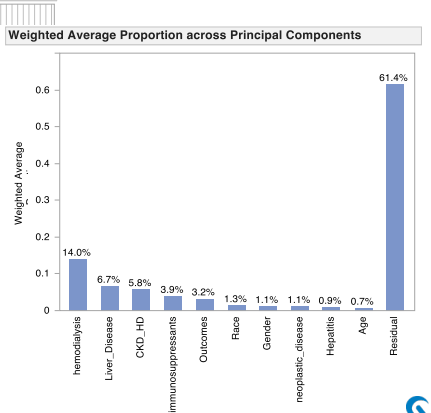
DISCOVERY AND PREDICTION

SEPSIS METABOLITE PROFILES

- Data exploration necessary to understand quality and drive further analysis
- Kernel densities, PCA of metabolite concentrations grouped by clinical dysfunctions. PVCA of factors contributing to metabolomic variability



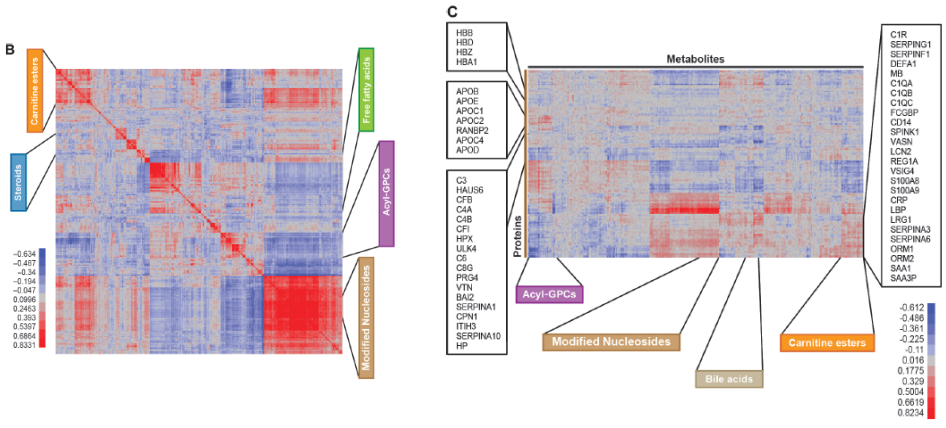




PATTERN DISCOVERY

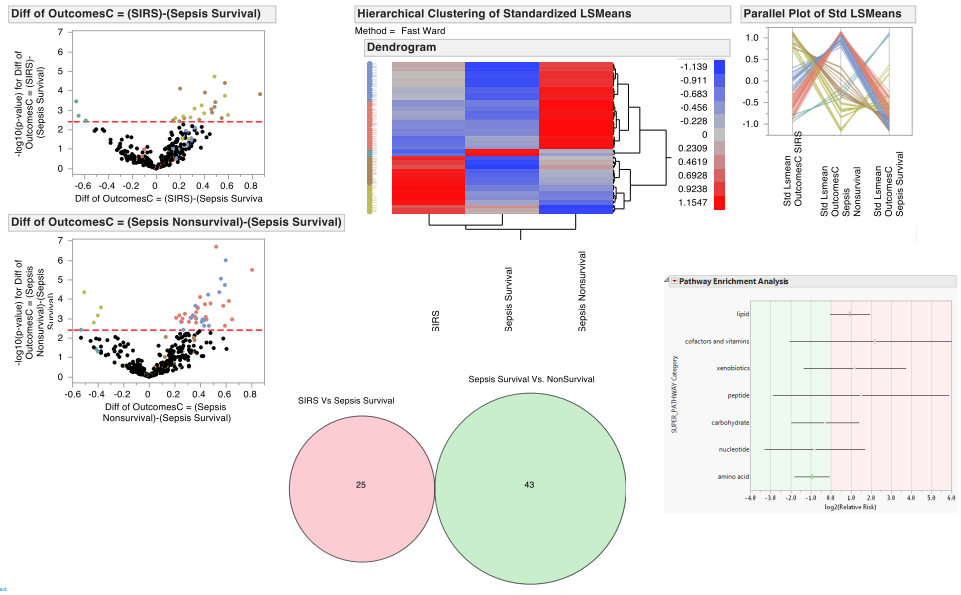
INTEGRATIVE EXPLORATION OF SEPSIS BIOMARKERS

- Cross-correlation analysis
  - Metabolites for sepsis survivors/nonsurvivors across time
  - Metabolites correlating with proteins
  - Transcriptome vs metabolome for “hypothetical association mapping” of genes to biochemical profiles



ANOVA MODELING

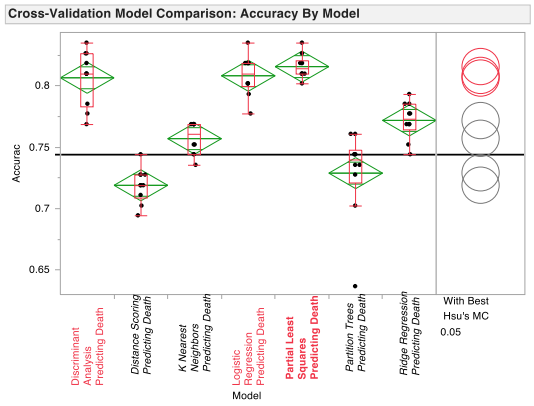
DIFFERENTIAL METABOLITE CONCENTRATIONS FOR SEPSIS SURVIVAL

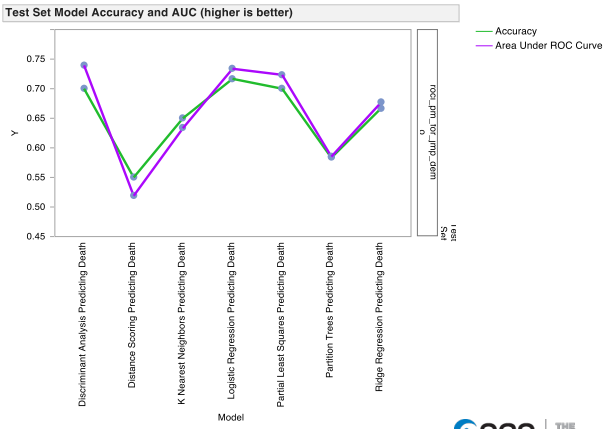


CLINICAL PREDICTION

DERIVATION AND TESTING PREDICTIVE SEPSIS BIOMARKER PANELS

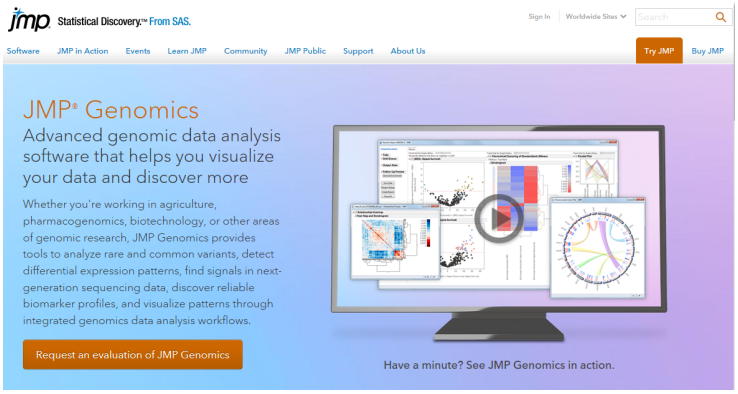
- Robust predictive modeling, advanced predictor filtering, cross-validation, model comparison, and test set evaluation
- Predictive utility for sepsis survival with clinical and biomarker signatures





JMP Genomics Online Resources

https://www.jmp.com/en_us/software/genomics-data-analysis-software.html



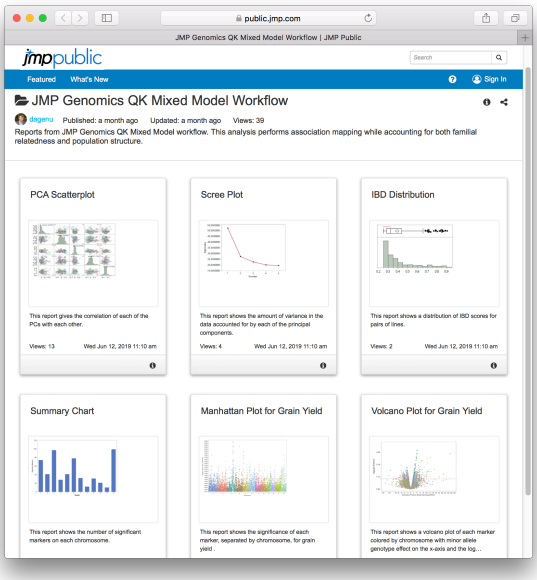
https://www.youtube.com/watch?v=DmaKz4NOURk

Other resources:

- www.jmp.com/jmpg
- Blog series ***Genetic Association with JMP Genomics*** (https://community.jmp.com/t5/JMPer-Cable/Genetic-Association-with-JMP-Genomics/ba-p/205372)
- Blog series ***Expression Analysis with JMP Genomics*** (https://community.jmp.com/t5/JMPer-Cable)

PUBLISH RESULTS AT PUBLIC.JMP.COM

Publish interactive results as web reports on JMP Public:
https://public.jmp.com/packages/JMP-Genomics-QK-Mixed-Model-Workflow-Rep/js-p/5cf6a6a92f411c0f2055177d



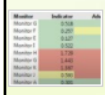
JMP CLINICAL

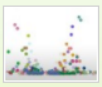
OVERVIEW

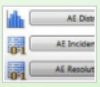
- Targeted Solution for safety and early efficacy in Clinical Trials
  - Data monitoring for operational site quality, medical safety monitoring and early efficacy, oncology
- Customized to automate report analyses using CDISC standard
  - (SDTM/ADaM/SEND) data structure
- Build role-based clinical trial analysis (shareable) reviews
- User Configurations to enable collaborative clinical trial analysis

Core Capabilities of JMP® Clinical

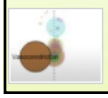
JMP Clinical gives you the tools to simplify the analysis and reporting of clinical trials data.


Risk-Based Monitoring


Data Integrity

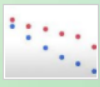

Data Visualization and Analysis


Data Monitoring


Biometrics and Biostatistics

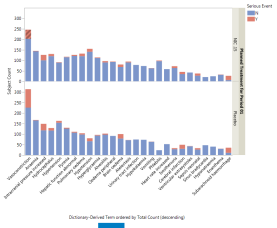

Pattern Discovery and Predicting Outcomes


Patient Profiles and Narratives

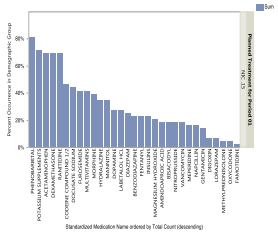

Interventions

CLINICAL DATA SCIENCE

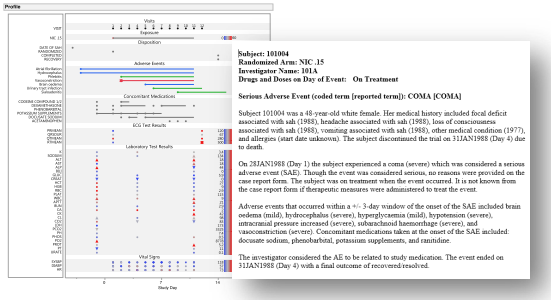
What count/percent of subjects on drug had a serious adverse event?



What medications were those subjects taking?



For selected subjects, what is the complete patient **profile** or **narrative**?



Subject: 101004
Randomized Arm: NIC_15
Investigator Name: 101A
Drugs and Doses on Day of Event: On Treatment

Serious Adverse Event (coded term [reported term]): COMA [COMA]

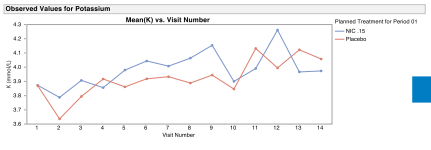
Subject 101004 was a 48-year-old white female. Her medical history included focal deficit associated with sah (1988), headache associated with sah (1988), loss of consciousness associated with sah (1988), vomiting associated with sah (1988), other medical condition (1977), and allergies (start date unknown). The subject discontinued the trial on 31JAN1988 (Day 4) due to death.

On 28JAN1988 (Day 1) the subject experienced a coma (severe) which was considered a serious adverse event (SAE). Though the event was considered serious, no reasons were provided on the case report form. The subject was on treatment when the event occurred. It is not known from the case report form if therapeutic measures were administered to treat the event.

Adverse events that occurred within a +/- 3-day window of the onset of the SAE included brain oedema (mild), hydrocephalus (severe), hypercrycaemia (mild), hypotension (severe), intracranial pressure increased (severe), subarachnoid haemorrhage (severe), and vasoconstriction (severe). Concomitant medications taken at the onset of the SAE included: docusate sodium, phenobarbital, potassium supplements, and ranitidine.

The investigator considered the AE to be related to study medication. The event ended on 31JAN1988 (Day 4) with a final outcome of recovered/resolved.

Did those subjects have abnormal lab results?



ONCOLOGY CLINICAL TRIALS

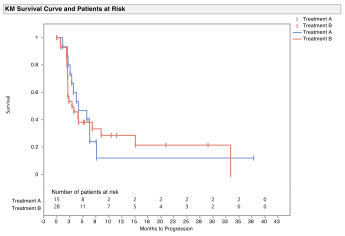
ANALYSIS CHALLENGES

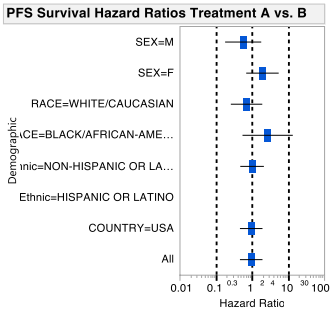
- Creating deterministic/consistent endpoints for tumor response
- Data capture and evaluation of solid tumor lesions
- **Appropriate Analysis and Visualization of early efficacy**
  - Complex trial designs and small sample sizes

EFFICACY SIGNALS

FDA INDUSTRY GUIDANCE FOR CLINICAL TRIAL ENDPOINTS

- Survival Analysis (OS)
  - Time to Death
- Progression Free Survival Curves (PFS)
  - Time to “disease progression” OR Death
- Objective Response Rate (ORR)
  - Trend and summaries in “Best” Response





Best Response Summary: Overall Response Test Results

	Description of Planned Arm					
	Treatment A (N = 17)		Treatment B (N = 33)		Total Subjects (N = 50)	
Objective Response Rate (ORR)	Count	%	Count	%	Total Count	Total %
CR + PR	4	23.5%	6	18.2%	10	20.0%
Best Response						
CR	.	.	3	9.1%	3	6.0%
PR	4	23.5%	3	9.1%	7	14.0%
SD	6	35.3%	8	24.2%	14	28.0%
PD	5	29.4%	14	42.4%	19	38.0%

DETECTING EARLY EFFICACY SIGNALS

Waterfall Plots

- Ordered Quantitative Best Response

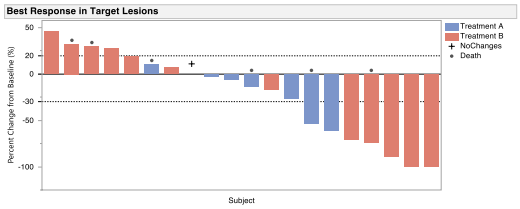
Time Trend Plots

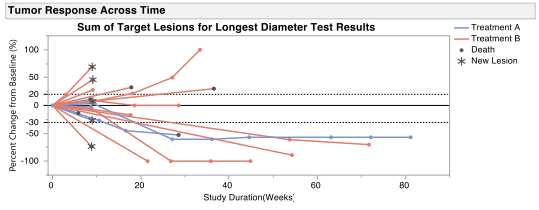
- Tumor Burden response across time
- Nicknames: Line, Spider, Spaghetti Plots

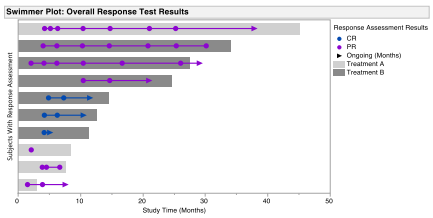
Swimmer Plots

- Qualitative response and duration

EFFECTIVE TUMOR RESPONSE VISUALIZATION





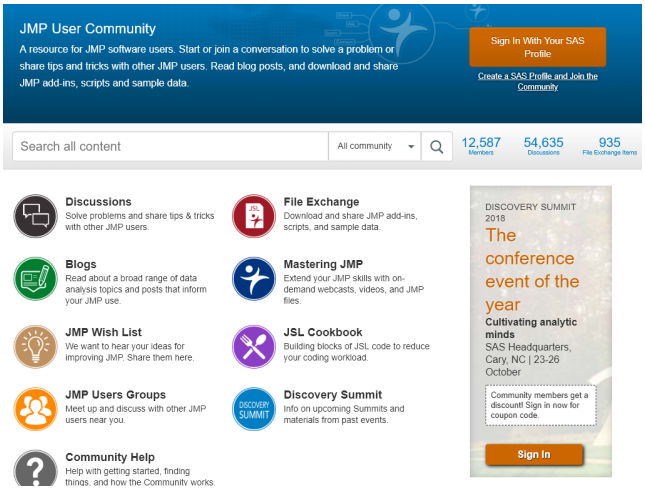


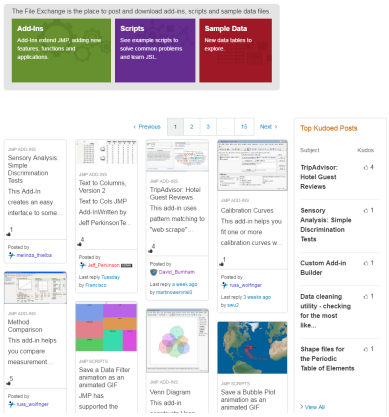
JMP INTEGRATION

ANALYTIC HUB

https://community.jmp.com/

- JMP integrates with SAS, R, Matlab, Python
- Load DLL functionality allows integration with other tools as well
- Add-in architecture (analogous to R packages) extends JMP functionality





JMP Life Sciences

Leading Professional Statistics Software for Data Sciences

- **Analytical**
  - Deep statistical and analytical capability
  - Statistical transformation and modeling through visualization
  - Dynamic model selection according to data
- **Graphical**
  - Drag and drop to create graphics
  - Interactive graphic for every statistical results
  - Statistical model application on the fly
- **Practical**
  - Communication hub
  - Easy to learn and use without coding
  - Seamless connection between graphic and data table
  - Beginning to End: design, prepare, analyze, mining and report
  - Instant discovery for meaningful conclusion
  - Statistical approach for every industry and every job function associated with data

Questions? Let us help!

support@jmp.com
ruth.hummel@jmp.com