

Responding to New Challenges: Statistics in Clinical and Translational Science



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The CTSA Consortium

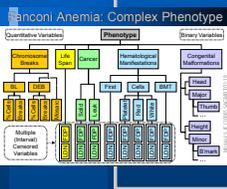


CTS: Statistical Challenges

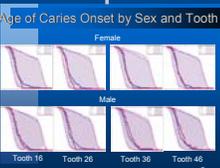
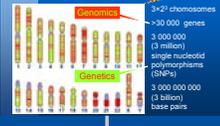
Non-linear Systems

Basic Science

The Human Genome



Different Scales
Complex Structures



Community Impact

U-Statistics for Translational Science

Advantage over methods based on linear models:

Do not assume that all differences of the same **magnitude** have the same **relevance**.

- **Insure** that statistical results are biologically meaningful
- Are **robust** to the effect of outliers
- Do **not require** data to be transformed prior to statistical analysis

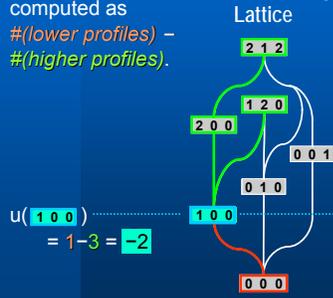
U-statistics lack of a unifying theory:

- Restricted to **uni/bi-variate data** and **simple designs**
- **Hodgepodge** of methods
- Risk of accidental **misspecification**

How to Score Multivariate Data

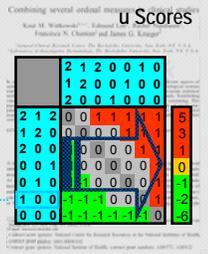
u scores are computed as
#(lower profiles) - #(higher profiles).

Partial Ordering Lattice



$$u(100) = 1 - 3 = -2$$

Pairwise Orderings

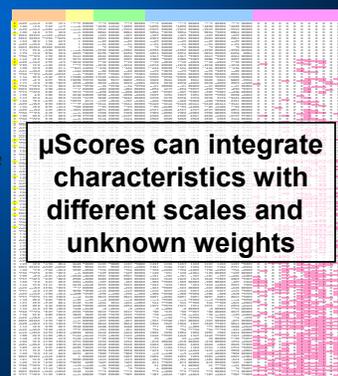


WITTKOWSKI KM (2004) *Stat Med* 23

μScores in Phenomics: FA

Fanconi Anemia Severity Indicators:

- DNA Damage
- Survival
- Cancer / Leukemia
- Bone Marrow Failure
- Birth Defects



μScores can integrate characteristics with different scales and unknown weights

Patients sorted by FA severity μScores

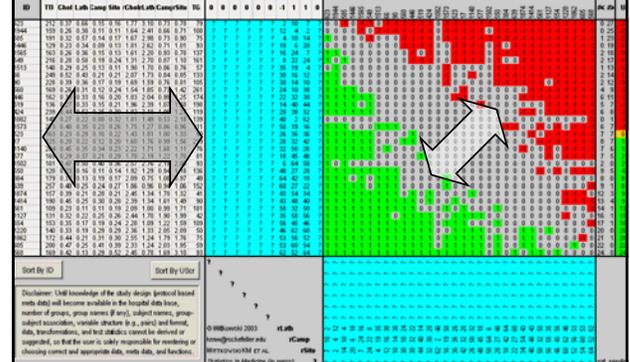
RUH.BERD Web Tools

1. Downloadable Statistical Tools

- A R/S-Plus script to implement a genetic test as described in [1]
- Statistically Valid Alternatives to the T-Test
- Spreadsheets for Multivariate U-Statistics

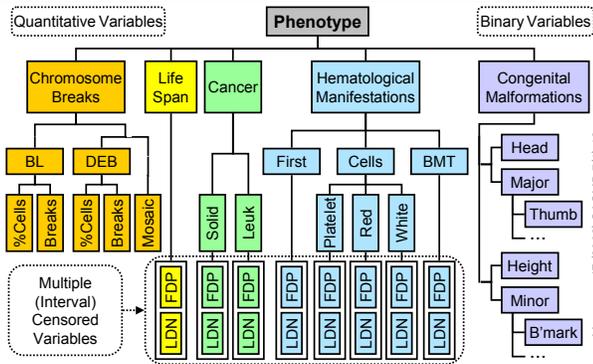
Transformation	one sample	two samples	k > 2 samples	Notes
none	U32x10N1	U32x10N2	U32x10Nk	Including the test by Wilcoxon/Mann-Whitney and Kruskal-Wallis
SVE (PH-NM)	U32x10S1			
Change (I-scale)	U32x10I1	U32x10I2	U32x10Ik	
Change (A-scale)	U32x10A1	U32x10A2	U32x10Ak	
Ranges (censored)	U32x10T1	U32x10T2	U32x10Tk	Including the tests by Gehan (1965) and Schemper
Haplotypes	U32x10H1	U32x10H2	U32x10Hk	

More Variables: Less Information Content



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Fanconi Anemia: Complex Phenotype



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AEs: Severity / Attribution

Patient No.	Severity										Attribution				
	Lightheadedness	Daytime sedation	Tinnitus	Dry skin/Puritus	Constipation	Lower extremity edema	Difficulty concentrating	Paresthesias	Visual accommodation problems	Hirsutism	Skin pigmentation changes	Changes in TFTs	Bradycardia	Palpitations	Other
17	1/3	1/3	1/4	1/4	1/3	1/4	1/4	1/3	1/3	1/3	1/3	3/3	renal failure*	3/3	
12	1/3	1/3	2/3	1/4	1/4	1/4	1/4	1/4	1/3	1/4	1/4				
14	1/2	1/3	2/3	1/3	1/4	1/4	1/4	1/3	1/3	1/3	1/3	1/3	1/2	2/3	dyspnea on exertion
13	1/2	1/3	2/3	1/3	1/3	1/3	1/3	1/3	1/3	1/3	1/3	1/3	1/2	2/3	dyspnea on exertion
18	1/3	1/3	2/3	1/3	1/3	1/3	1/3	1/3	1/3	1/3	1/3	1/3	1/2	2/3	dyspnea on exertion
19	1/3	1/3	2/3	1/3	1/3	1/3	1/3	1/3	1/3	1/3	1/3	1/3	1/2	2/3	dyspnea on exertion

*SAE

Tests Based on μ -Scores

The new function 'prentice.test' integrates / extends (at twice the speed) several well-known tests:

	Conditions	Granularity	Replications	Blocks
mcnemar.test	2	2	≥ 2	1
SMN.pvalue	2	2	≥ 2	3
wilcox.test	2	≥ 2	≥ 2	1
kruskal.test	≥ 2	≥ 2	≥ 2	1
friedman.test	≥ 2	≥ 2	1	≥ 2
prentice.test	≥ 2	≥ 2	≥ 0	≥ 2



CRAN
http://cran.r-project.org/index.html

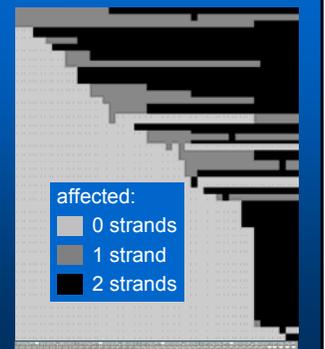


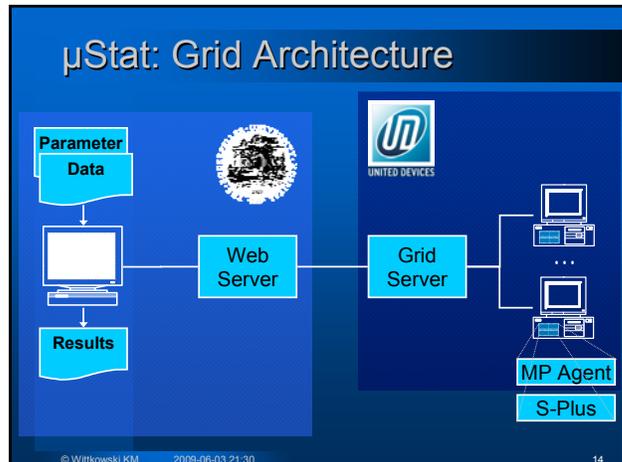
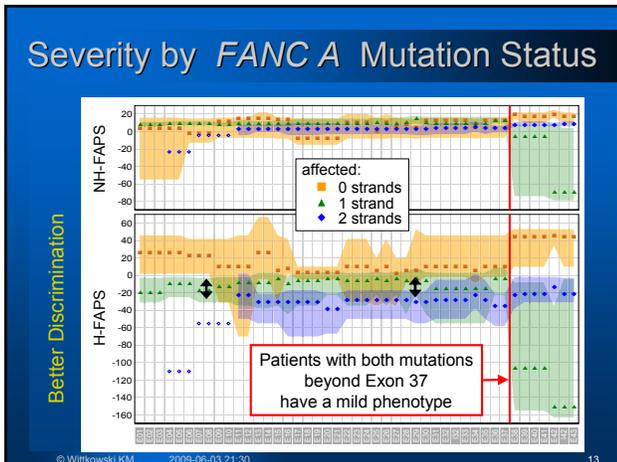
CSAN
http://csan.insightful.com/Default.aspx

Subjects by Mutation Status

For a subject to develop FA, both strands of the same gene need to be affected.

Fig.: Mutation map for 100 FANCA subjects (rows) by exons or introns with variations. The effect of frame-shift, splicing, indels, and stop codon mutations are assumed to affect the protein encoded in all downstream gene regions.





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muStat available on CTSPedia

CTSPedia: A Knowledge Base for Clinical & Translational Sciences

You are here: TWiki > CTSPedia Web > StatisticalTools > RScripts

Tags: create new tag

R/S-PLUS Packages/Scripts/Functions & Tools

- muStat package for multivariate ordinal data** (download from CRAN) [CSAN] [discuss]
 Kouf M. Wittkowski, The Rockefeller University muStat@rockefeller.edu
 maintained by Tingting Song tsong@rockefeller.edu
 - `muStat.score`: a generalization of `ELUSCO`, `net` and `ocaml.cox`
 - `muStat.pvalue`: a replacement of the `ttpt` for family-based association studies
 - `muStat.score`: a function to score multivariate, censored, and structured ordinal data
- muStat Web server for analyzing multivariate ordinal data** (grid powered) [multivariate RSS feed] [discuss]
 Kouf M. Wittkowski, The Rockefeller University muStat@rockefeller.edu
 maintained by Tingting Song tsong@rockefeller.edu
 - screening microarrays for gene expression profiles (sets of collaborating genes)
 - screening whole genome scans for epistasis between multipoint ranges (diplotypes)

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muStat Discussion Forums

CTSPedia: A Knowledge Base for Clinical & Translational Sciences

You are here: TWiki > Forum Web > StatToolsForum > muStatPackage

Tags: Censored Data | Doubly Interval Censored Data | Interval Censored Data | Multivariate | Nonparametric Statistics | Ordinal Data | Software Development | create new tag

Discussion Forum > R Discussion Forum > muStat package

Welcome to the muStat Package discussion forum. Please check the [multivariate RSS feed](#) before posting.

Add comment

DiscussionTopicForm

Title: muStat package
 Forum: RDiscussionForum

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μStat Discussion Forums

CTSPedia: A Knowledge Base for Clinical & Translational Sciences

You are here: TWiki > Forum Web > StatToolsForum > muStatServer

Tags: Censored Data | Doubly Interval Censored Data | Interval Censored Data | Multivariate | Nonparametric Statistics | Ordinal Data | create new tag

Discussion Forum > General Statistical Tools Q&A > μStat Server

Welcome to the muStat Server discussion forum. Please check the [multivariate RSS feed](#) before posting.

Add comment

DiscussionTopicForm

Title: μStat Server
 Forum: StatToolsForum

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μStat Usage Metrics

Period	RU users	RU jobs	.edu users	.edu jobs	Other users	Other jobs	Dev users	Dev jobs	USCr
Prft1	1	1	2	2	3	3			
Prft2	1	2	3	4	5	6			
Pol	1	1	1	1	1	1			
<hr/>									
Dat	June	2	5	0	0	1	57	1	11
Dat	July	2	20	0	0	1	9	2	2
Dat	August	2	7	0	0	4	30	1	1
Dat	September	2	25	0	0	12	82	1	6
Dat	October	2	11	1	3	1	11	1	6
Dat	November	2	12	0	0	3	50	1	7
Dat	December	1	4	0	0	0	0	1	53
Dat	January	1	21	0	0	2	51	1	4
Dat	February	2	5	1	1	2	13	1	11
Dat	March	1	2	0	0	2	24	1	5
Dat	April	1	12	0	0	2	32	1	10
Dat	May	1	18	1	1	2	35	2	2
	Total	2	140	3	5	13	381	2	119

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How to Specify Complex Phenotypes?

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WISDOM for Research Support

Goal:
to make knowledge about the design of the study available to the software an investigator uses for

- Protocol Writing
- Study Management
- Data Management
- Statistical Analysis
- Data Sharing

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WISDOM as a Knowledge Broker

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Layers of Meta-Data

WITTKOWSKI KM (1988) KB support for statistical databases LN Comp Sci 339:62
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WISDOM Knowledge Acquisition

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WISDOM: Data Base Creation

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RU CCTS – VICTR / YCCI

WISDOM for REDCap

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WISDOM as a μ Stat User Interface

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NIH Data Sharing Policy

“To ensure that others can use” data, meta-data is needed that documents

- “definitions of variables, details about codes
- the methodology and procedures used to collect the data,
- variable field locations, [...].

The precise content of *only the DOMAIN* documentation will vary by the

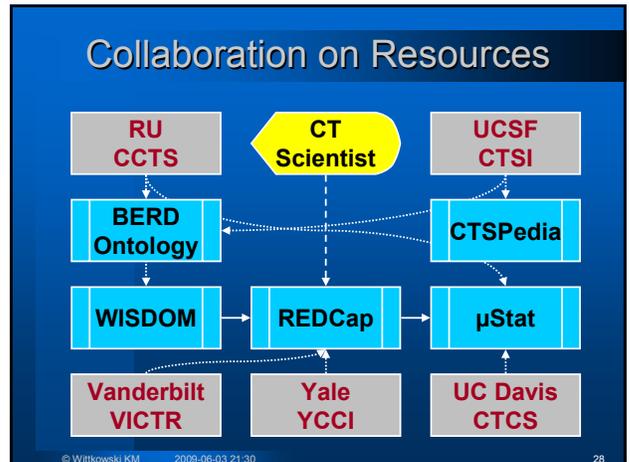
- scientific area,
- type of data collected,
- study design, and
- characteristics of the dataset.”

MODEL
DESIGN
DATA

DOMAIN
MODEL
DESIGN
DATA

http://grants.nih.gov/grants/policy/data_sharing/data_sharing_guidance.htm

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Plans to Meet Challenges

Develop

- Best Practices and Resources

to assist clinical and translational scientists with

- Experimental Design
- Protocol Writing
- Data Management (Oracle)
- Data Acquisition (REDCap)
- Safety Monitoring
- Statistical Analyses (μ Stat)
- Data Sharing

Using the CTSA environment to

- Develop an *ontology* and
- Build and share *tools* (*muStat*, *WISDOM*)

Based on novel non-parametric approaches (u-statistics) and on biostatistical knowledge at the layers

MODEL
DESIGN
DATA

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