Statistics (part 2)

Ting Xu

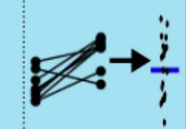
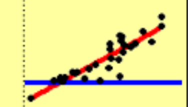
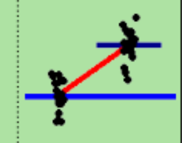
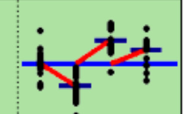
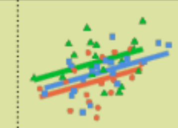
Regression

$$Y_i = \beta_0 + \beta_1 X_1 + \beta_2 X_2 + \epsilon$$

Common statistical tests are linear models

Last updated: 02 April, 2019

See worked examples and more details at the accompanying notebook: https://lindeloev.github.io/tests-as-linear

	Common name	Built-in function in R	Equivalent linear model in R	Exact?	The linear model in words	Icon
Simple regression: lm(y ~ 1 + x)	**y is independent of x** P: One-sample t-test N: Wilcoxon signed-rank	t.test(y) wilcox.test(y)	lm(y ~ 1) lm(signed_rank(y) ~ 1)	✓ for N >14	One number (intercept, i.e., the mean) predicts **y**. - (Same, but it predicts the *signed rank* of **y**.)	
	P: Paired-sample t-test N: Wilcoxon matched pairs	t.test(y_1, y_2, paired=TRUE) wilcox.test(y_1, y_2, paired=TRUE)	lm(y_2 - y_1 ~ 1) lm(signed_rank(y_2 - y_1) ~ 1)	✓ for N >14	One intercept predicts the pairwise **y_2-y_1** differences. - (Same, but it predicts the *signed rank* of **y_2-y_1**.)	
	y ~ continuous x P: Pearson correlation N: Spearman correlation	cor.test(x, y, method='Pearson') cor.test(x, y, method='Spearman')	lm(y ~ 1 + x) lm(rank(y) ~ 1 + rank(x))	✓ for N >10	One intercept plus **x** multiplied by a number (slope) predicts **y**. - (Same, but with *ranked* **x** and **y**)	
	y ~ discrete x P: Two-sample t-test P: Welch's t-test N: Mann-Whitney U	t.test(y_1, y_2, var.equal=TRUE) t.test(y_1, y_2, var.equal=FALSE) wilcox.test(y_1, y_2)	lm(y ~ 1 + G_2)[A] gls(y ~ 1 + G_2, weights=…[B])[A] lm(signed_rank(y) ~ 1 + G_2)[A]	✓ ✓ for N >11	An intercept for **group 1** (plus a difference if **group 2**) predicts **y**. - (Same, but with one variance *per group* instead of one common.) - (Same, but it predicts the *signed rank* of **y**.)	
Multiple regression: lm(y ~ 1 + x_1 + x_2 +...)	P: One-way ANOVA N: Kruskal-Wallis	aov(y ~ group) kruskal.test(y ~ group)	lm(y ~ 1 + G_2 + G_3 +...+ G_N)[A] lm(rank(y) ~ 1 + G_2 + G_3 +...+ G_N)[A]	✓ for N >11	An intercept for **group 1** (plus a difference if group ≠ 1) predicts **y**. - (Same, but it predicts the *rank* of **y**.)	
	P: One-way ANCOVA	aov(y ~ group + x)	lm(y ~ 1 + G_2 + G_3 +...+ G_N + x)[A]	✓	- (Same, but plus a slope on **x**.) *Note: this is discrete AND continuous. ANCOVAs are ANOVAs with a continuous x.*	
	P: Two-way ANOVA	aov(y ~ group * sex)	lm(y ~ 1 + G_2 + G_3 + ... + G_N + S_2 + S_3+ ... + S_K + G_2*S_2+G_3*S_3+...+G_N*S_K)	✓	Interaction term: changing **sex** changes the **y ~ group** parameters. *Note: **$G_{2 \text{ to } N}$** is an indicator (0 or 1) for each non-intercept levels of the **group** variable. Similarly for **$S_{2 \text{ to } K}$** for sex. The first line (with G_i) is main effect of group, the second (with S_i) for sex and the third is the **group × sex** interaction. For two levels (e.g. male/female), line 2 would just be "S_2" and line 3 would be S_2 multiplied with each G_i.*	*[Coming]*
	Counts ~ discrete x N: Chi-square test	chisq.test(groupXsex_table)	**Equivalent log-linear model** glm(y ~ 1 + G_2 + G_3 + ... + G_N + S_2 + S_3+ ... + S_K + G_2*S_2+G_3*S_3+...+G_N*S_K, family=...)[A]	✓	Interaction term: (Same as Two-way ANOVA.) *Note: Run glm using the following arguments: `glm(model, family=poisson())` As linear-model, the Chi-square test is $\log(y_i) = \log(N) + \log(\alpha_i) + \log(\beta_j) + \log(\alpha_i\beta_j)$ where α_i and β_j are proportions. See more info in the accompanying notebook.*	*Same as Two-way ANOVA*
	N: Goodness of fit	chisq.test(y)	glm(y ~ 1 + G_2 + G_3 +...+ G_N, family=...)[A]	✓	(Same as One-way ANOVA and see Chi-Square note.)	*1W-ANOVA*

List of common parametric (P) non-parametric (N) tests and equivalent linear models. The notation y ~ 1 + x is R shorthand for y = 1·b + a·x which most of us learned in school. Models in similar colors are highly similar, but really, notice how similar they *all* are across colors! For non-parametric models, the linear models are reasonable approximations for non-small sample sizes (see "Exact" column and click links to see simulations). Other less accurate approximations exist, e.g., Wilcoxon for the sign test and Goodness-of-fit for the binomial test. The signed rank function is `signed_rank = function(x) sign(x) * rank(abs(x))`. The variables G_i and S_i are "dummy coded" indicator variables (either 0 or 1) exploiting the fact that when Δx = 1 between categories the difference equals the slope. Subscripts (e.g., G_2 or y_1) indicate different columns in data. lm requires long-format data for all non-continuous models. All of this is exposed in greater detail and worked examples at https://lindeloev.github.io/tests-as-linear.

[A] See the note to the two-way ANOVA for explanation of the notation.
[B] Same model, but with one variance per group: `gls(value ~ 1 + G₂, weights = varIdent(form = ~1|group), method="ML")`.

Jonas Kristoffer Lindeløv
https://lindeloev.net

Regression

$$Y_i = \beta_0 + \beta_1 X_1 + \beta_2 X_2 + \epsilon$$

Conventional linear regression (LM)

$$Y = \beta X + \epsilon$$

General Linear Model (GLM)

$$g(E[Y]) = \beta X + \epsilon$$

Linear Mixed Model

$$Y = \beta X + Zb + \epsilon$$

Example: Intraclass correlation in LMM (link)

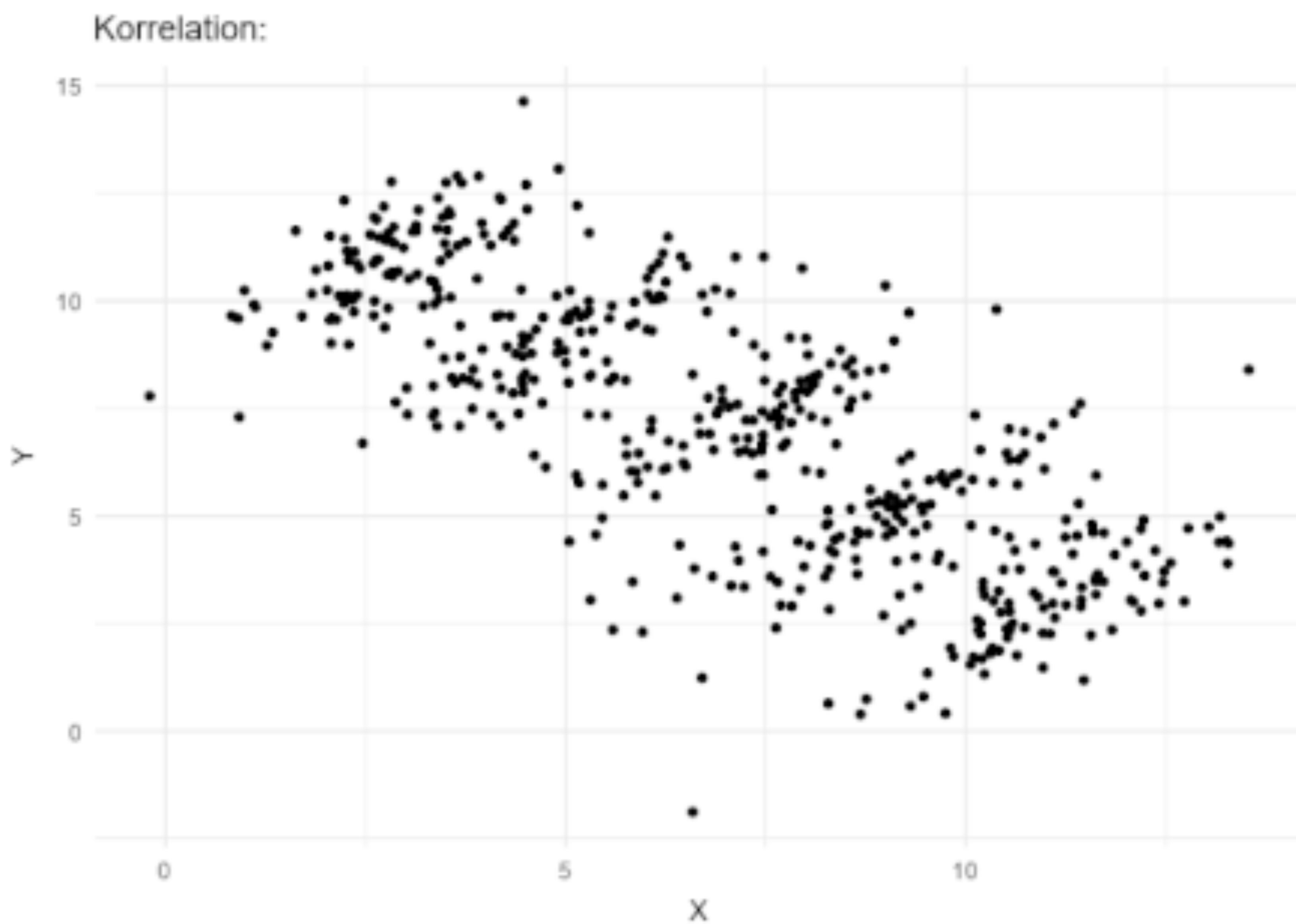
Generalized Additive Model (GAM)

$$g(E[Y]) = \beta_0 + f_1(X_1) + f_2(X_2) + \ldots + f_m(X_m)$$

Generalized Additive Model for Location, Scale and Shape (GAMLSS)

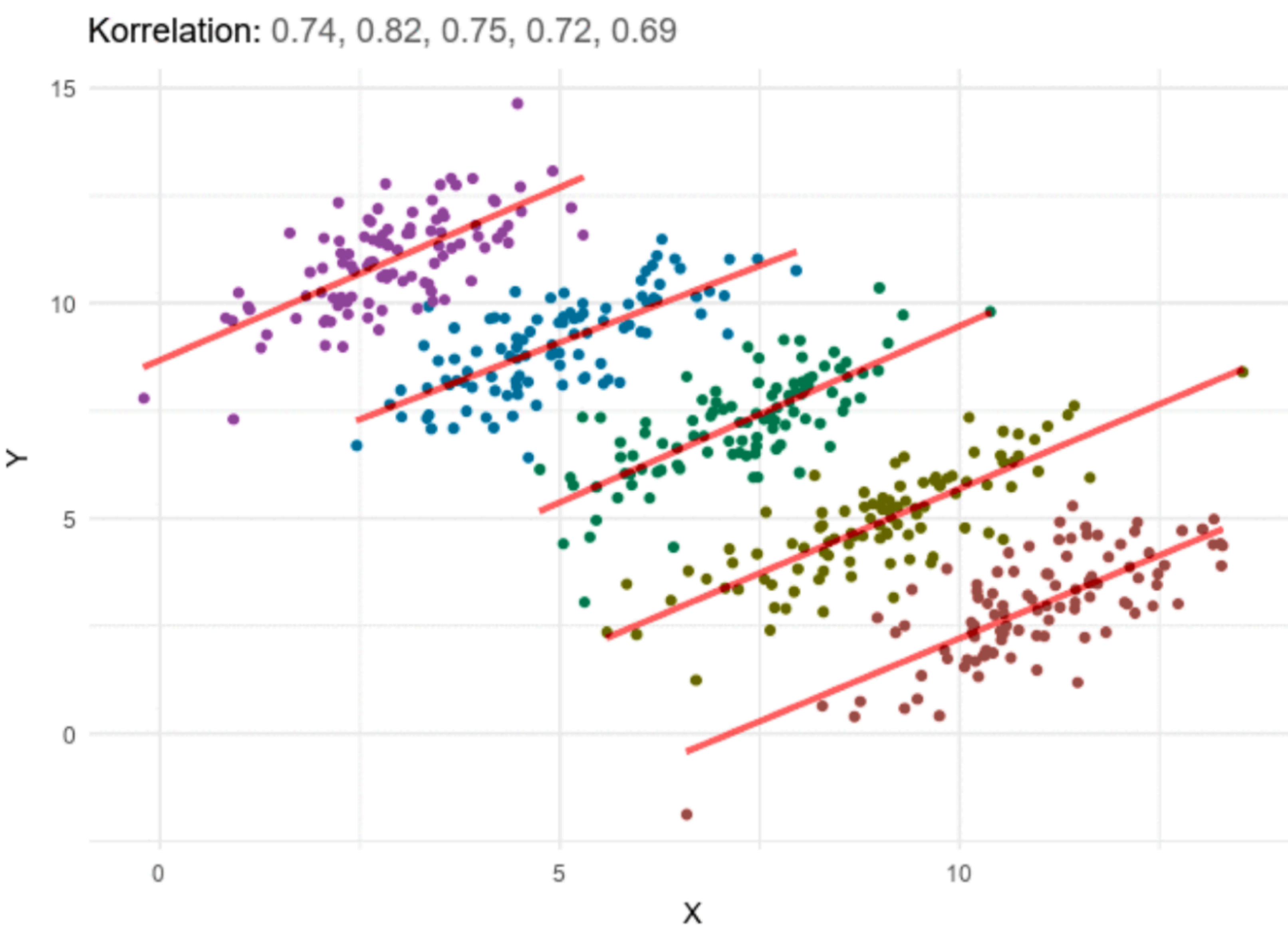
$$f(y_i|\mu_i, \sigma_i, \nu_i, \tau_i)$$

Linear Mixed Model (Random Intercept)

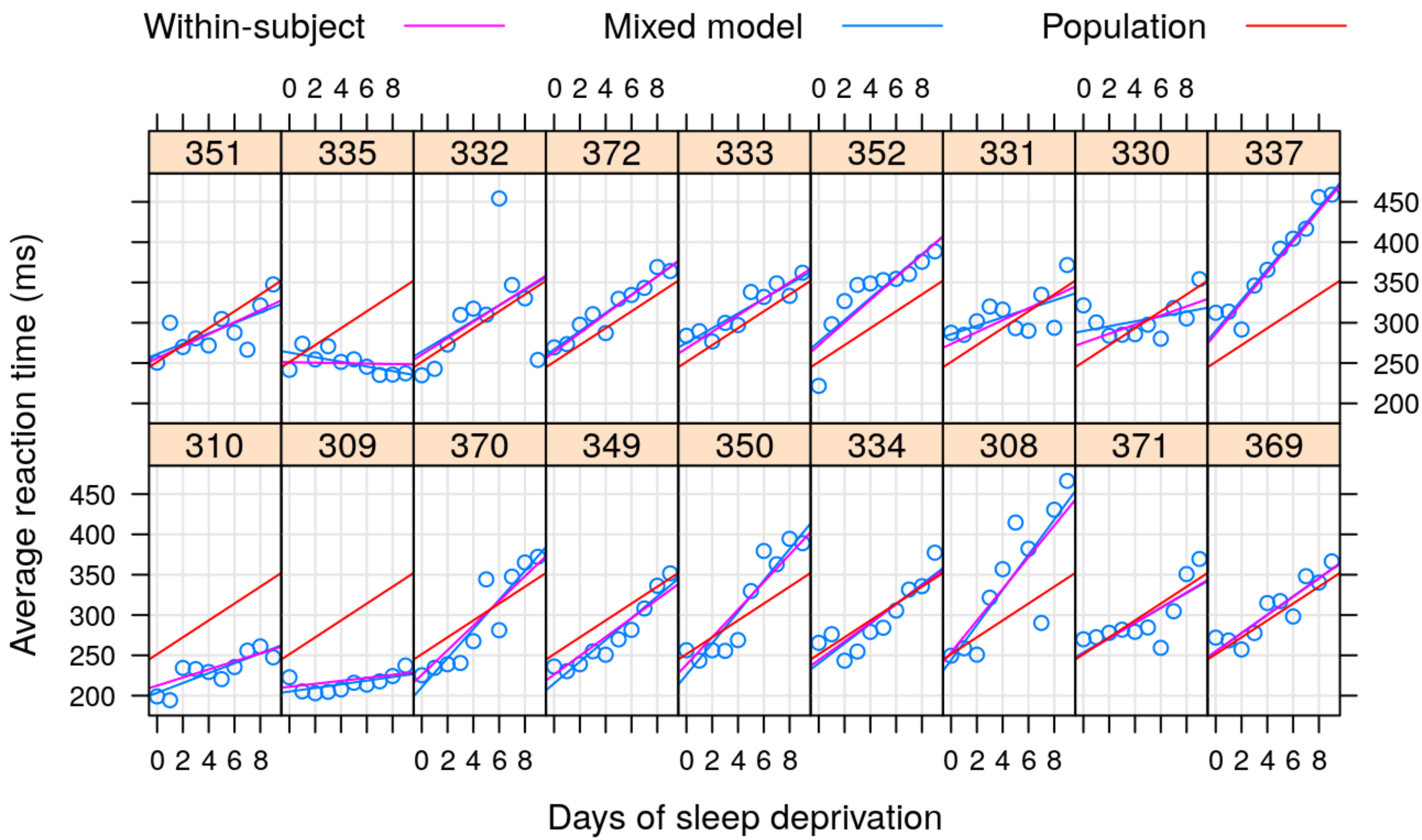


Wikipedia Simpson's Paradox

Linear Mixed Model (Random Intercept)



Linear Mixed Model (Random Slope)



http://www.john-ros.com/Rcourse/lme.html

GAMM

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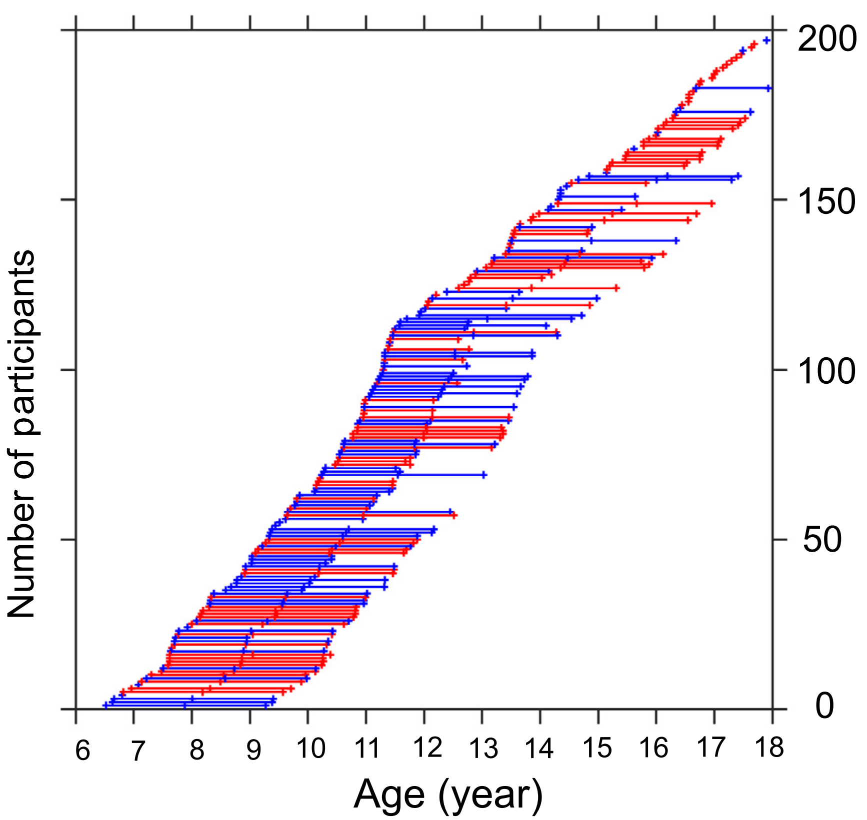
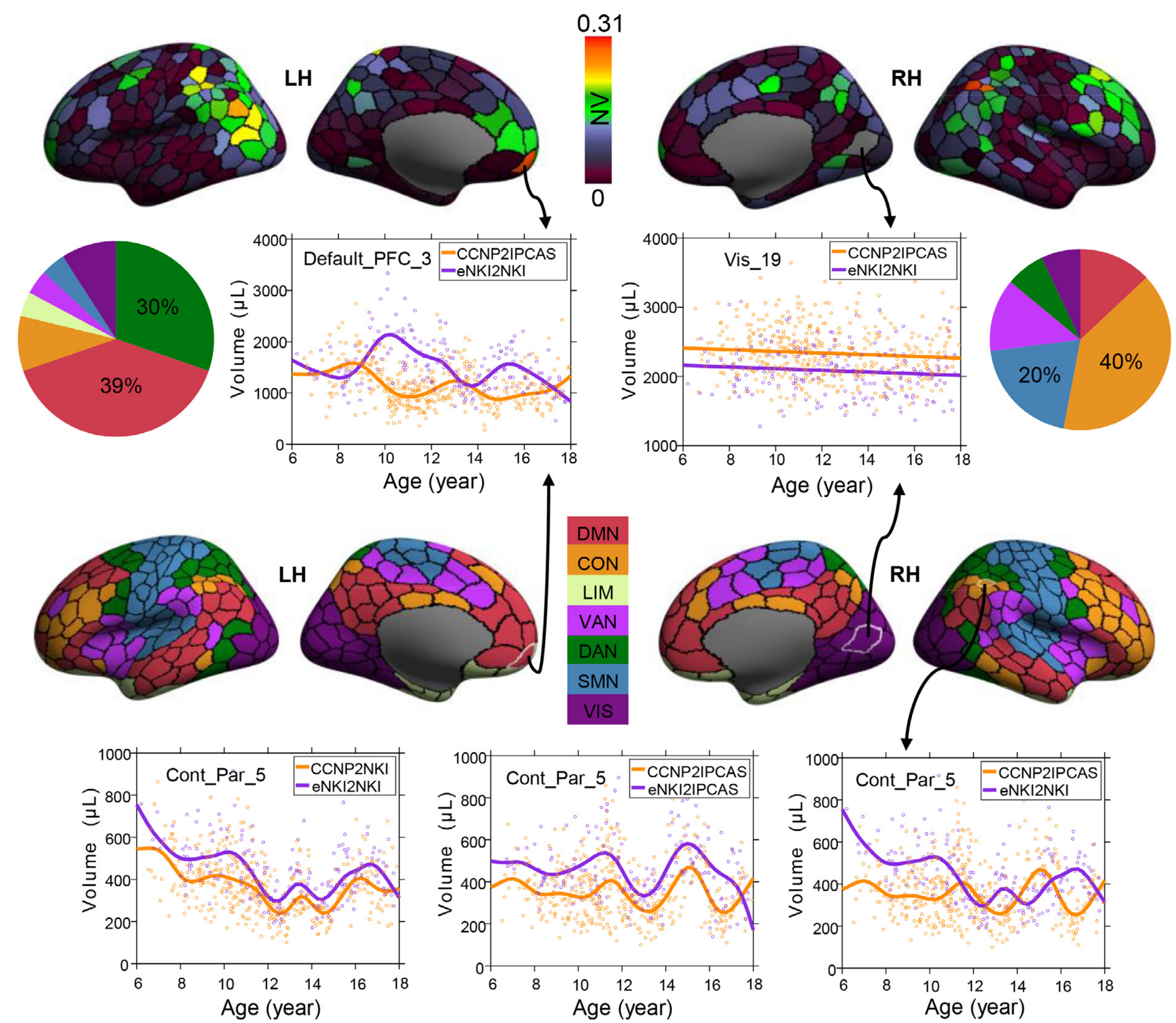
Article

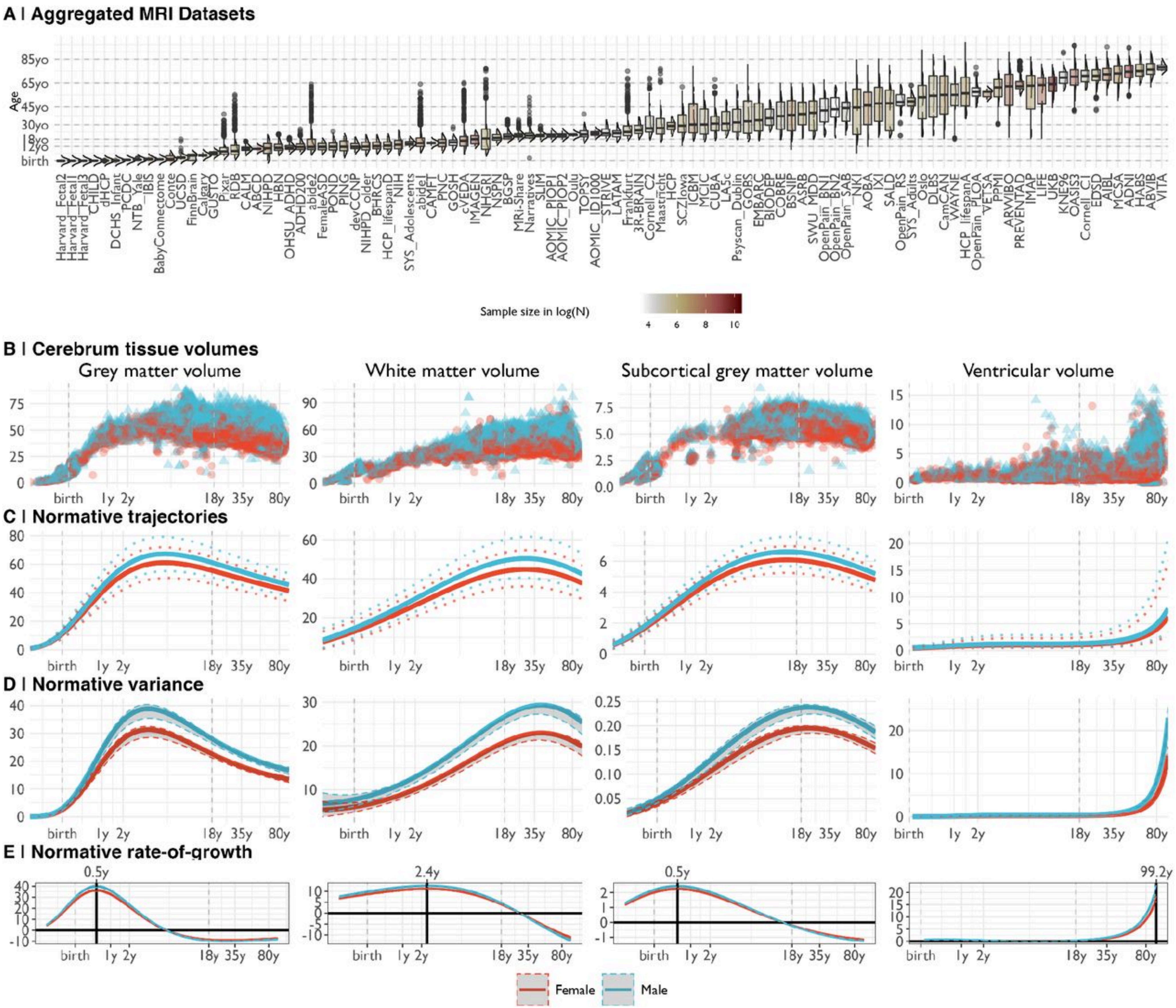
Charting brain growth in tandem with brain templates at school age

Hao-Ming Dong[a,b], F. Xavier Castellanos[c,d], Ning Yang[a,b], Zhe Zhang[a], Quan Zhou[e], Ye He[f], Lei Zhang[a], Ting Xu[g], Avram J. Holmes[h], B.T. Thomas Yeo[i], Feiyan Chen[j], Bin Wang[k], Christian Beckmann[l], Tonya White[m,n], Olaf Sporns[f], Jiang Qiu[o], Tingyong Feng[o], Antao Chen[o], Xun Liu[a], Xu Chen[o], Xuchu Weng[a,p], Michael P. Milham[d,g], Xi-Nian Zuo[b,e,p,q,r,s,t,*]



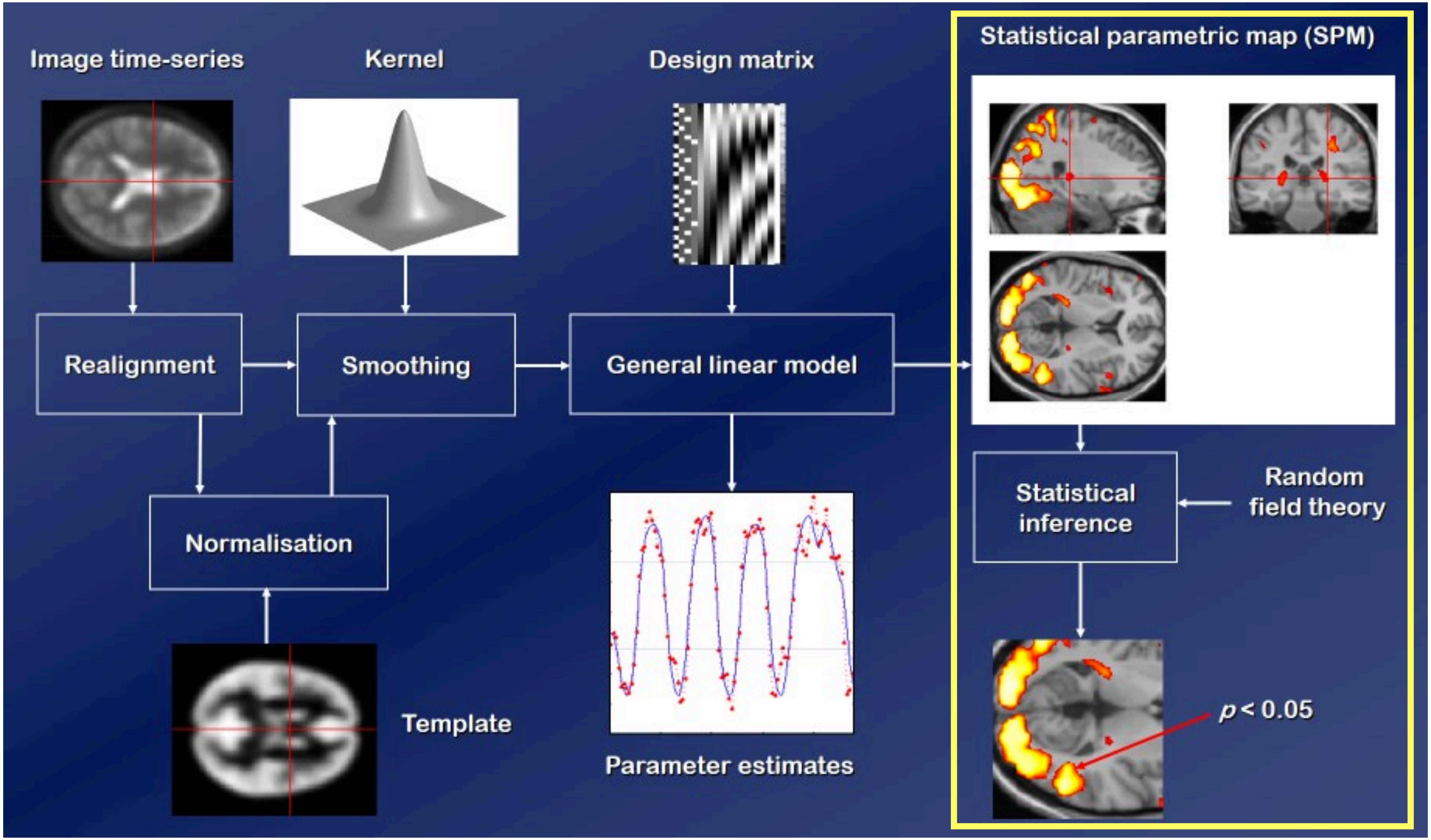


GAMLSS



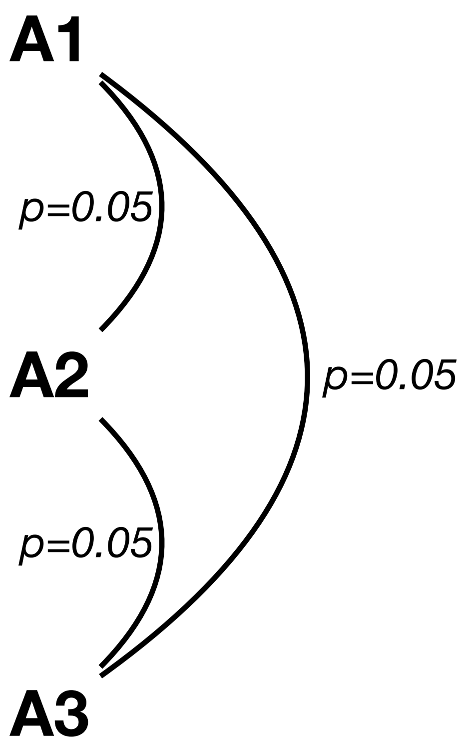
Brain charts for the human lifespan. Bethlehem & Seidlitz et al., biorxiv

Statistics in Neuroimaging



https://www.fil.ion.ucl.ac.uk/spm/

Multiple Comparison Correction



Any significant difference(s)?

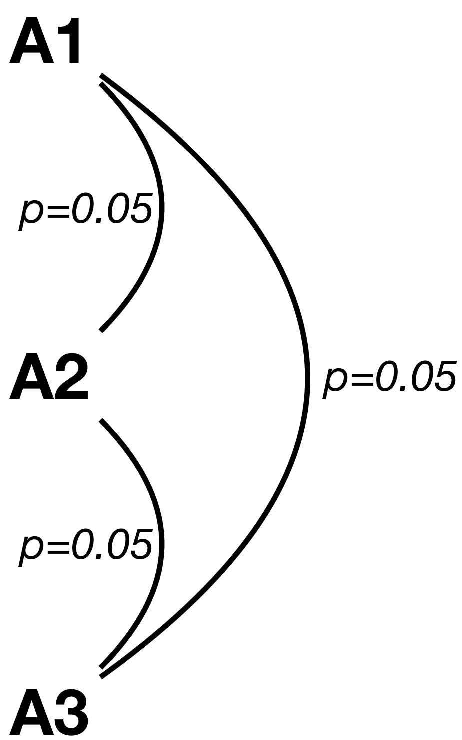
P(at least one significant result between any two levels)
= 1 - P(no significant result between any two levels)
= 1 - (1-0.05)^3
= 0.1426

Family-wise error rate (FWER): the probability of making one or more false discoveries (type I errors) when performing multiple hypotheses tests

Multiple Comparison Correction

Bonferroni correction
alpha=0.05/n

0.05/3=0.0166667

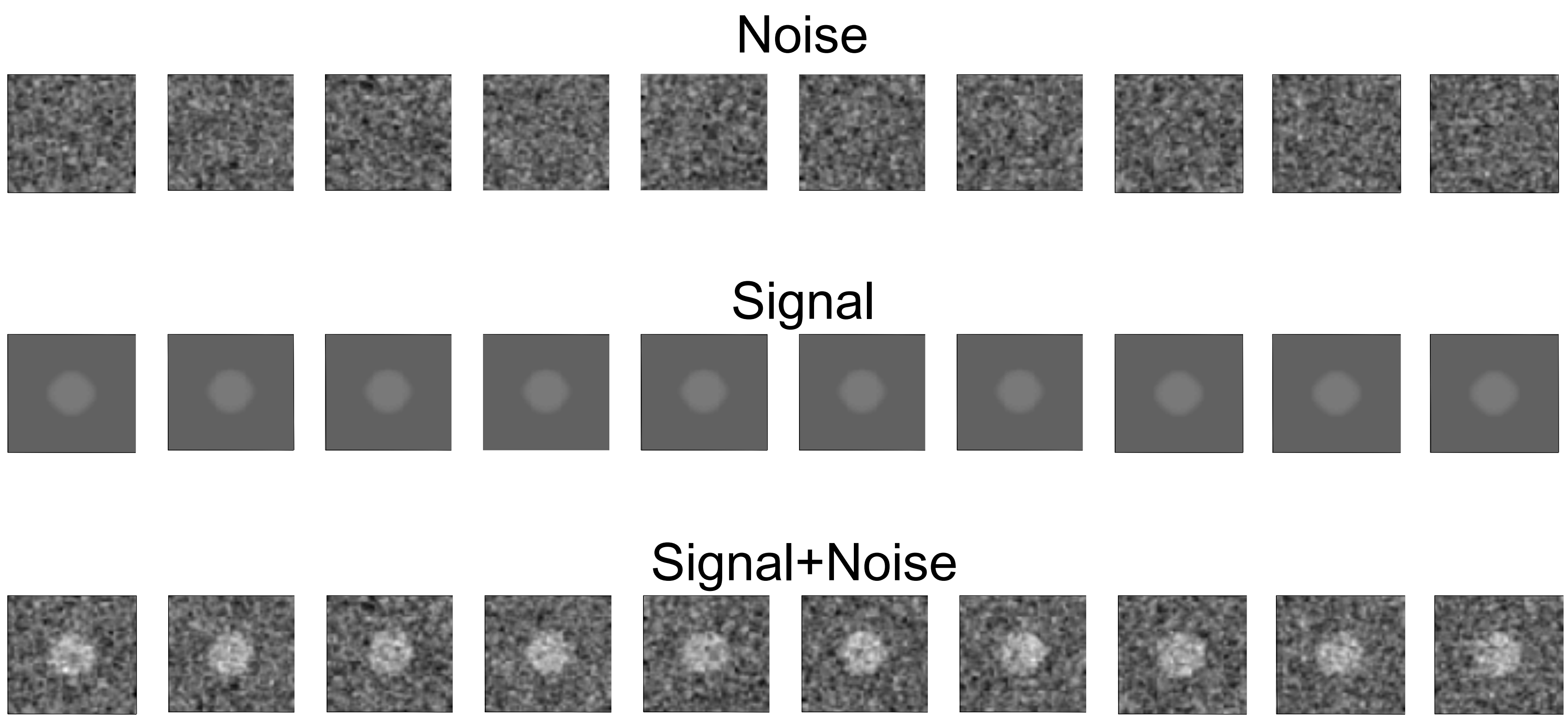


Any significant difference(s)?

P(at least one significant result between any two levels)
= 1 - P(no significant result between any two levels)
= 1 - (1-0.0166667)^3
= 0.04917

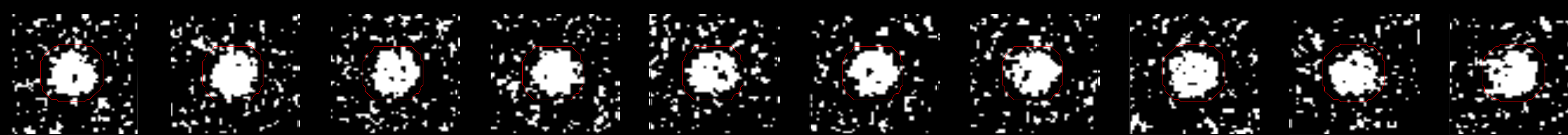
Statistics in Neuroimaging

Inference on images



Slide: Thomas Nichols. Introduction to Functional Neuroimaging

Use of ‘uncorrected’ p-value, α=0.1



Percentage of Null Pixels that are False Positives

Using an ‘uncorrected’ p-value of 0.1 will lead us to conclude on average that 10% of voxels are active when they are not.

This is clearly undesirable. To correct for this we can define a null hypothesis for images of statistics.

Multiple Comparison Correction

Bonferroni correction

Family-wise Error Rate (FWER)
- Random Field Methods

False Discovery Rate (FDR): With a false discovery rate of $q < 0.05$ one would accept that 5% of the discovered (supra-threshold) voxels would be false positives.

Cluster Corrections

Cluster failure: Why fMRI inferences for spatial extent have inflated false-positive rates

Anders Eklund[a,b,c,1], Thomas E. Nichols[d,e], and Hans Knutsson[a,c]

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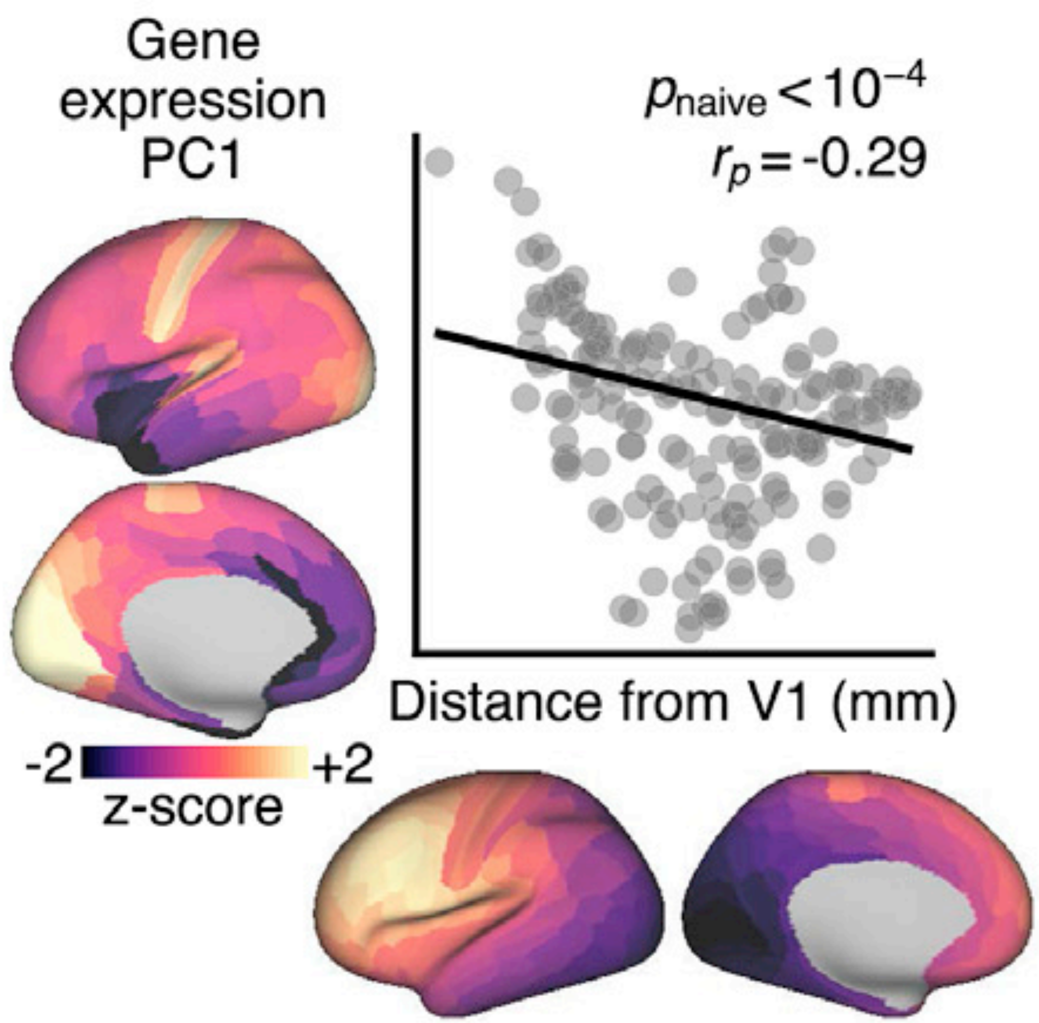
Edited by Emery N. Brown, Massachusetts General Hospital, Boston, MA, and approved May 17, 2016 (received for review February 12, 2016)

Correction for spatial autocorrelation



Correction for spatial autocorrelation

Spin Permutations

Here, we use the spin permutations approach previously proposed in (Alexander-Bloch et al., 2018), which preserves the auto-correlation of the permuted feature(s) by rotating the feature data on the spherical domain. We will start by loading the conte69 surfaces for left and right hemispheres, their corresponding spheres, midline mask, and t1w/t2w intensity as well as cortical thickness data, and a template functional gradient.

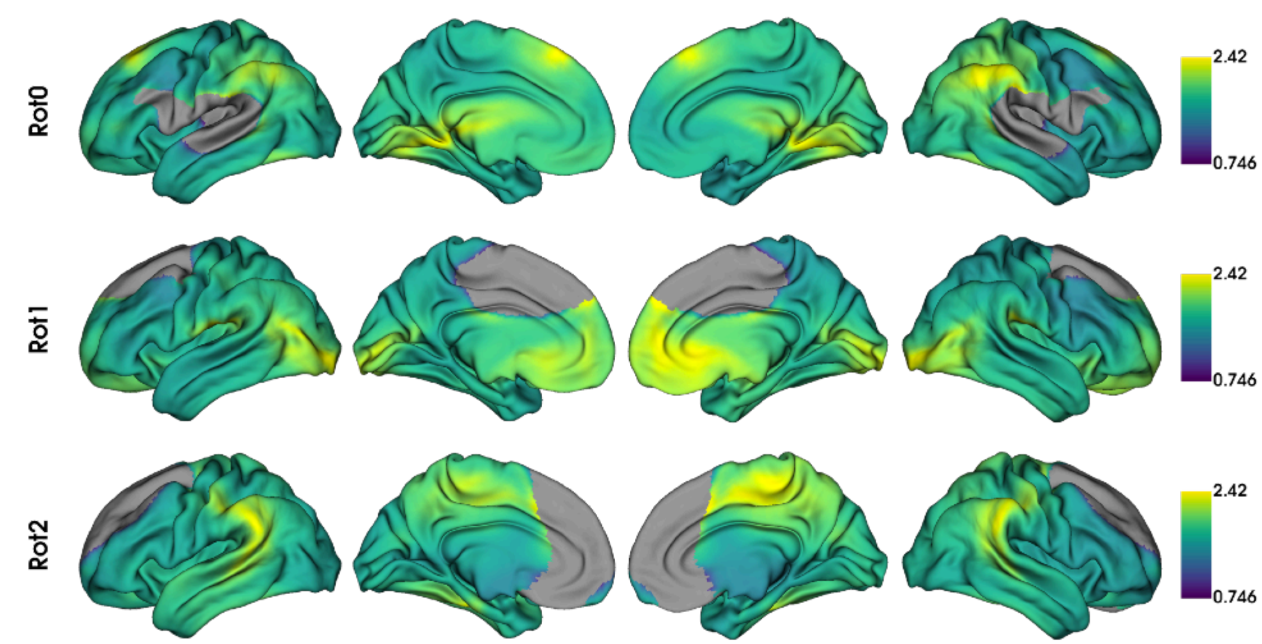
Cerebral Cortex January 2016;26:288–303
doi:10.1093/cercor/bhu239
Advance Access publication October 14, 2014

Generation and Evaluation of a Cortical Area Parcellation from Resting-State Correlations

Evan M. Gordon[1], Timothy O. Laumann[1], Babatunde Adeyemo[1], Jeremy F. Huckins[5], William M. Kelley[5] and Steven E. Petersen[1,2,3,4]

[1]Department of Neurology, [2]Department of Psychology, [3]Department of Radiology, [4]Department of Anatomy and Neurobiology, Washington University School of Medicine, St. Louis, MO, USA and [5]Department of Psychological and Brain Sciences, Dartmouth College, Hanover, NH, USA

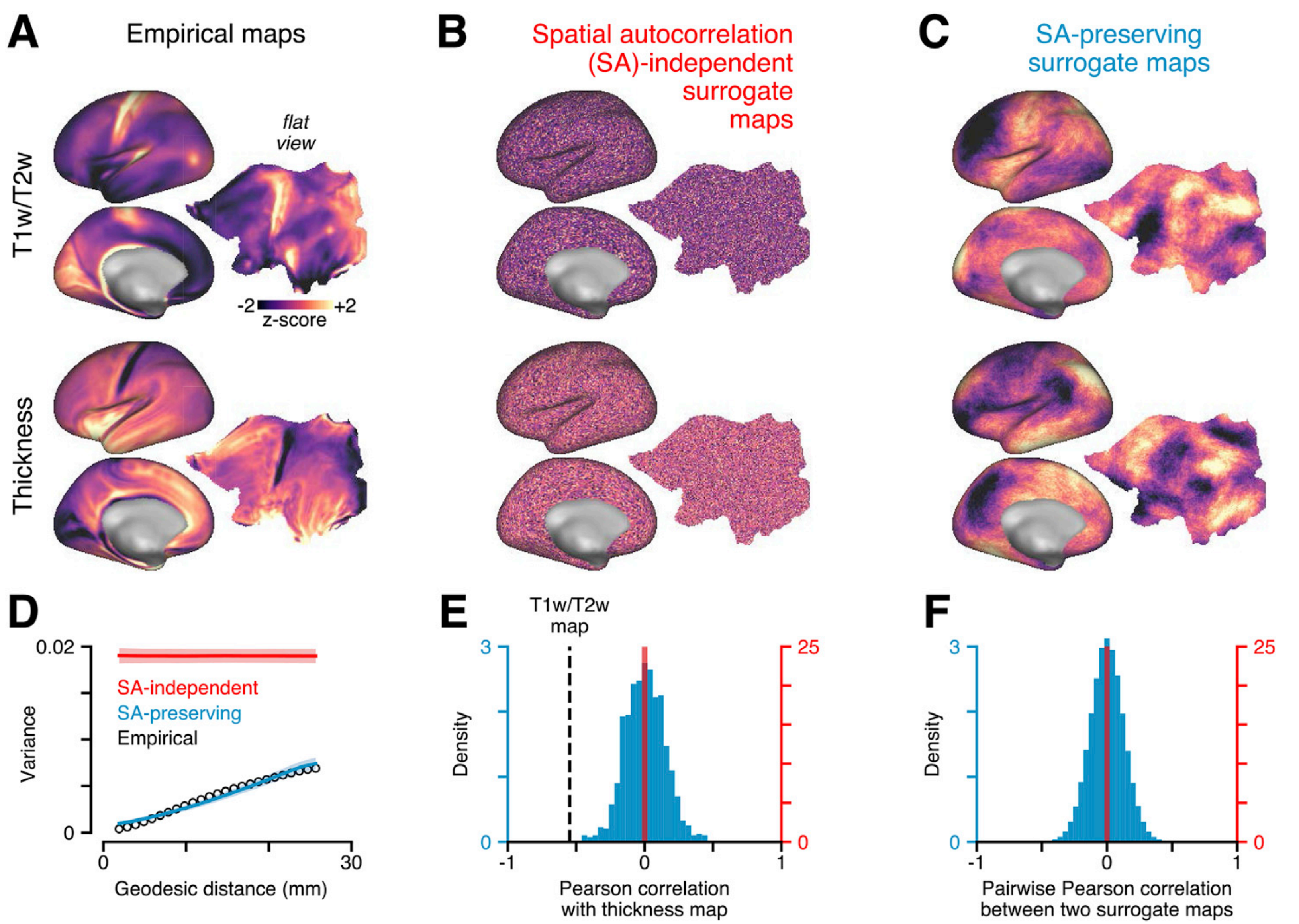
To create such random parcellations, we rotated each hemisphere of the original parcellation a random amount around each of the x, y, and z axes on the spherical expansion of the 32k fs_LR cortical surface. This procedure randomly relocated each parcel while maintaining the relative positions of parcels to each other. Each parcel was then slightly dilated or contracted to adjust for vertices gained or lost due to the non-uniform vertex density across the surface of the sphere, thus maintaining the same number of vertices within the rotated parcel while approximately maintaining the same shape. Random rotation was repeated 1000 times to generate distributions of average homogeneities calculated from randomly placed versions of each tested parcellation.



Toolbox: BrainSpace (Vos de Wael 2018)

Correction for spatial autocorrelation

SA-preserving permutation
Toolbox: BrainSMASH (Burt et al., 2020)



Q&A