STATISTICAL PARAMETRIC MAPPING (SPM): THEORY, SOFTWARE AND FUTURE DIRECTIONS

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DESCRIPTION

Overview— Statistical Parametric Mapping (SPM) [1] was developed in Neuroimaging in the mid 1990s [2], primarily for the analysis of 3D fMRI and PET images, and has recently appeared in Biomechanics for a variety of applications with dataset types ranging from kinematic and force trajectories [3] to plantar pressure distributions [4] (Fig.1) and cortical bone thickness fields [5].

SPM's fundamental observation unit is the "*m*D*n*D" continuum, where *m* and *n* are the dimensionalities of the observed variable and spatiotemporal domain, respectively, making it ideally suited for a variety of biomechanical applications including:

- (*m*=1, *n*=1) Joint flexion trajectories
- (*m*=3, *n*=1) Three-component force trajectories
- (*m*=1, *n*=2) Contact pressure distributions
- (*m*=6, *n*=3) Bone strain tensor fields.

SPM handles all data types in a single, consistent statistical framework, generalizing to arbitrary data dimensionalities and geometries through Eulerian topology.

Although SPM may appear complex it is relatively easy to show that SPM reduces to common software implementations (SPSS, R, MATLAB, etc.) when *m*=1 and *n*=0. Identically, it is conceptually easy to show how common tests, ranging from t tests and regression to MANCOVA, all generalize to SPM when one's data move from 0D scalars (1D0D) to *m*D*n*D continua (Table 1).

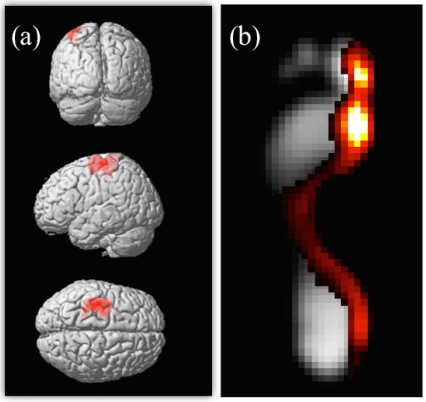

Figure 1: SPM first made the jump from Neuroimaging (a) to Biomechanics (b) in 2008 in plantar pressure analysis [5] and has since emerged in a variety of biomechanics applications including: kinematics/ force trajectory analysis and finite element modeling. SPM using topological inference to identify continuum regions (depicted as warm colors) that significantly co-vary with an experimental design.

Table 1: Many types of biomechanical data are *m*D*n*D, but most statistical tests in the literature are 1D0D: t tests, regression and ANOVA, and based on the relatively simple Gaussian distribution, despite nearly a century of theoretical development in *m*D0D and *m*D*n*D statistics.

	0D data		**1D data**	
	Scalar	Vector	Scalar	Vector
	1D0D	*m*D0D	1D1D	*m*D1D
Theory	Gaussian	Multivariate Gaussian	Random Field Theory	
Applied	T tests Regression ANOVA	T2 tests CCA MANOVA	**SPM**	

The purposes of this workshop are:

1. To review SPM's historical context.
2. To demonstrate how SPM generalizes common tests (including t tests, regression and ANOVA) to the domain of *m*D*n*D data.
3. To clarify potential pitfalls associated with the use of 0D approaches to analyze *n*D data.
4. To provide an overview of spm1d (www.spm1d.org), open-source software (Python, MATLAB) for the analysis of *m*D1D continua, and how it can be used to analyze a variety of biomechanical datasets.
5. To discuss future directions for SPM in Biomechanics.

Target Audience— Scientists, clinicians and engineers who deal with spatiotemporally continuous data, and all individuals interested in alternatives to simple classical hypothesis testing.

Expected audience background—

- Experience analyzing kinematics / dynamics time series
- Basic familiarity with MATLAB
- Familiarity with t tests, regression and ANOVA

Additionally, advanced topics toward the end of the workshop will be directed toward attendees who have familiarity with or who are interested in:

- Repeated measures modeling
- Multivariate statistics
- Bayesian modeling and analysis

Learning Objectives—

1) How and why SPM works: its fundamental concepts.
2) How to access and use spm1d software to conduct common analyses of 1D biomechanics data.
3) How to interpret and report SPM results.

PROGRAM

Time	*Speaker*	*Content*
0:00 – 0:30	Pataky	Background & Theory
0:30 – 1:00	Robinson	Software
1:00 – 1:30	Vanrenterghem	Interpretation & Reporting
1:30 – 1:45	Pataky	Future Directions
1:45 – 2:00	(None)	Open Discussion

(*The last 5 minutes of each session will be devoted to Q&A*)

Background & Theory— First we promote critical thinking regarding statistics by interactively reviewing the meaning of experimentation, random sampling and probability values. Through random simulations of 0D data and 1D data we clarify that statistical tests, while used for experimental analyses, are more aptly summarized as descriptors of randomness. This will prepare attendees to make the apparent leap but actual small step into the world of SPM: by observing what 1D randomness looks like (Fig.2), and how it can be funneled into t tests, just like the 0D Gaussian, it will become easy for attendees to conceptually connect the simple t test to its *n*D SPM manifestations (Table 1). Just as t tests' p values emerge directly from Gaussian theory, SPM's p values emerge directly from RFT. Coupled with an explanation of SPM's evolution in both Neuroimaging and Biomechanics, attendees will understand that SPM represents a natural progression of classical statistics concepts.

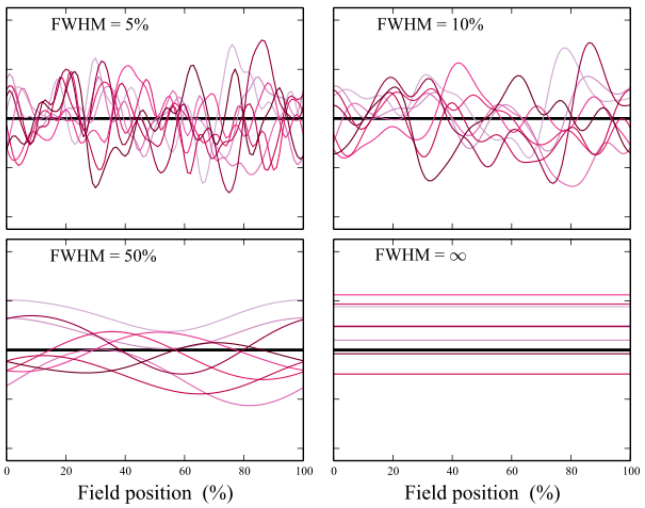

Figure 2: Depiction of Random Field Theory's model of 1D randomness. Fluctuations about means are modeled as smooth continua, parameterized by the FWHM (full-width at half-maximum) of a Gaussian kernel which is convolved with pure 1D noise. As FWHM approaches ∞, the data approach 0D, and SPM results approach those from common software implementations. By seeing how both 0D Gaussian data and these random can be routed into a t test, attendees will realize that t tests (and all other tests) simply funnel randomness into a test statistic, and thus the only difference between SPM and common 0D techniques is the form of randomness one assumes.

Software— Procedural knowledge will be stressed through a Matlab demonstration of spm1d basics (www.spm1d.org), its relation to other software packages, and its broader capabilities. Data organization and tests' optional parameters (e.g. one- vs. two-tailed, sphericity assumptions, etc.) will be described through example and with reference to online documentation. Additionally, spm1d's collection of real and simulated datasets will be introduced and explored. We'll finally introduce spm1d's online forums for free software support and general statistics discussion.

Interpretation & Reporting— We will next guide attendees through experimental design, scientific interpretation and reporting of SPM results. Necessary details including experimental design parameters, SPM-specific parameters, will be emphasized. Key literature references will be summarized. For a practical demonstration we will revisit some datasets from our own papers to discuss real Methods and Results reporting. We emphasize these points through hypothetical examples of bad SPM reporting. We finish by summarizing literature and internet resources for continued SPM learning.

Future Directions— We will provide an update regarding spm1d's current state, including a variety of functionality we have in the development pipeline including: normality, power analysis, and Bayesian inference. We will also discuss spm1d's possible expansion into the 2D and 3D domains, as a light-weight Biomechanics-friendly version of gold-standard Neuroimaging software. We will also briefly revisit theory to summarize SPM's relation to other whole-dataset techniques from the Biomechanics literature including: principal components analysis, wavelet analysis and functional data analysis. We will end with an open Q&A session regarding our spm1d software, SPM methodology in general, and other aspect of the workshop.

LIST OF SPEAKERS

(page 3)

REFERENCES

1. Friston KJ, et al. *Statistical Parametric Mapping: The Analysis of Functional Brain Images*, Elsevier, 2007.
2. Friston KJ, et al. *Human Brain Mapping*. **2**(4), 189-210, 1995.
3. Pataky TC, et al. *Journal of Biomechanics* **46**(14): 2394-2401, 2013.
4. Pataky TC, et al. *Journal of Biomechanics*, **41**(9), 1987-1994, 2008.
5. Li W, et al. *Bone*, **44**(4), 596-602, 2009.

LIST OF SPEAKERS

Todd C. Pataky, Ph.D., Associate Professor
Institute for Fiber Engineering, Shinshu University
Department of Bioengineering
Tokida 3-15-1, Ueda, Nagano, JAPAN 386-8567
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Todd Pataky received a Ph.D. in Kinesiology and Mechanical Engineering from the Pennsylvania State University in 2004 and pursued postdoctoral research positions in functional neuroimaging and biomechanical continuum analysis in Japan (ATR International, Kyoto) and the UK (University of Liverpool). He is currently an Associate Professor in the Institute for Fiber Engineering, Shinshu University (Japan) where his research focuses on the development of continuum statistics techniques and their applications in Biomechanics. He has over 60 peer-reviewed publications in Biomechanics, many of which focus on SPM and its applications. Notable honors include: Young Investigator Award (bronze) at the World Congress on Biomechanics (2010), Nike Award for Athletic Footwear Research (2009), and William Evans Fellow at the University of Otago, New Zealand (2014).

Mark Robinson, Ph.D., Senior Lecturer
Research Institute for Sport and Exercise Sciences
Liverpool John Moores University
Tom Reilly Building, Byrom Street
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Mark is currently a Senior Lecturer in Biomechanics and Programme Leader for the BSc(Hons) Sport and Exercise Sciences degree at LJMU. He completed his doctorate in 2011 in the School of Sport and Exercise Sciences, LJMU. His research interests are related to musculoskeletal loading, injury and impairment in the lower limbs, specifically during dynamic sporting activities. Of particular interest are knee injuries, player loading in soccer, and gait analysis. His research also includes the development of SPM as a method to provide biomechanists with the appropriate statistical tools to analyze complex biomechanical data. He has published over 30 journal articles in these areas since 2012 and was awarded a UEFA Research Grant in 2014.

Jos Vanrenterghem, Ph.D., Associate Professor
KU Leuven, Department of Rehabilitation Sciences
Tervuursevest 101 - box 1501
3001 Leuven, Belgium
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Jos received a PhD in Biomechanics from Ghent University in 2004. After having lectured at the School of Sport and Exercise Sciences at Liverpool John Moores University for 10 years, he is now an Associate Professor at the University of Leuven. He has published over 50 articles in peer-reviewed Biomechanics journals, with research interests in lower extremity musculoskeletal loading mechanisms and injury prevention in sport. He has been teaching biomechanics across undergraduate and postgraduate levels, providing him with a good insight in the common issues that students face when analyzing biomechanical data. He has also delivered a series of workshops on research practice in Biomechanics, and devotes much of his work to making biomechanics available in applied and clinical contexts, including through the use of SPM.

STATISTICAL PARAMETRIC MAPPING

THEORY, SOFTWARE AND FUTURE DIRECTIONS

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Todd Pataky

Dept. of Bioengineering

KU LEUVEN

Jos Vanrenterghem

Dept. of Rehabilitation Sciences

liverpool JMU

Mark Robinson

Institute for Sport and Exercise Sciences

spm1D 0.4

26 July 2017

ISB Brisbane

Overview

- 17:00 – 17:30 Background & Theory
- 17:30 – 18:00 Software
- 18:00 – 18:30 Interpretation & Reporting
- 18:30 – 18:40 Future Directions
- 18:40 – Open Discussion

BACKGROUND & THEORY

Todd Pataky

26 July 2017
ISB Brisbane

S

STATISTICAL

Probabilistic inferences regarding experimental data

P

PARAMETRIC

- Based on **mean** & **SD** & **sample size**
- Also non-parametric (SnPM)
- Parameterized model of cerebral blood flow

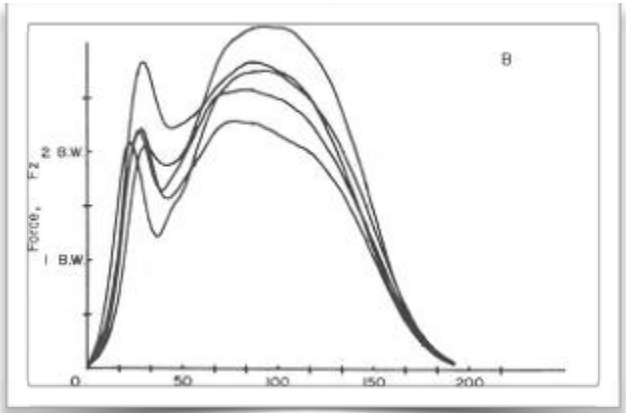
M

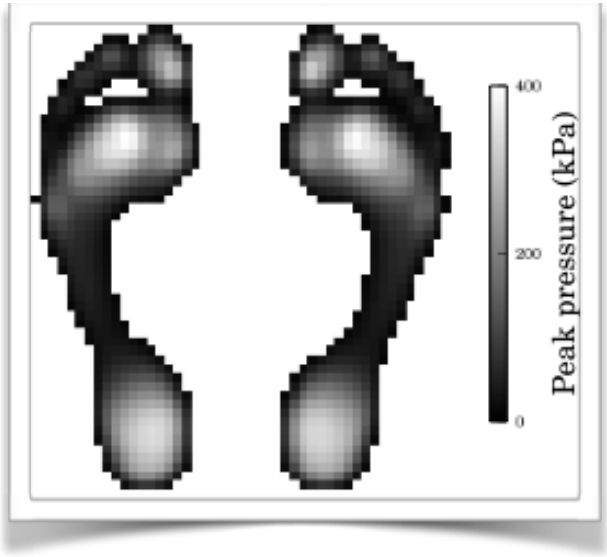
MAPPING

Results form an *n*-Dimensional "map" in the same space as the original data

(i.e. test statistics [t and F] are *n*-D continua)

n-D continua





Smooth, bounded

n-D, *m*-D continua

continuum | dependent variable

continuum	dependent variable		
Univariate **0D**	Body mass	0D, 1D	SPSS, MATLAB, R
Multivariate **0D**	GRF at t = 50 ms	0D, 3D	SPSS, MATLAB, R
Univariate **1D**	Knee flexion	1D, 1D	
Multivariate **1D**	Knee posture	1D, 6D	
Univariate ***n*D**	Foot pressure	2D, 1D	
Multivariate ***n*D**	Bone strain tensor	3D, 6D	

A brief history of SPM

1976 Adler & Hasofer, *Annals of Prob*.

1990 Friston et al. *J Cerebral Blood Flow*

1995 Friston et al. *Human Brain Mapping*

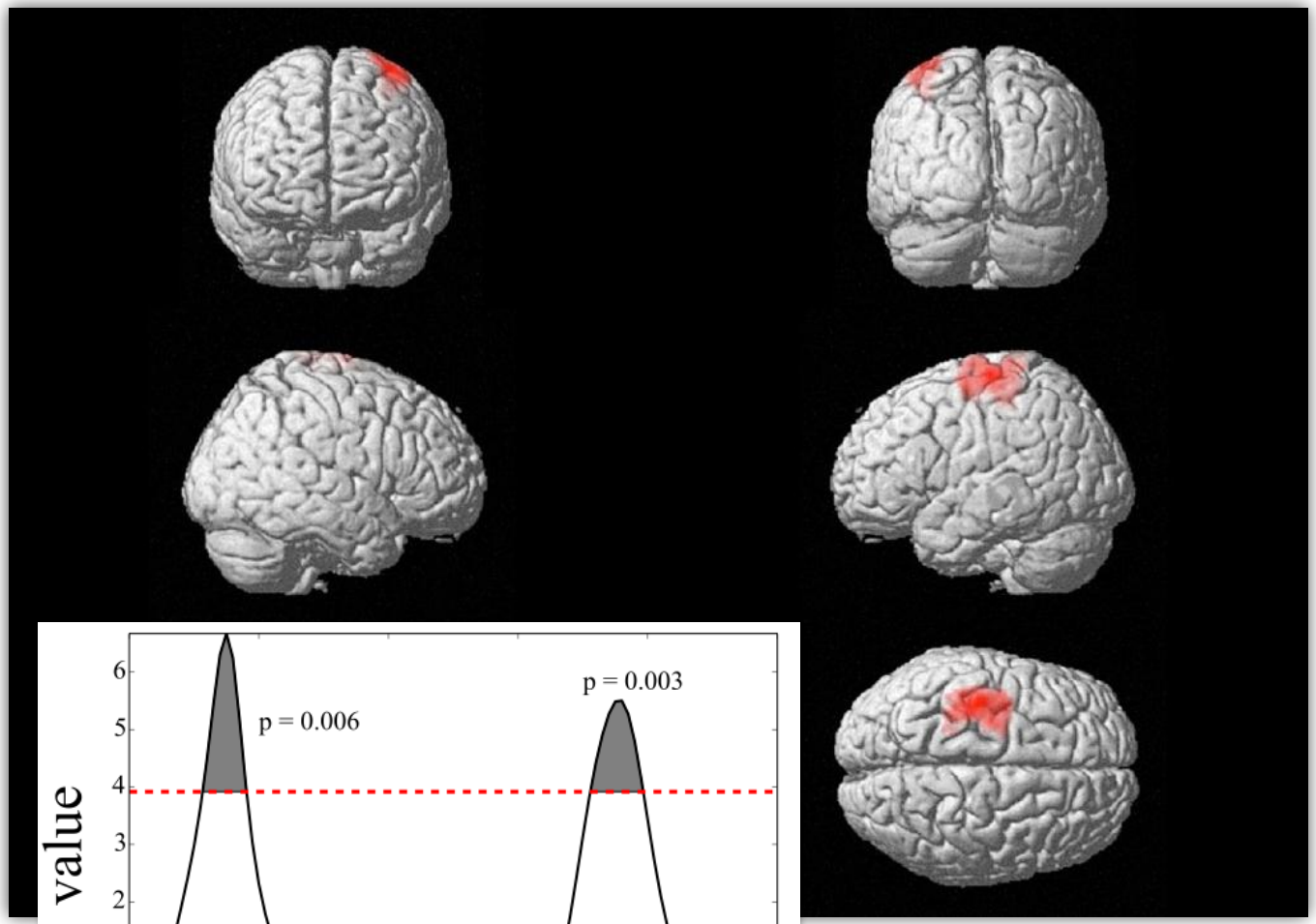
8663 citations
H-index: 202
i-10-index: 758

2004 Worsley et al. *NeuroImage*

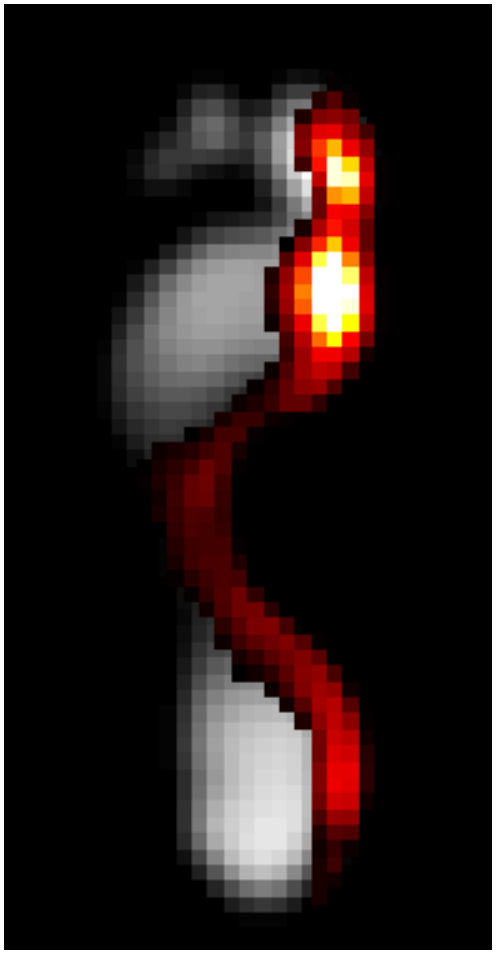
2008 Pataky et al. New insights into the plantar pressure correlates of walking speed using pedobarographic statistical parametric mapping *J Biomech* 41: 1987-1994.

2009 Li et al. Identify fracture-critical regions inside the proximal femur using statistical parametric mapping, *Bone* 44: 596-602

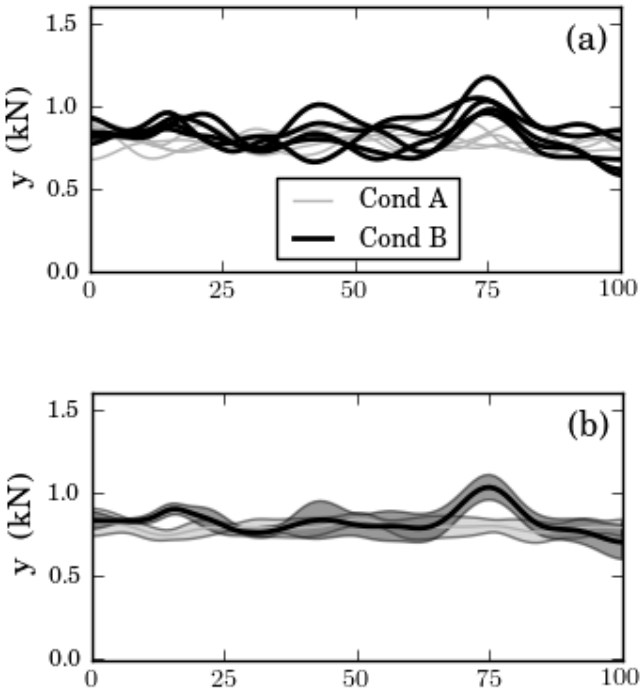
spm1D 0.4

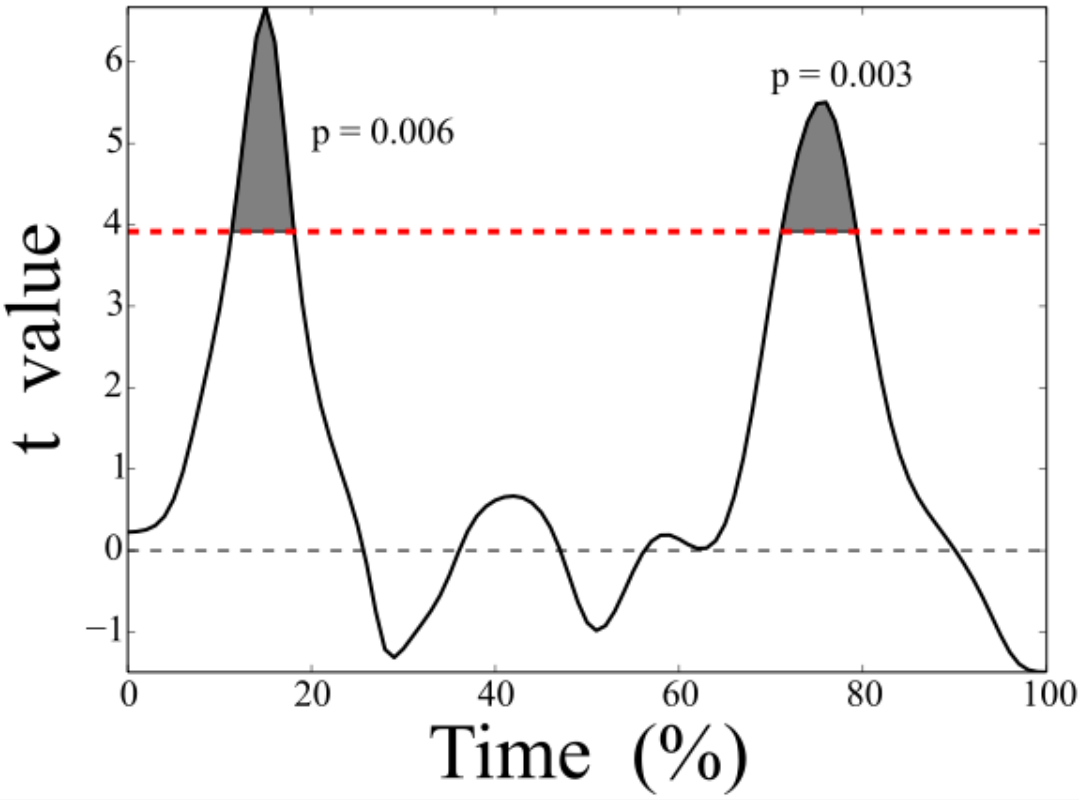


p = 0.006
p = 0.003
t value
Time (%)
6
5
4
3
2
1
0
−1
0
20
40
60
80
100



Example


(a)
(b)
y (kN)
1.5
1.0
0.5
0.0
0
25
50
75
100
Cond A
Cond B

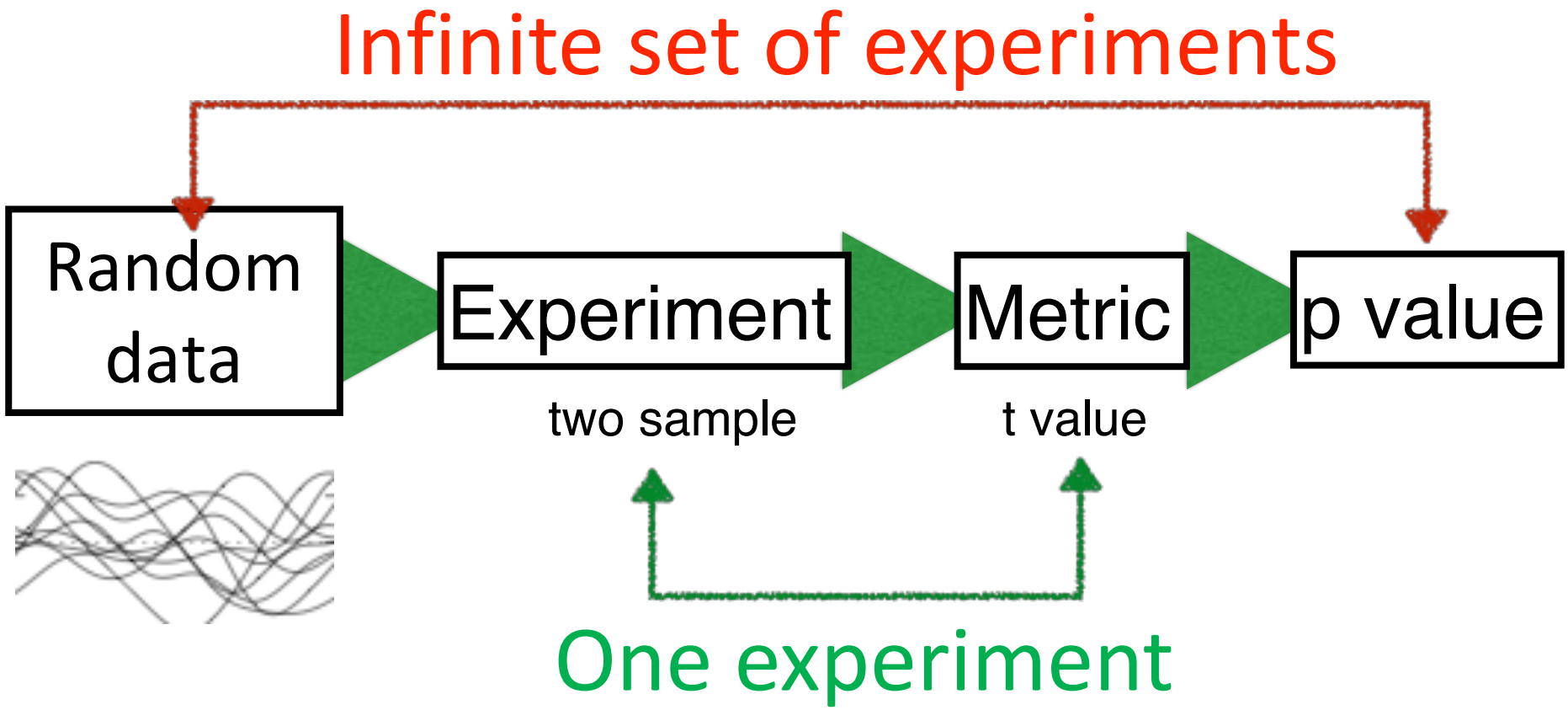

t value
Time (%)
p = 0.006
p = 0.003
6
5
4
3
2
1
0
−1
0
20
40
60
80
100

What is a *p* value?

Demo

What is a *p* value?

The probability that a random process will yield a particular result.


Infinite set of experiments
Random data
Experiment
two sample
Metric
t value
p value
One experiment

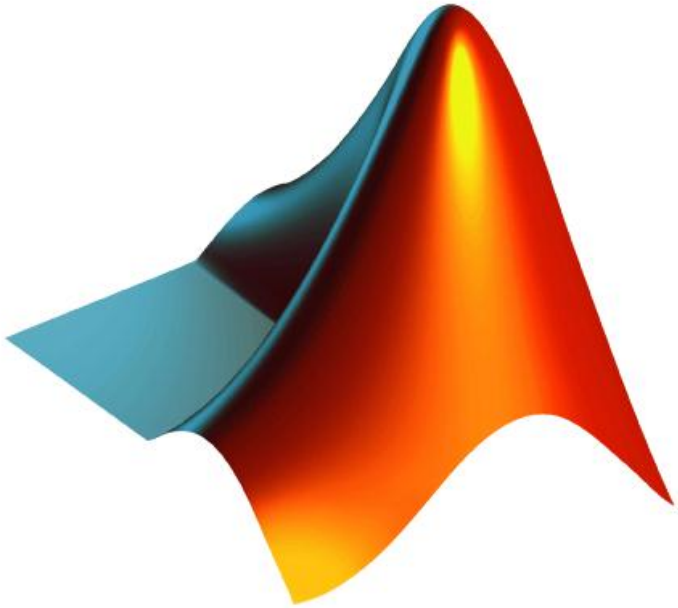
t and F values describe one experiment

p values describe the behavior of random data in an infinite set of experiments

Use ***n*D random data** to make probabilistic conclusions regarding ***n*D experimental data**

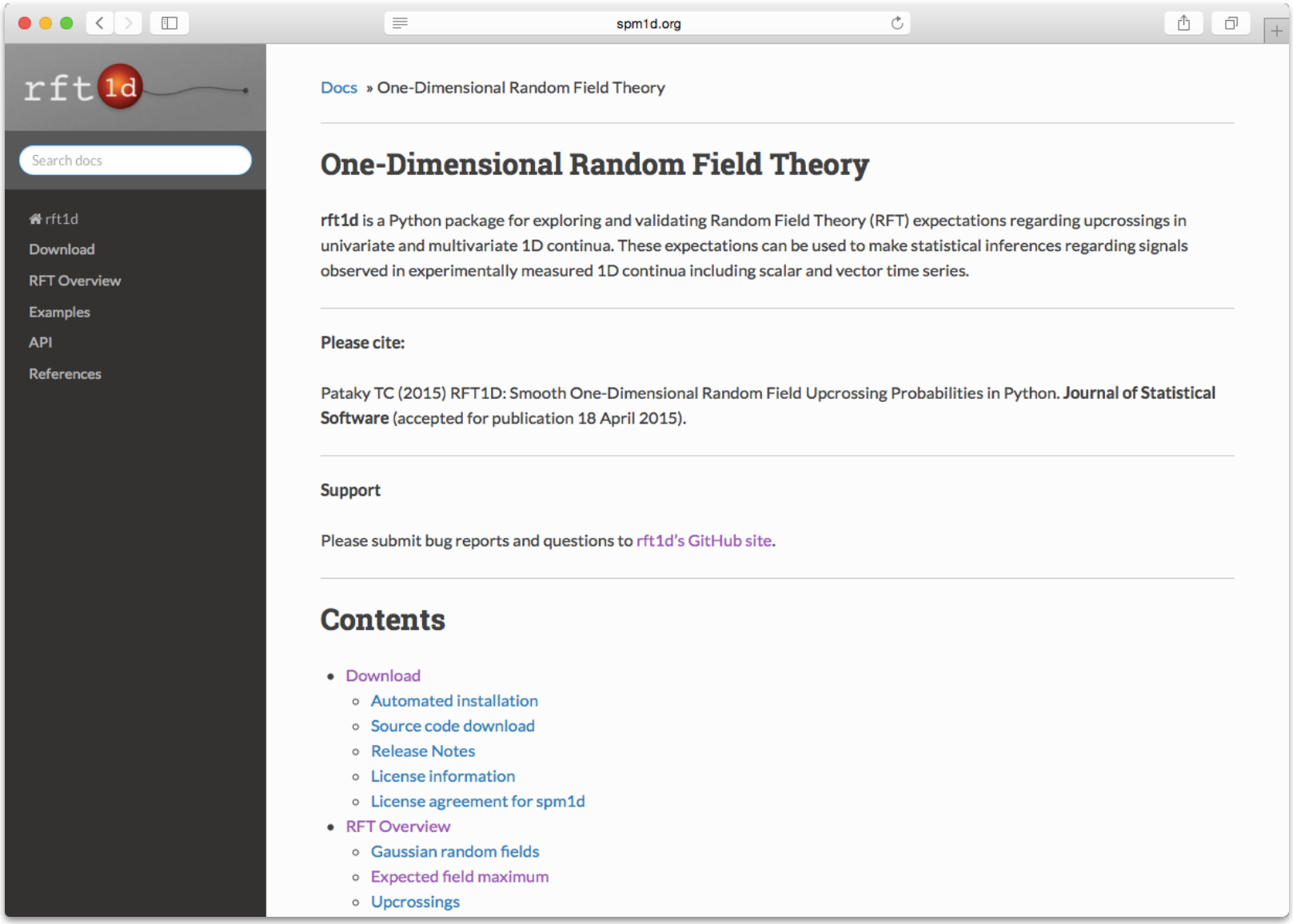
www.spm1d.org

spm1D 0.4

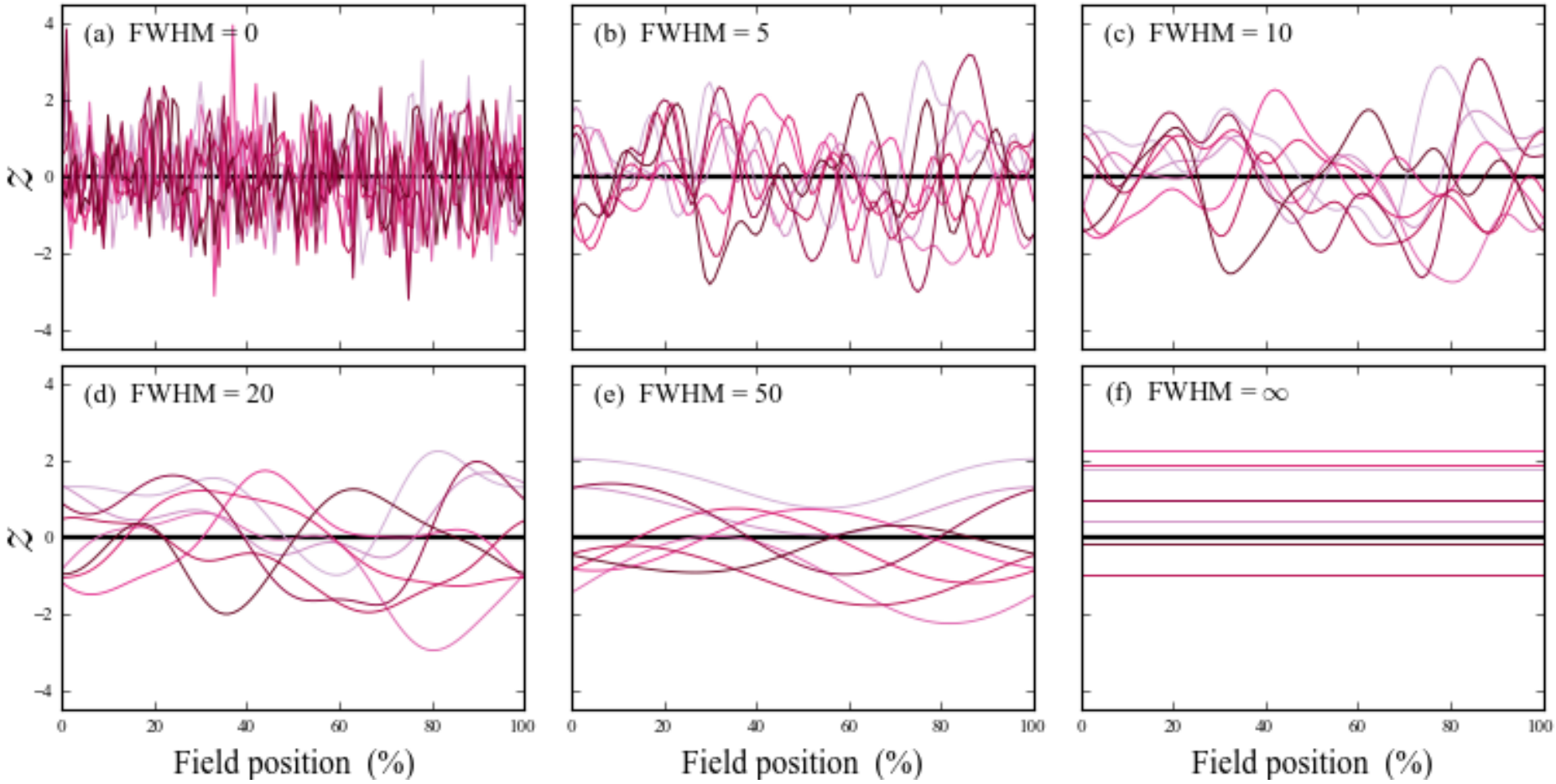


spm1d.org/rft1d

Pataky (2016) *J. Statistical Software*



rft 1d

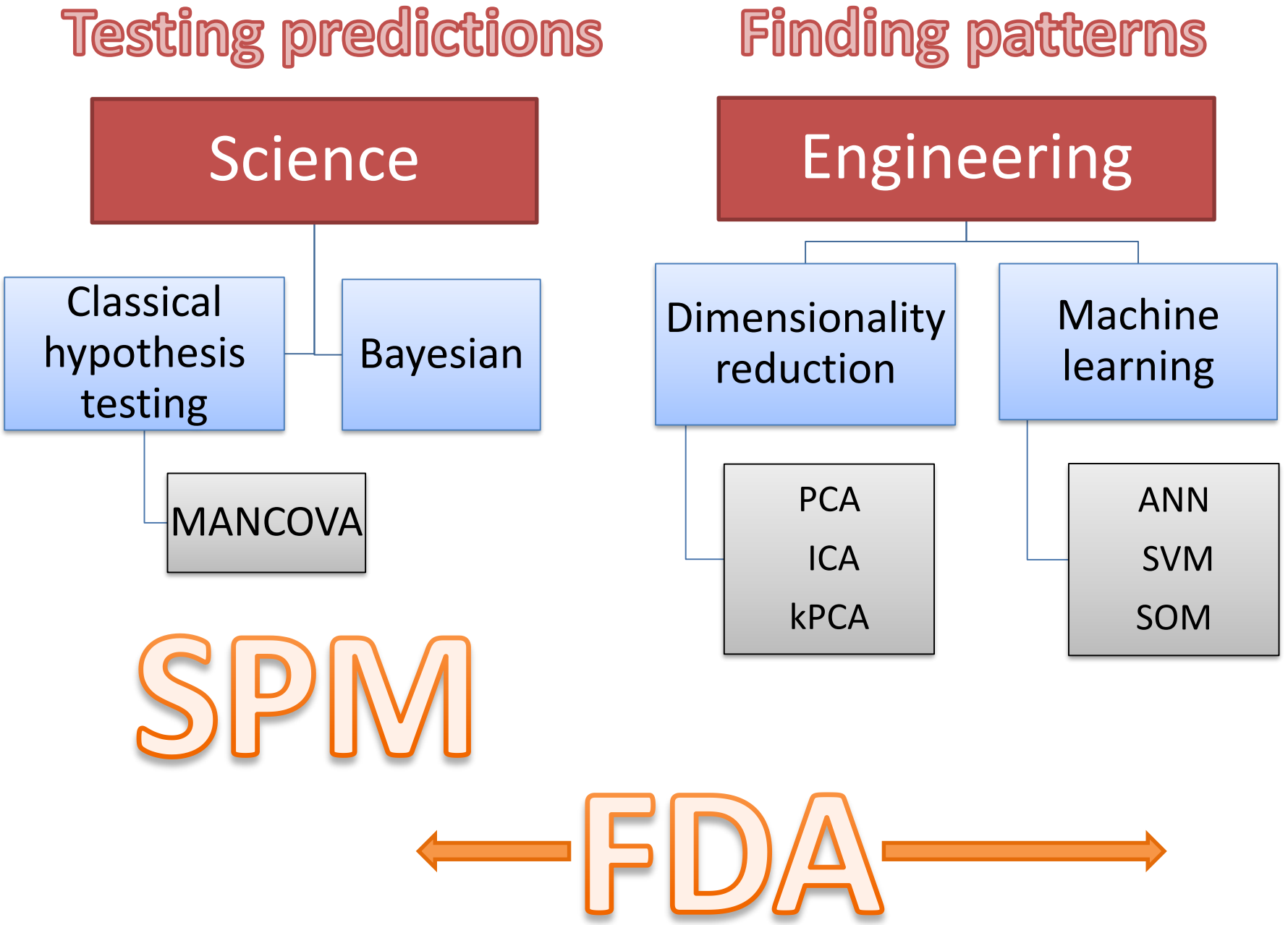

(a) FWHM = 0
(b) FWHM = 5
(c) FWHM = 10
(d) FWHM = 20
(e) FWHM = 50
(f) FWHM = ∞
Z
4
2
0
-2
-4
0
20
40
60
80
100
Field position (%)

Statistics

- z
- t
- F
- χ^2
- T^2

Distribution Functions

- probability density
- survival function
- inverse survival function


Testing predictions
Finding patterns
Science
Engineering
Classical hypothesis testing
Bayesian
MANCOVA
Dimensionality reduction
Machine learning
PCA
ICA
kPCA
ANN
SVM
SOM
SPM
FDA

www.spm1d.org

spm1d tutorial, ISB 2017

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This tutorial will focus on using the software and will cover:

1. getting "spm1d"
2. input data organisation
3. statistical tests: t-tests, regression, ANOVA, CCA
4. keywords
5. help
6. questions?

1. Software

"spm1d" is an open source package for one-dimensional Statistical Parametric Mapping.

The current version is 0.4

The python code repository is: https://github.com/0todd0000/spm1d/ (https://github.com/0todd0000/spm1d/)
The matlab code repository is: https://github.com/0todd0000/spm1dmatlab (https://github.com/0todd0000/spm1dmatlab)

2. Input data organisation

2. Input data organisation

Univariate spm1d uses a (J x Q) array, where J is the number of 1D responses (i.e. trials or subjects) and Q is the number of nodes in the 1D continuum.

> e.g. 10 subject means normalized to 101 nodes will give a 10x101 array

Multivariate spm1d analysis the data should be arranged as a (J x Q x I) array, where I is the number of vector components in the 1D continuum.

> e.g. 10 subject means normalized to 101 nodes for GRF X,Y,Z, will give a 10x101x3 vector field

3. Statistical tests

a. 1D two-sample t-test

```
/examples/stats1d/ex1d_ttest2.m
```

In [2]:

```
% load some data
dataset = spm1d.data.uv1d.t2.PlantarArchAngle();
[YA,YB] = deal(dataset.YA, dataset.YB);

dataset
```

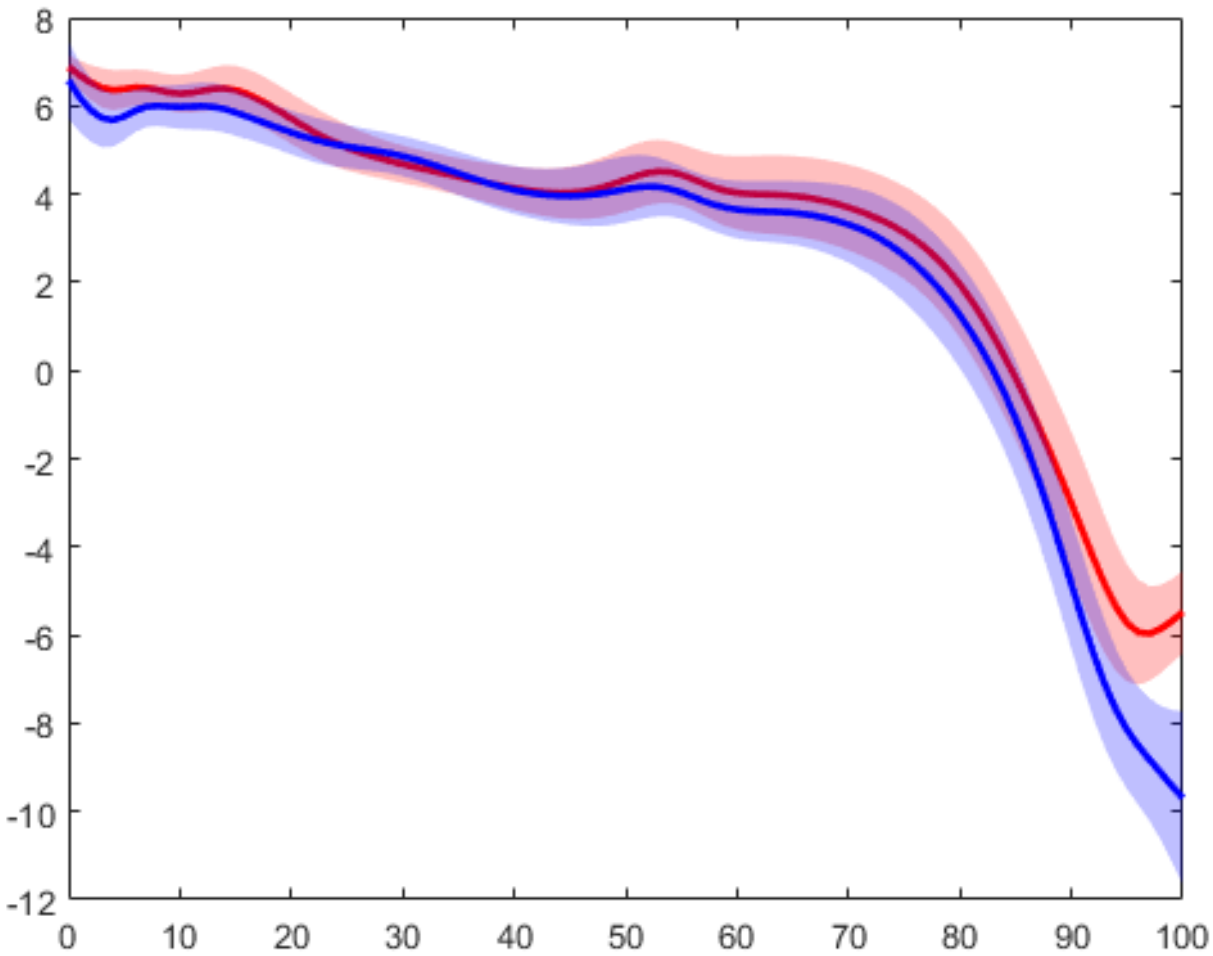
```
dataset =

  struct with fields:

    cite: 'Caravaggi, P., Pataky, T., G?nther, M., S
avage, R., & Crompton, R. (2010). Dynamics of longit
udinal arch support in relation to walking speed: co
ntribution of the plantar aponeurosis. Journal of An
atomy, 217(3), 254?261. http://doi.org/10.1111/j.146
9-7580.2010.01261.x'
      YA: [10×101 double]
      YB: [10×101 double]
```

This dataset has two variables both of size 10x101

spm1d has built in plotting functions for data e.g. plot_meanSD

In [3]:

```
% Plot the data
spm1d.plot.plot_meanSD(YA,'color','r');
hold on
spm1d.plot.plot_meanSD(YB,'color','b');
```



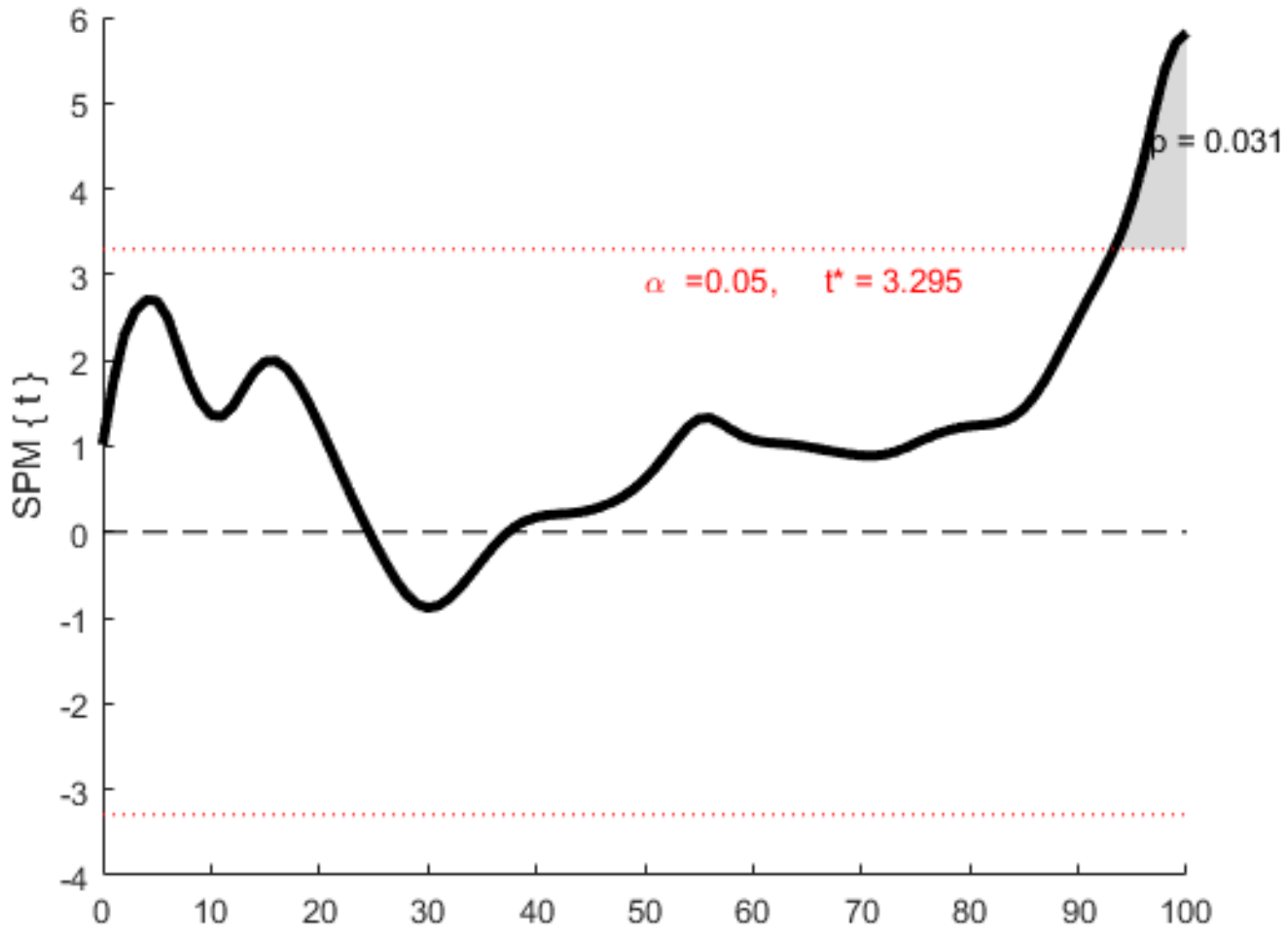
In [4]:

```
%(1) Conduct SPM analysis:
spm       = spm1d.stats.ttest2(YA, YB);
spmi      = spm.inference(0.05, 'two_tailed',true);
disp(spmi)
```

```
SPM{t} inference
         z: [1×101 double]
        df: [1 18]
      fwhm: 20.5956
    resels: [1 4.8554]
     alpha: 0.0500
     zstar: 3.2947
     p_set: 0.0312
         p: 0.0312
```

In [5]:

```
% Plot SPM analysis outcome
spmi.plot();
spmi.plot_threshold_label();
spmi.plot_p_values();
```



In [6]:

```
% For descriptive information about clusters
spmi.clusters{1,1}
```

```
ans =

  Cluster with properties:

    endpoints: [93.2746 100]
        csign: 1
    iswrapped: 0
       extent: 6.7254
      extentR: 0.3265
            h: 3.2947
           xy: [96.5343 4.5976]
            P: 0.0312
```

b. 1D Linear Regression

/examples/stats1d/ex1d_regression.m

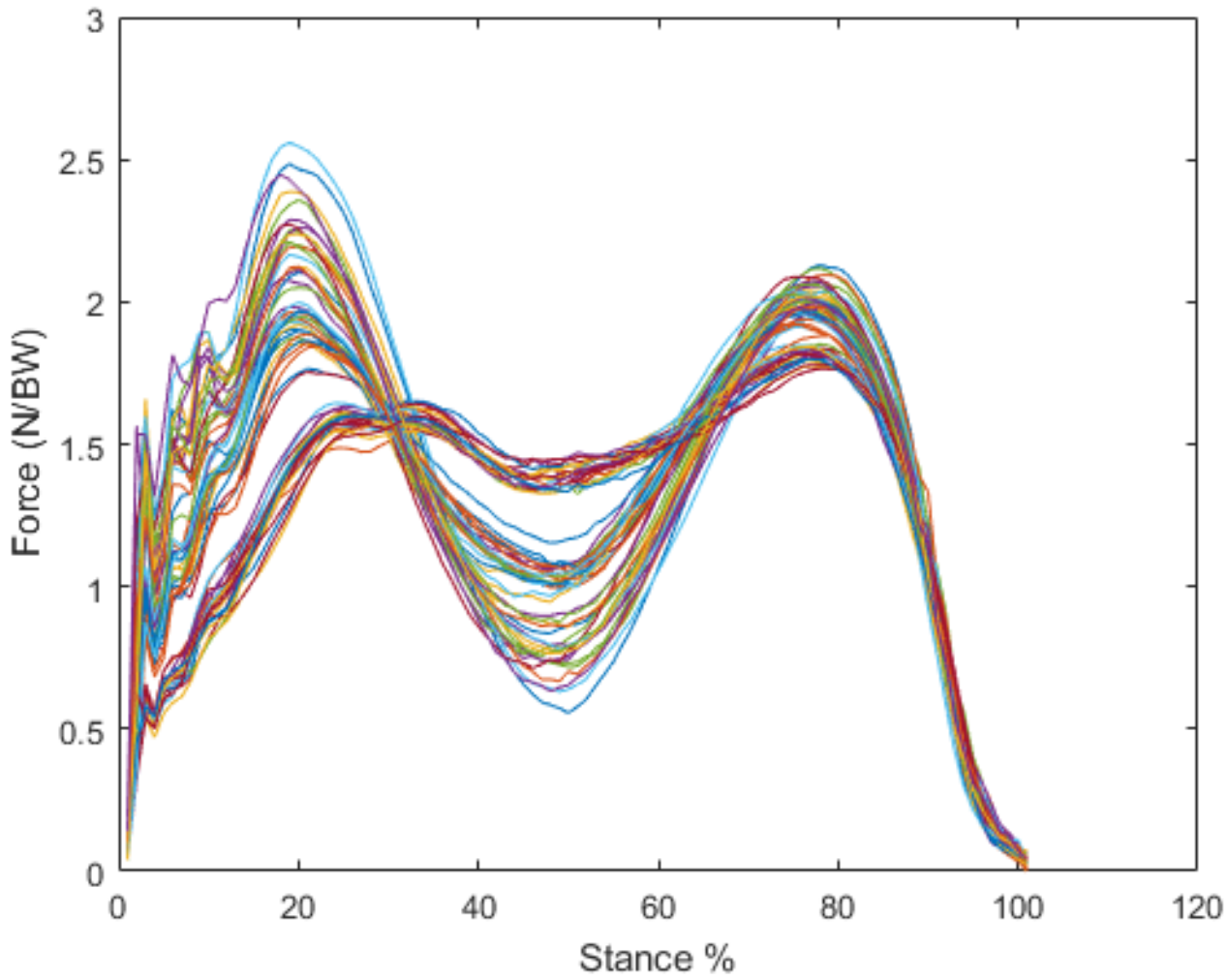
In [7]:

```
% Load example data
dataset = spm1d.data.uv1d.regress.SpeedGRF();
[Y,x]  = deal(dataset.Y, dataset.x);

dataset
```

```
dataset =

  struct with fields:

    cite: 'Pataky, T. C., Caravaggi, P., Savage, R.,
Parker, D., Goulermas, J., Sellers, W., & Crompton,
R. (2008). New insights into the plantar pressure co
rrelates of walking speed using pedobarographic stat
istical parametric mapping (pSPM). Journal of Biomec
hanics, 41(9), 1987?1994.'
    Y: [60×101 double]
    x: [60×1 double]
```

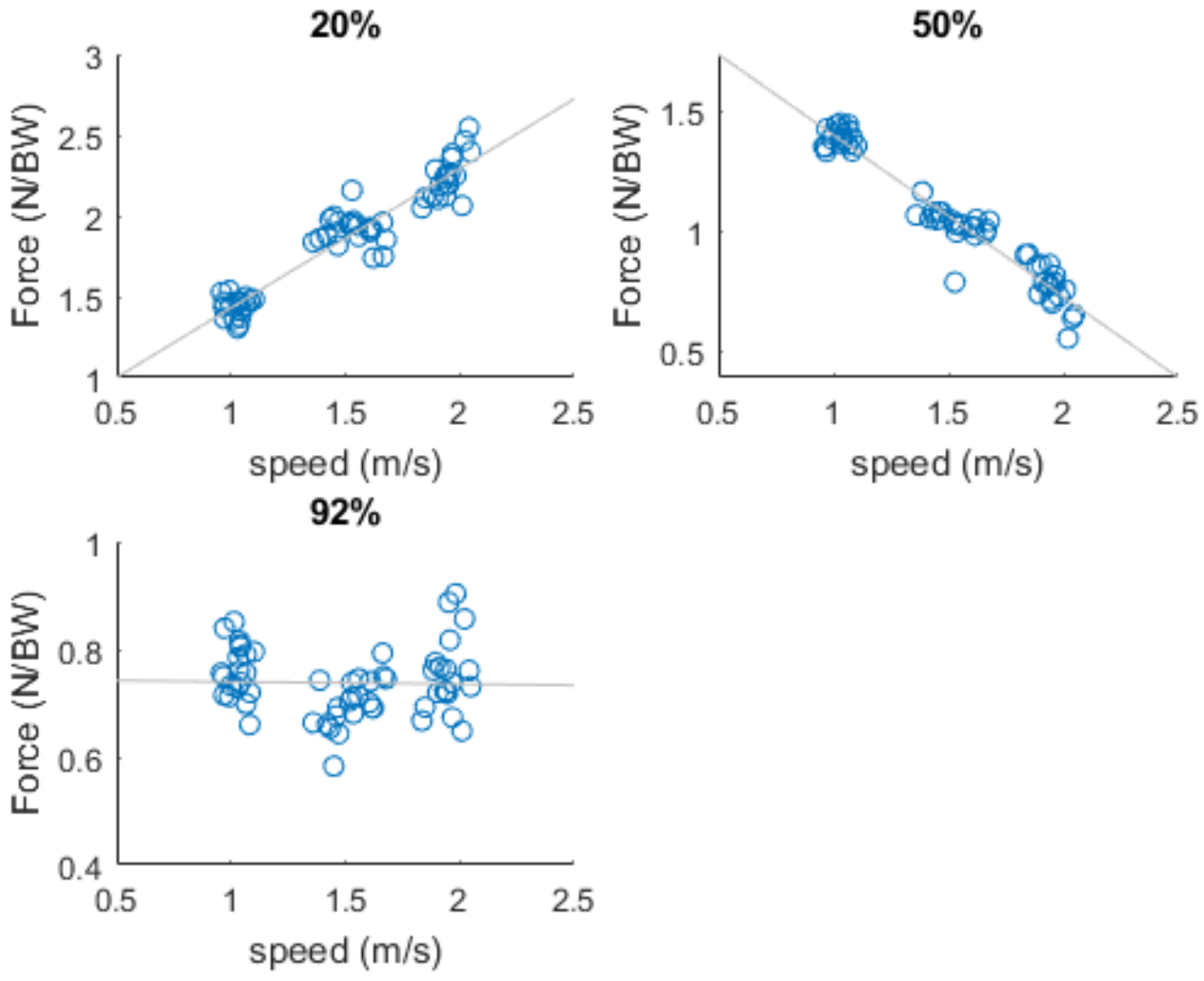
In [8]:

```
% Plot the GRF data
plot(Y');
xlabel('Stance %');
ylabel('Force (N/BW)');
```



In [9]:

```
subplot(221);
    scatter(x,Y(:,20));  title('20%');  xlabel('speed (m/s)');  yla
bel('Force (N/BW)'); lsline()
subplot(222);
    scatter(x,Y(:,50));  title('50%');  xlabel('speed (m/s)');  yla
bel('Force (N/BW)'); lsline()
subplot(223);
    scatter(x,Y(:,92));  title('92%');  xlabel('speed (m/s)');  yla
bel('Force (N/BW)'); lsline()
```



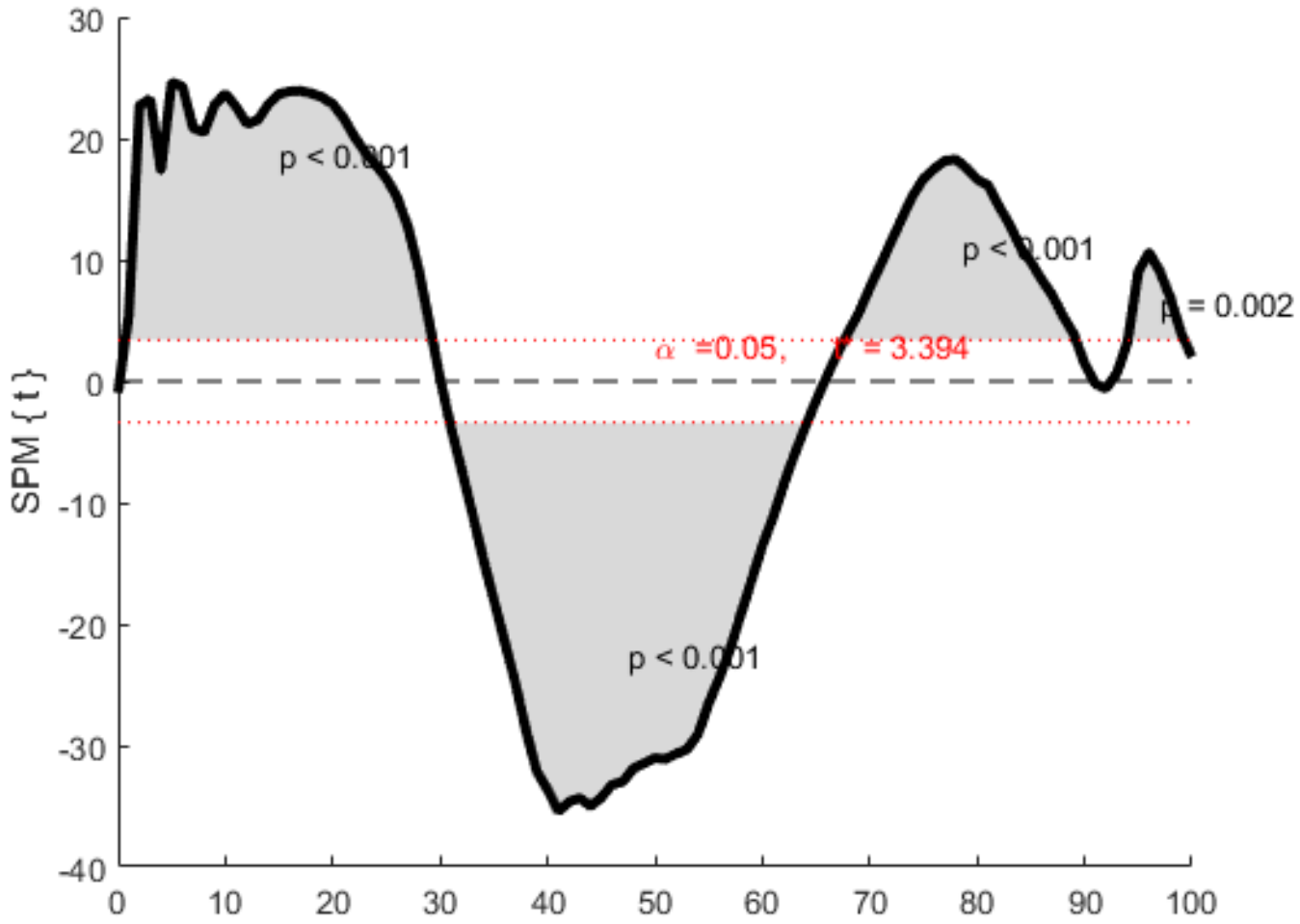
In [10]:

```
% Conduct SPM analysis:
spm       = spm1d.stats.regress(Y, x);
spmi      = spm.inference(0.05, 'two_tailed', true);
disp(spmi)
```

```
SPM{t} inference
         z: [1×101 double]
        df: [1 58]
      fwhm: 6.1343
    resels: [1 16.3017]
     alpha: 0.0500
     zstar: 3.3945
     p_set: 4.0634e-14
         p: [0 0 0 0.0017]
```

In [11]:

```
% Plot SPM output
spmi.plot();
spmi.plot_threshold_label();
spmi.plot_p_values();
```



c. ANOVA - between groups

/examples/stats1d/ex1d_anova1.m

In [12]:

```
% Load data:
dataset    = spm1d.data.uv1d.anova1.SpeedGRFcategorical();
[Y,A]      = deal(dataset.Y, dataset.A);
```

```
disp('Data Loaded')
dataset
 A
```

```
Data Loaded

dataset =

  struct with fields:

    cite: 'Pataky, T. C., Caravaggi, P., Savage, R.,
Parker, D., Goulermas, J., Sellers, W., & Crompton,
R. (2008). New insights into the plantar pressure co
rrelates of walking speed using pedobarographic stat
istical parametric mapping (pSPM). Journal of Biomec
hanics, 41(9), 1987?1994.'
       Y: [60×101 double]
       A: [60×1 uint8]

A =

  60×1 uint8 column vector

   3
   1
   1
   1
   3
   1
   1
   2
   2
   2
   3
   3
```

2
1
3
1
3
1
3
2
1
1
3
3
3
2
3
2
2
2
2
3
1
3
2
2
1
3
3
1

```
1
2
2
1
1
3
2
1
1
3
3
3
```

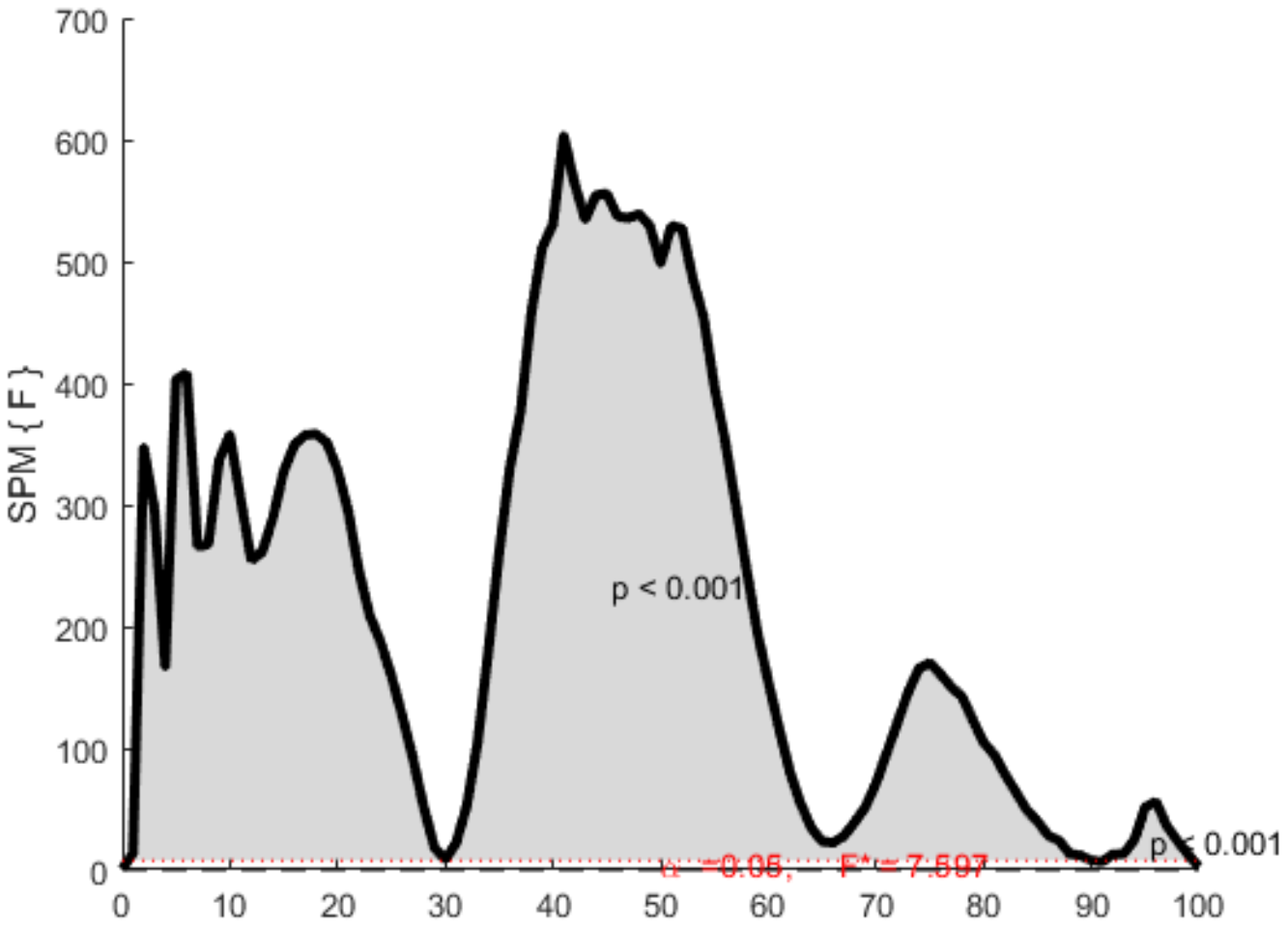
In [13]:

```
% Run SPM analysis
spm       = spm1d.stats.anova1(Y, A);
spmi      = spm.inference(0.05);
disp(spmi)
```

```
SPM{F} inference
         z: [1×101 double]
        df: [2 57]
      fwhm: 6.1179
    resels: [1 16.3455]
     alpha: 0.0500
     zstar: 7.5969
     p_set: 5.2921e-12
         p: [2.2204e-16 3.2533e-06]
```

In [14]:

```
% Plot
spmi.plot();
spmi.plot_threshold_label();
spmi.plot_p_values();
```

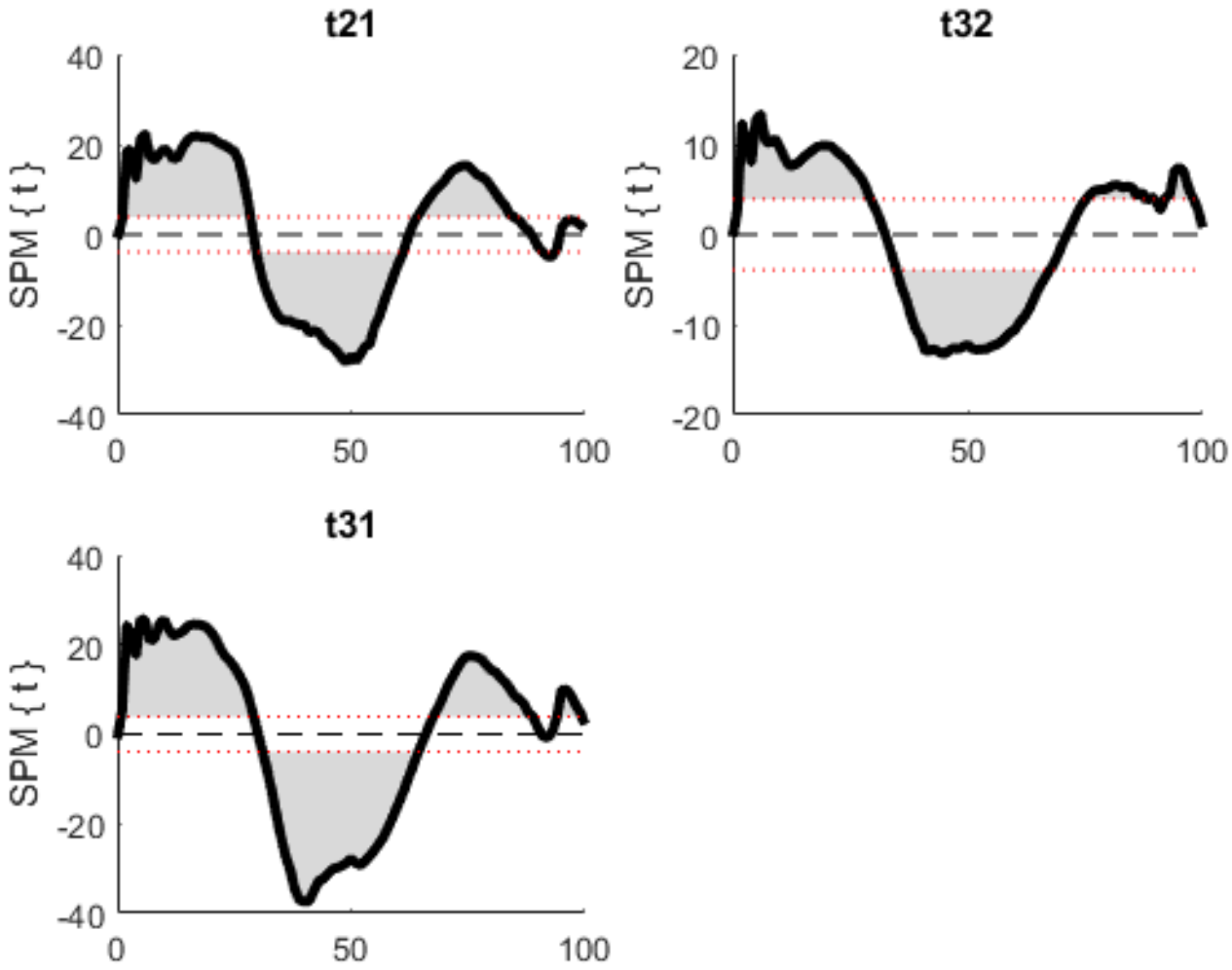


In [15]:

```
% Post-hoc Analysis

% separate into groups:
Y1          = Y(A==1,:);
Y2          = Y(A==2,:);
Y3          = Y(A==3,:);

% Conduct post-hoc analysis:
t21         = spm1d.stats.ttest2(Y2, Y1);
t32         = spm1d.stats.ttest2(Y3, Y2);
t31         = spm1d.stats.ttest2(Y3, Y1);

% inference:
alpha       = 0.05;
nTests      = 3;
p_critical = spm1d.util.p_critical_bonf(alpha, nTests);

t21i        = t21.inference(p_critical, 'two_tailed',true);
t32i        = t32.inference(p_critical, 'two_tailed',true);
t31i        = t31.inference(p_critical, 'two_tailed',true);
```

In [16]:

```
subplot(221);  t21i.plot(); title('t21')
subplot(222);  t32i.plot(); title('t32')
subplot(223);  t31i.plot(); title('t31')
```



d. Canonical Correlation Analysis

/examples/stats1d/ex1d_cca.m

In [17]:

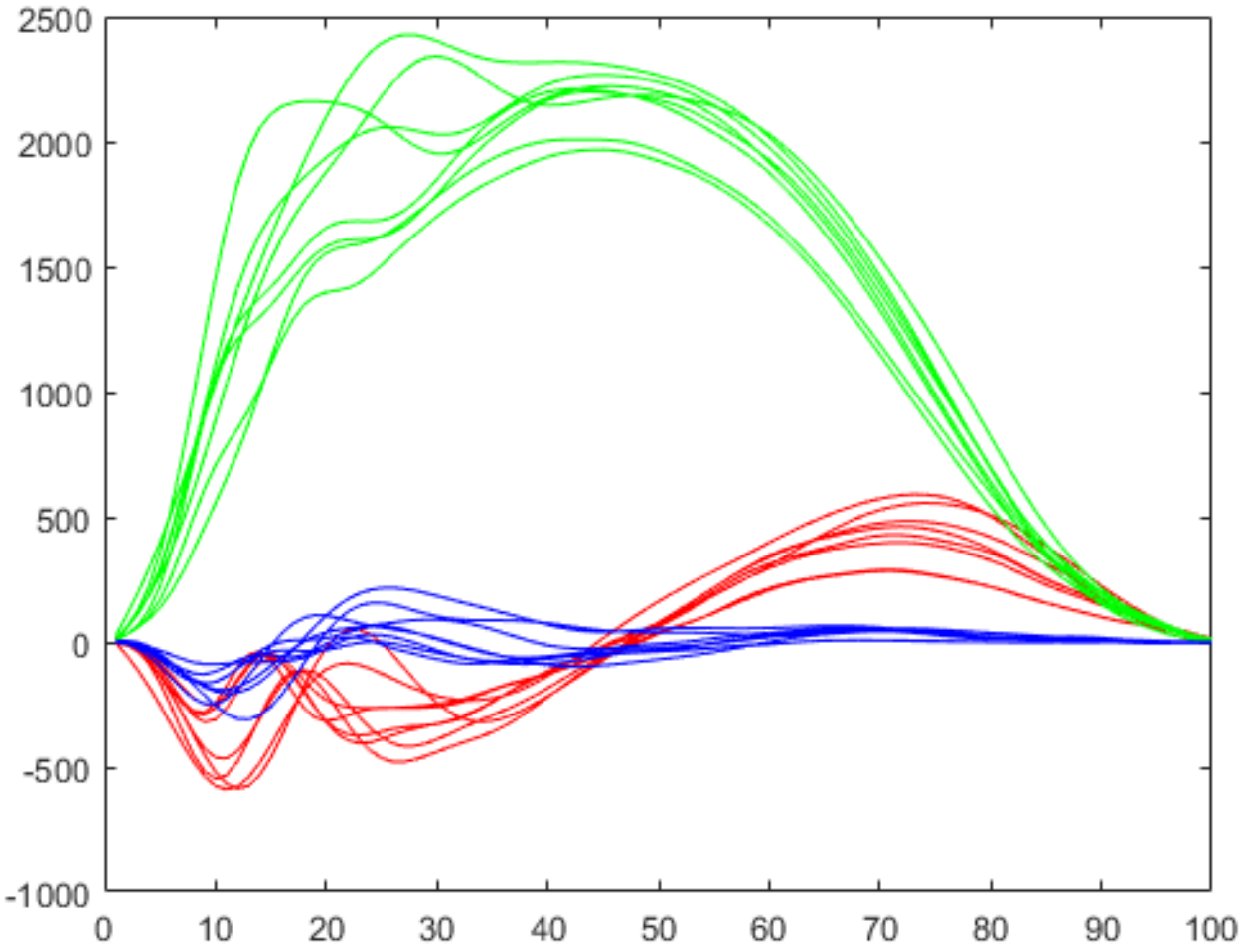
```
%(0) Load data:
dataset    = spm1d.data.mv1d.cca.Dorn2012();
[Y,x]      = deal(dataset.Y, dataset.x);

dataset
x
```

```
dataset =

  struct with fields:

    cite: 'Dorn, T. W., Schache, A. G., & Pandy, M.
G. (2012). Muscular strategy shift in human running:
dependence of running speed on hip and ankle muscle
performance. Journal of Experimental Biology, 215(11
), 1944?1956. http://doi.org/10.1242/jeb.064527'
     www: 'https://simtk.org/home/runningspeeds'
       Y: [8×100×3 double]
       x: [8×1 double]


x =

    3.5600
    3.5600
    5.2000
    5.2000
    7.0000
    7.0000
    9.4900
    9.4900
```

In [18]:

```
% Visualise this dataset
plot(Y(:,:,1)','r');
hold on
plot(Y(:,:,2)','g');
plot(Y(:,:,3)','b');
x
```

```
x =

    3.5600
    3.5600
    5.2000
    5.2000
    7.0000
    7.0000
    9.4900
    9.4900
```



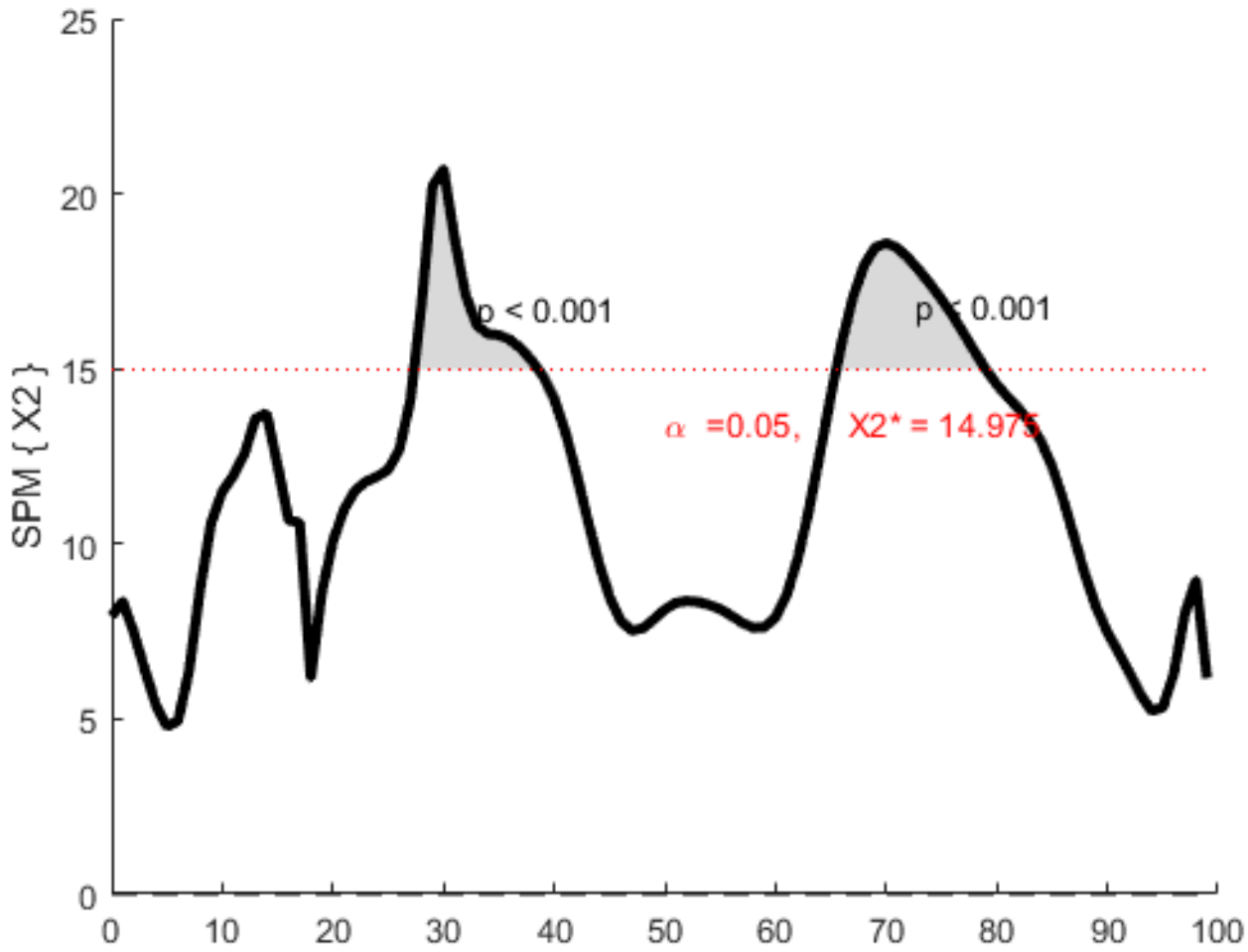
In [19]:

```
%(1) Conduct SPM analysis:
spm       = spm1d.stats.cca(Y, x);
spmi      = spm.inference(0.05);
disp(spmi)
```

```
SPM{X2} inference
         z: [1×100 double]
        df: [1 3]
      fwhm: 8.8974
    resels: [1 11.1269]
     alpha: 0.0500
     zstar: 14.9752
     p_set: 5.6243e-10
         p: [3.3539e-05 1.2275e-06]
```

In [20]:

```
%(2) Plot
spmi.plot();
spmi.plot_threshold_label();
spmi.plot_p_values();
```



4. Keywords

Equality of variance

```
t = spm1d.stats.ttest2(YA, YB, 'equal_var', false)
```

One or two-tailed Interpolation of clusters

```
ti = t.inference(0.05, 'two_tailed', false, 'interp', true)
```

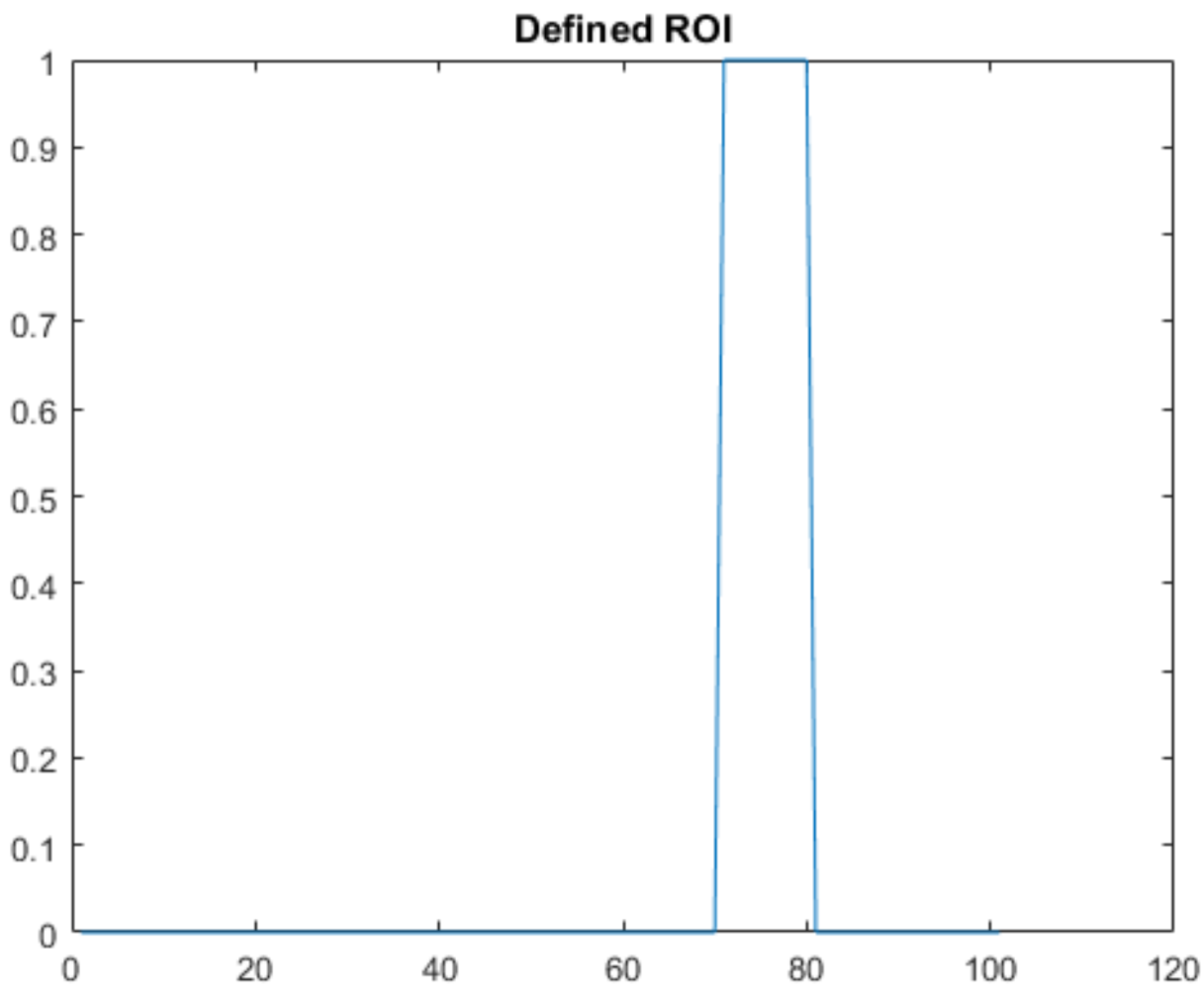
Circular fields

```
ti = t.inference(0.05, 'circular', true)
```

Region of interest

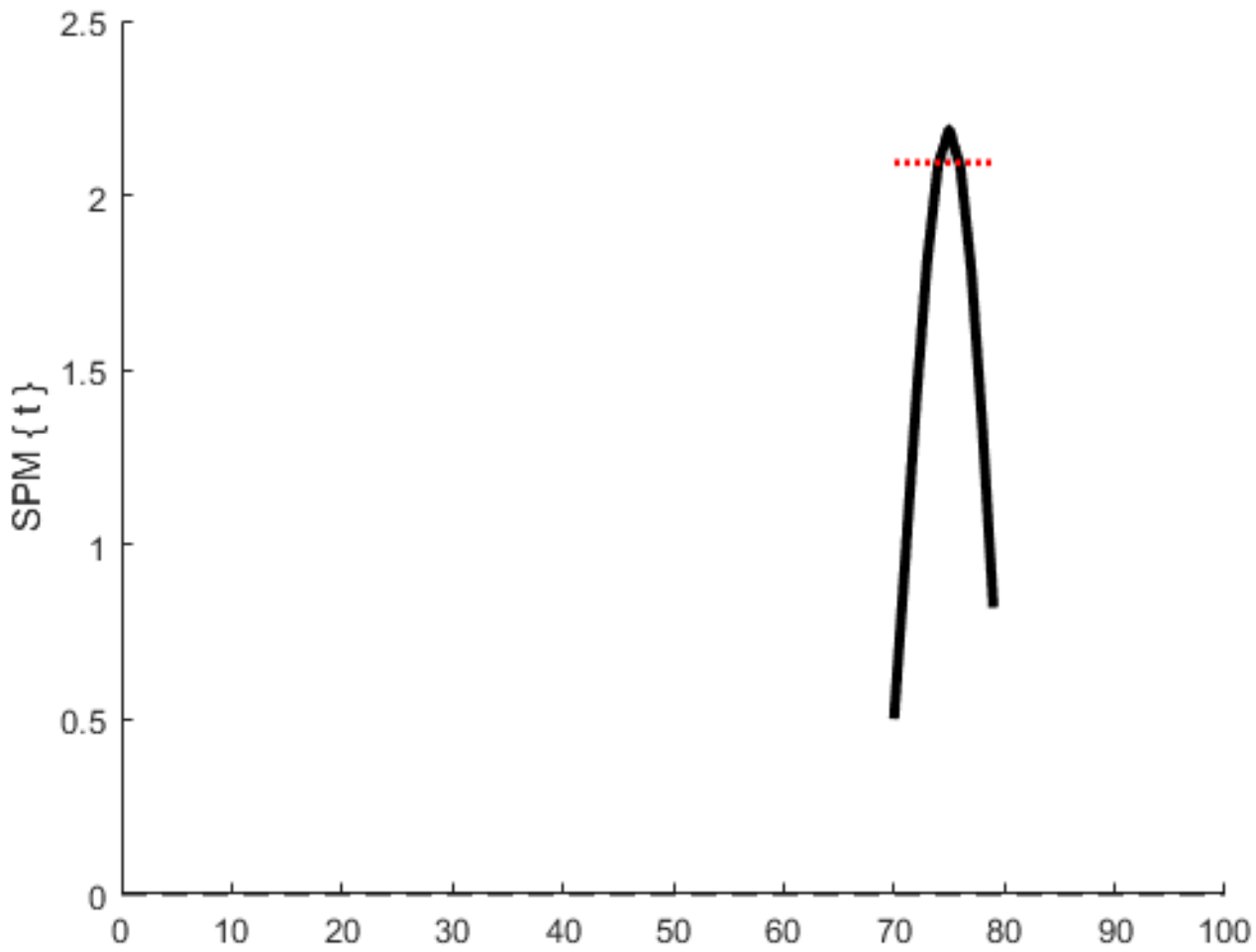
In [21]:

```
dataset = spm1d.data.uv1d.t1.SimulatedPataky2015a();
[Y,mu]  = deal(dataset.Y, dataset.mu);

% Create a region  of interest (ROI):
roi         = false( 1, size(Y,2) );
roi(71:80) = true;
plot(roi); title('Defined ROI');
```



In [22]:

```
%(1) Conduct SPM analysis:
spm        = spm1d.stats.ttest(Y - mu, 'roi', roi);
spmi       = spm.inference(0.05, 'two_tailed', false, 'interp',true)
;
plot(spmi)
```



5. Help

spm1d website: www.spm1d.org

matlab help forum: https://github.com/0todd0000/spm1dmatlab/issues (https://github.com/0todd0000/spm1dmatlab/issues)
Python help forum: https://github.com/0todd0000/spm1d/issues (https://github.com/0todd0000/spm1d/issues)

INTERPRETATION & REPORTING

Jos Vanrenterghem

26 July 2017
ISB Brisbane

Reporting SPM methods

26 July 2017
ISB Brisbane

SPM Methods

[Data treatment – smoothing, averaging]

a) Statistical tests used

b) SPM code & analysis software

c) Refer to key SPM/RFT literature

- Friston KJ, Holmes AP, Worsley KJ, Poline JB, Frith CD, Frackowiak RSJ (1995). Statistical parametric maps in functional imaging: a general linear approach. *Human Brain Mapping* **2**, 189–210.
- SPM documentation repository, Wellcome Trust Centre for Neuroimaging: http://www.fil.ion.ucl.ac.uk/spm/doc/

SPM Methods

[Data treatment – smoothing, averaging]

a) Statistical tests used
b) SPM code & analysis software
c) Refer to key SPM/RFT literature
d) Define terminology
e) Specify alpha – correction?
f) How results will be interpreted

Example

Statistical parametric mapping (SPM, Friston et al., 2007) was used to statistically compare walking speeds. Specifically a SPM two-tailed paired *t*-test was used to compare the longitudinal arch angle during normal versus fast walking (α=0.05). The scalar output statistic, SPM{*t*}, was calculated separately at each individual time node and is referred to as a Statistical Parametric Map. At this stage it is worth noting that SPM refers to the overall methodological approach, and SPM{*t*} to the scalar trajectory variable. The calculation of SPM{*t*} simply indicates the magnitude of the Normal-Fast differences, therefore with this variable alone we cannot accept or reject our null hypothesis. To test our null hypothesis we next calculated the critical threshold at which only α % (5%) of smooth random curves would be expected to traverse. This threshold is based upon estimates of trajectory smoothness via temporal gradients [Friston et al., 2007] and, based on that smoothness, Random Field Theory expectations regarding the field-wide maximum [Adler and Taylor, 2007]. Conceptually, a SPM paired t-test is similar to the calculation and interpretation of a scalar paired t-test; if the SPM{*t*} trajectory crosses the critical threshold at any time node, the null hypothesis is rejected. Typically, due to waveform smoothness and the inter-dependence of neighbouring points, multiple adjacent points of the SPM{*t*} curve often exceed the critical threshold, we therefore call these "supra-threshold clusters". SPM then uses Random Field Theory expectations regarding supra-threshold cluster size to calculate cluster specific *p*-values which indicate the probability with which supra-threshold clusters could have been produced by a random field process with the same temporal smoothness [Adler and Taylor, 2007]. All SPM analyses were implemented using the open-source spm1d code (v.M0.1, www.spm1d.org) in Matlab (R2014a, 8.3.0.532, The Mathworks Inc, Natick, MA).

Example

Statistical parametric mapping (SPM, Friston et al., 2007) was used to statistically compare walking speeds. Specifically a SPM two-tailed paired *t*-test was used to compare the longitudinal arch angle during normal versus fast walking (α=0.05). The scalar output statistic, SPM{*t*}, was calculated separately at each individual time node and is referred to as a Statistical Parametric Map. At this stage it is worth noting that SPM refers to the overall methodological approach, and SPM{*t*} to the scalar trajectory variable. The calculation of SPM{*t*} simply indicates the magnitude of the Normal-Fast differences, therefore with this variable alone we cannot accept or reject our null hypothesis. To test our null hypothesis we next calculated the critical threshold at which only α % (5%) of smooth random curves would be expected to traverse. This threshold is based upon estimates of trajectory smoothness via temporal gradients [Friston et al., 2007] and, based on that smoothness, Random Field Theory expectations regarding the field-wide maximum [Adler and Taylor, 2007]. Conceptually, a SPM paired t-test is similar to the calculation and interpretation of a scalar paired t-test; if the SPM{*t*} trajectory crosses the critical threshold at any time node, the null hypothesis is rejected. Typically, due to waveform smoothness and the inter-dependence of neighbouring points, multiple adjacent points of the SPM{*t*} curve often exceed the critical threshold, we therefore call these "supra-threshold clusters". SPM then uses Random Field Theory expectations regarding supra-threshold cluster size to calculate cluster specific *p*-values which indicate the probability with which supra-threshold clusters could have been produced by a random field process with the same temporal smoothness [Adler and Taylor, 2007]. All SPM analyses were implemented using the open-source spm1d code (v.M0.1, www.spm1d.org) in Matlab (R2014a, 8.3.0.532, The Mathworks Inc, Natick, MA).

midfoot, medial and lateral forefoot, and hallux (Fig. 1). Markers were placed by the same researcher for all subjects. First, a static measurement was recorded for 5 s to define the different segments of the Ghent Foot Model (GFM). During this measurement, the subject had to perform a tandem stand with the tested leg in front and the front knee slightly flexed so that the lower leg was perpendicular to the floor.

During the gait measurements, speed was monitored using [illegible]Hz), which was [illegible] to walk bare-[illegible]6 m·s^{-1}) while [illegible]l. During run-[illegible]ed of 3.5 m·s^{-1} [illegible] running was [illegible] first allowed [illegible]cedure by per-[illegible] The actual test [illegible]aptured. Trials [illegible]ge, if two feet [illegible]een to show an [illegible] attempt to hit [illegible]essed by using [illegible] The dependent [illegible] joint angles of [illegible]he GFM. Be-[illegible]nates were fil-[illegible]-pass filter at [illegible] with 50 points [illegible]sing Euler ro-[illegible], Y-, and Z-axis [illegible]agittal plane), [illegible]ction/adduction [illegible]ance phase was [illegible]e ground reac-[illegible]n each point in [illegible] rigid foot was [illegible]teral malleolus,

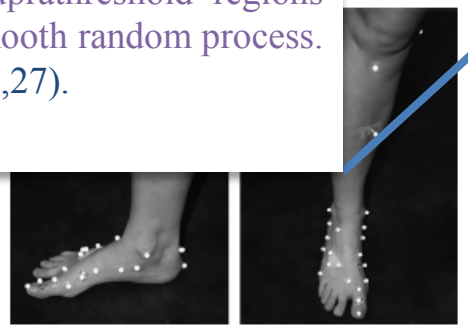


FIGURE 1—Marker locations according to the Ghent Foot Model.

and the head of the first and fifth metatarsal heads. The other segments were defined according to the multisegmented GFM (7). For each subject, the three trials per condition were averaged.

To compare between groups, a curve analysis was performed using statistical parametric mapping (SPM) (13). Initially, ANOVA over the normalized time series was used to establish the presence of any significant differences between the three groups. If statistical significance was reached, *post hoc* *t*-tests over the normalized time series were used to determine between which groups significant differences occurred. For both the ANOVA and *t*-test analyses, SPM involved four steps. The first was computing the value of a test statistic at each point in the normalized time series. The second was estimating temporal smoothness on the basis of the average temporal gradient. The third was computing the value of test statistic above which only $\alpha = 5\%$ of the data would be expected to reach had the test statistic trajectory resulted from an equally smooth random process. The last was computing the probability that specific suprathreshold regions could have resulted from an equivalently smooth random process. Technical details are provided elsewhere (13,27).

RESULTS

Curve Analyses

Overall, rotations in the frontal plane representing inversion/eversion showed significant ANOVA results ($P < 0.05$) for the rigid foot, the rear foot, the midfoot, and the medial forefoot during midstance and late stance. Furthermore, ANOVA results ($P < 0.05$) indicated differences in rotations in the sagittal and transversal plane for the rear foot during walking. *Post hoc* analysis results are presented below and showed similar findings for both the CAI and coper group compared with the control group. No differences were found for plantarflexion/dorsiflexion and abduction/adduction angles for both running and walking data in the *post hoc* analysis.

Foot (rigid foot in relation to the shank). Walking analysis showed a significantly greater eversion angle in the CAI group, from 11% to 73% of the stance phase (average difference of 2.17°, $P < 0.001$), and in the coper group, from 19% to 73%, compared with that in the control group (average difference of 2.19°, $P < 0.001$). During the significant period of this midstance phase, the foot first progressed toward a maximally everted position and then subsequently inverted toward the end of this phase (Fig. 2). No significant differences were found for the running data.

Rear foot (in relation to the shank). The running trials exhibited a significantly greater eversion of the rear foot in the CAI group, from 56% to 73% of the stance phase (average difference of 2.72°, $P = 0.045$), and in the coper group, from 29% to 86% (average difference of 3.47°, $P = 0.001$), compared with controls. The rear foot reached a maximally everted position in the beginning of the midstance

To compare between groups, a curve analysis was performed using statistical parametric mapping (SPM) (13). Initially, ANOVA over the normalized time series was used to establish the presence of any significant differences between the three groups. If statistical significance was reached, post hoc t-tests over the normalized time series were used to determine between which groups significant differences occurred. For both the ANOVA and t-test analyses, SPM involved four steps. The first was computing the value of a test statistic at each point in the normalized time series. The second was estimating temporal smoothness on the basis of the average temporal gradient. The third was computing the value of test statistic above which only > = 5% of the data would be expected to reach had the test statistic trajectory resulted from an equally smooth random process. The last was computing the probability that specific suprathreshold regions could have resulted from an equivalently smooth random process. Technical details are provided elsewhere (13,27).

Reporting SPM results

t-tests

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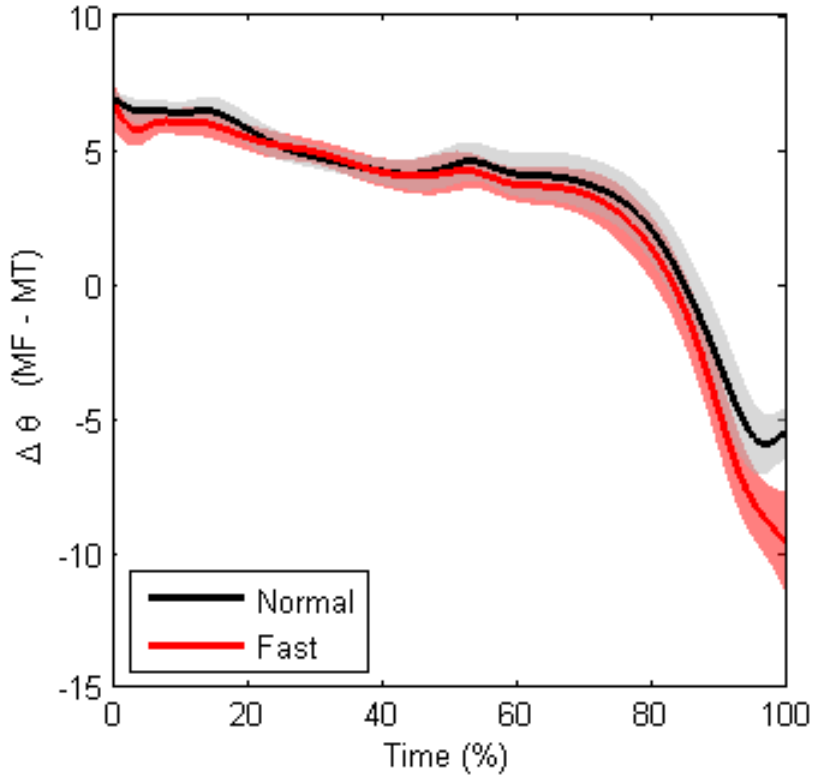
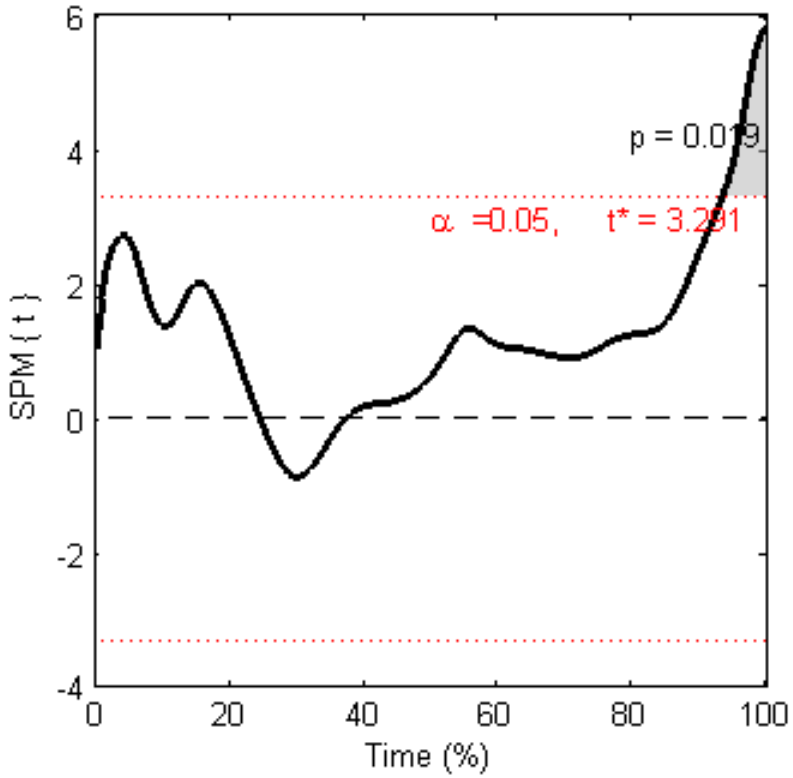
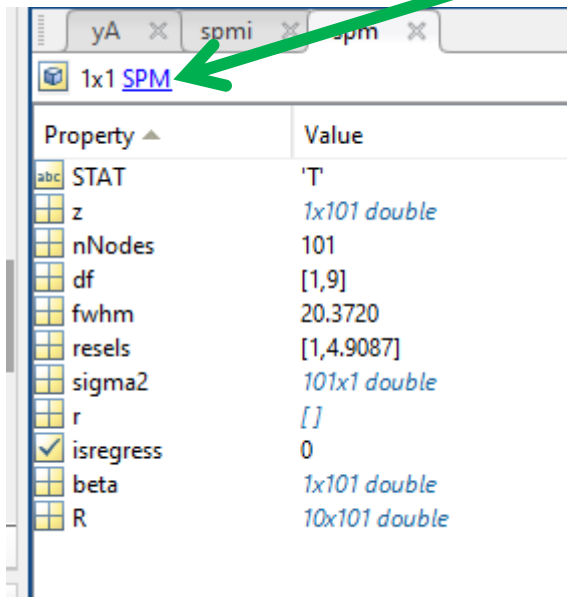
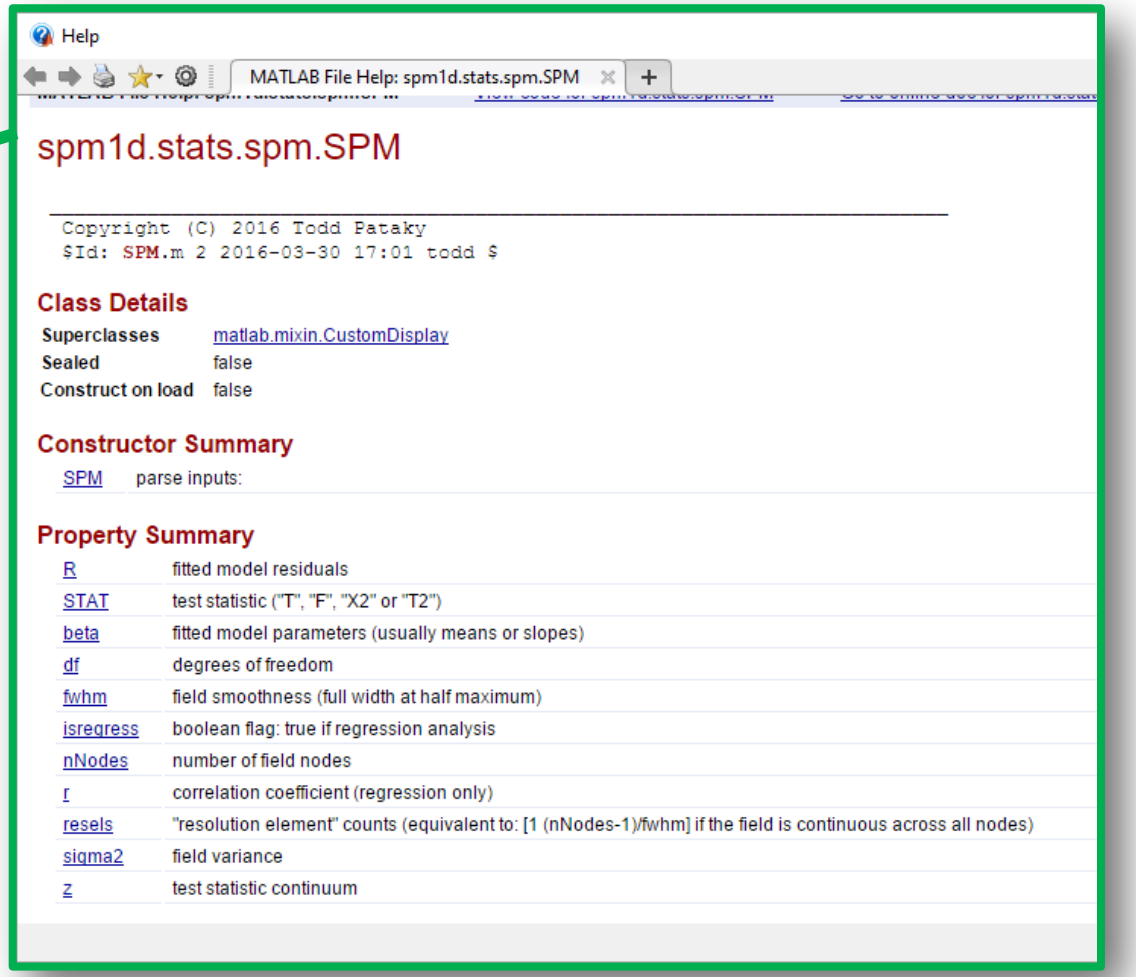

10
5
0
-5
-10
-15
Δ θ (MF - MT)
0
20
40
60
80
100
Time (%)
Normal
Fast

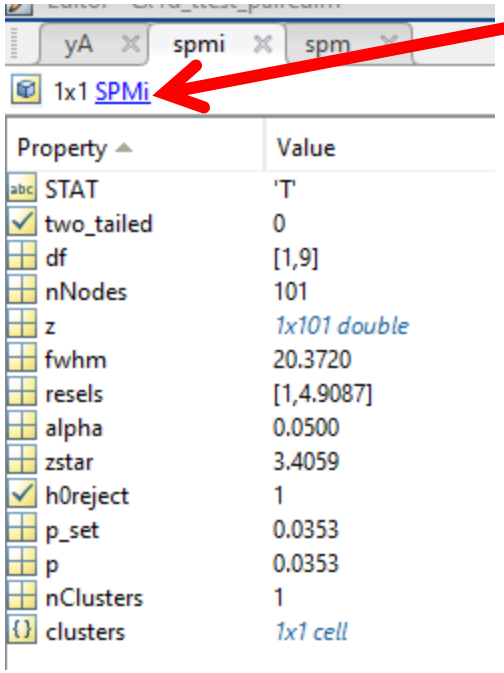

6
4
2
0
-2
-4
SPM { t }
p = 0.019
α =0.05,
t* = 3.291
0
20
40
60
80
100
Time (%)

the “SPM” variable





the “SPMi” variable



spm1d.stats.spm.SPMi

```
Copyright (C) 2016 Todd Pataky
$Id: SPMi.m 1 2016-01-04 16:07 todd $
```

Class Details

Superclasses	matlab.mixin.CustomDisplay, handle
Sealed	false
Construct on load	false

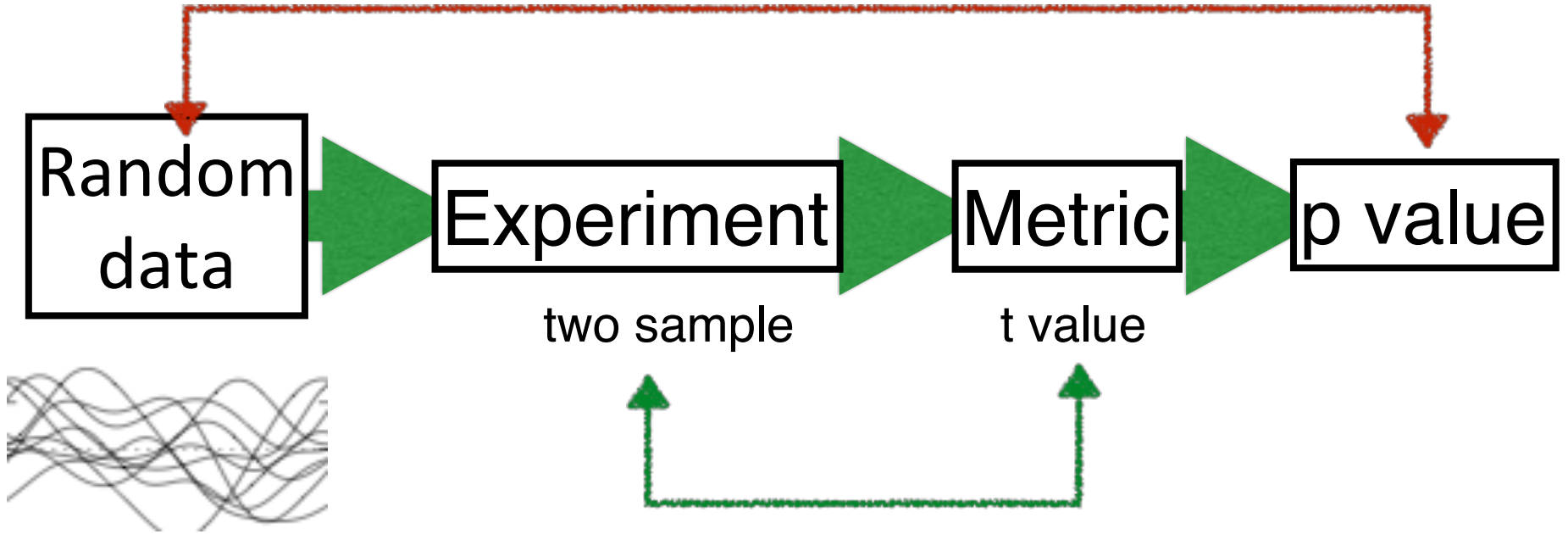
Constructor Summary

SPMi

Property Summary

STAT	test statistic ("T", "F", "X2" or "T2")
alpha	type I error rate
clusters	cluster objects
df	degrees of freedom
fwhm	field smoothness (full width at half maximum)
h0reject	null hypothesis rejected?
nClusters	number of supra-threshold clusters
nNodes	number of continuum nodes
p	cluster-level inference
p_set	set-level inference
resels	"resolution element" counts
two_tailed	
z	test statistic continuum
zstar	critical test statistic threshold (at alpha)

Infinite set of experiments



One experiment

SPM and SPMi

SPM	
Name	Size or value
STAT	T
z	1x100 double
nNodes	100
df	[1,9]
fwhm	11.2192
resels	[1,8.8242]
sigma2	1x100 double
r	[]
isregress	0
beta	1x100 double
R	10x100 double

SPMi	
Name	Size or value
alpha	0.05
two_tailed	0
zstar	3.8213
h0reject	1
p_set	0.031
p	0.031
nClusters	1
clusters	1x1 cell

Results

Key information to present:

a) Was the critical threshold exceeded?

b) Direction of effect

c) Consequence for the null hypothesis

d) Descriptive data:

critical threshold, p-value/s, number of supra-threshold clusters, extent of clusters, degrees of freedom.

Results section bad example

The mean arch angles during normal and fast walking were highly similar for the majority of time except for the very last bit of the walking cycle (figure 1a). The arch angle during fast walking were significantly different between normal and fast walking (figure 1b, p=0.024).

Results section ‘better’ example

The mean arch angles during normal and fast walking were highly similar for the majority of time (figure 1a). However one supra-threshold cluster (96-100%) exceeded the critical threshold of 3.933 as the arch angle during fast walking was significantly more negative than during normal walking (figure 1b). The precise probability that a supra-threshold cluster of this size would be observed in repeated random samplings was p=0.024. The null hypothesis was therefore rejected.

Figure caption

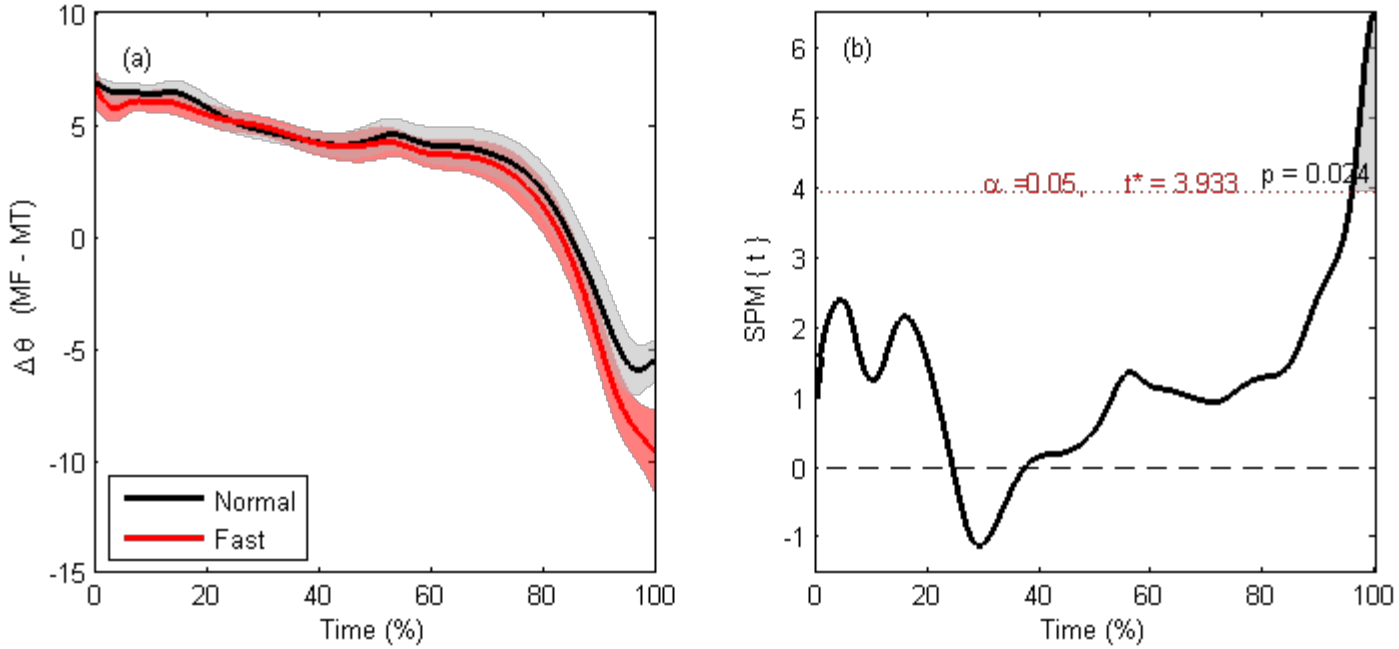


Figure 1 a) Mean trajectories for longitudinal arch angles during normal (black) and fast (red) walking. b) The paired samples t-test statistic SPM {*t*}. The critical threshold of 3.933 (red dashed line) was exceeded at time = 96% with a supra-threshold cluster probability value of p=0.024 indicating a significantly more negative angle in the fast condition.

Reporting SPM results

Regression

26 July 2017
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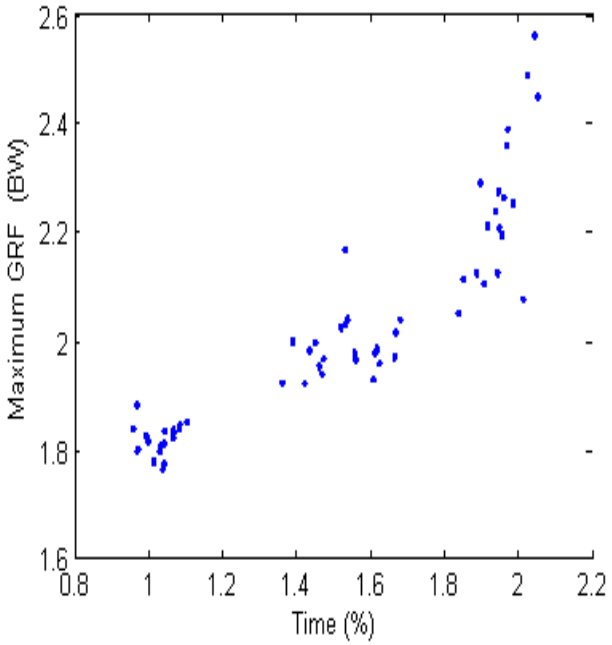
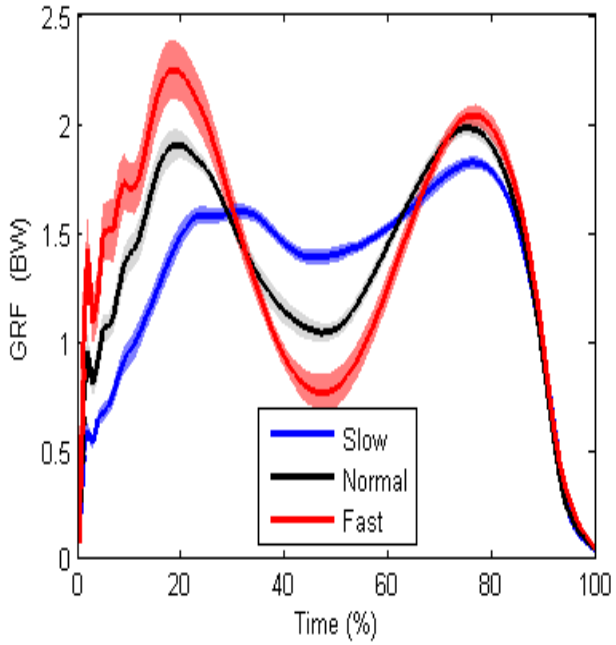
Regression

```
spm  = spm1d.stats.regress(Y, x);
spmi = spm.inference(0.05, 'two_tailed', true);
```

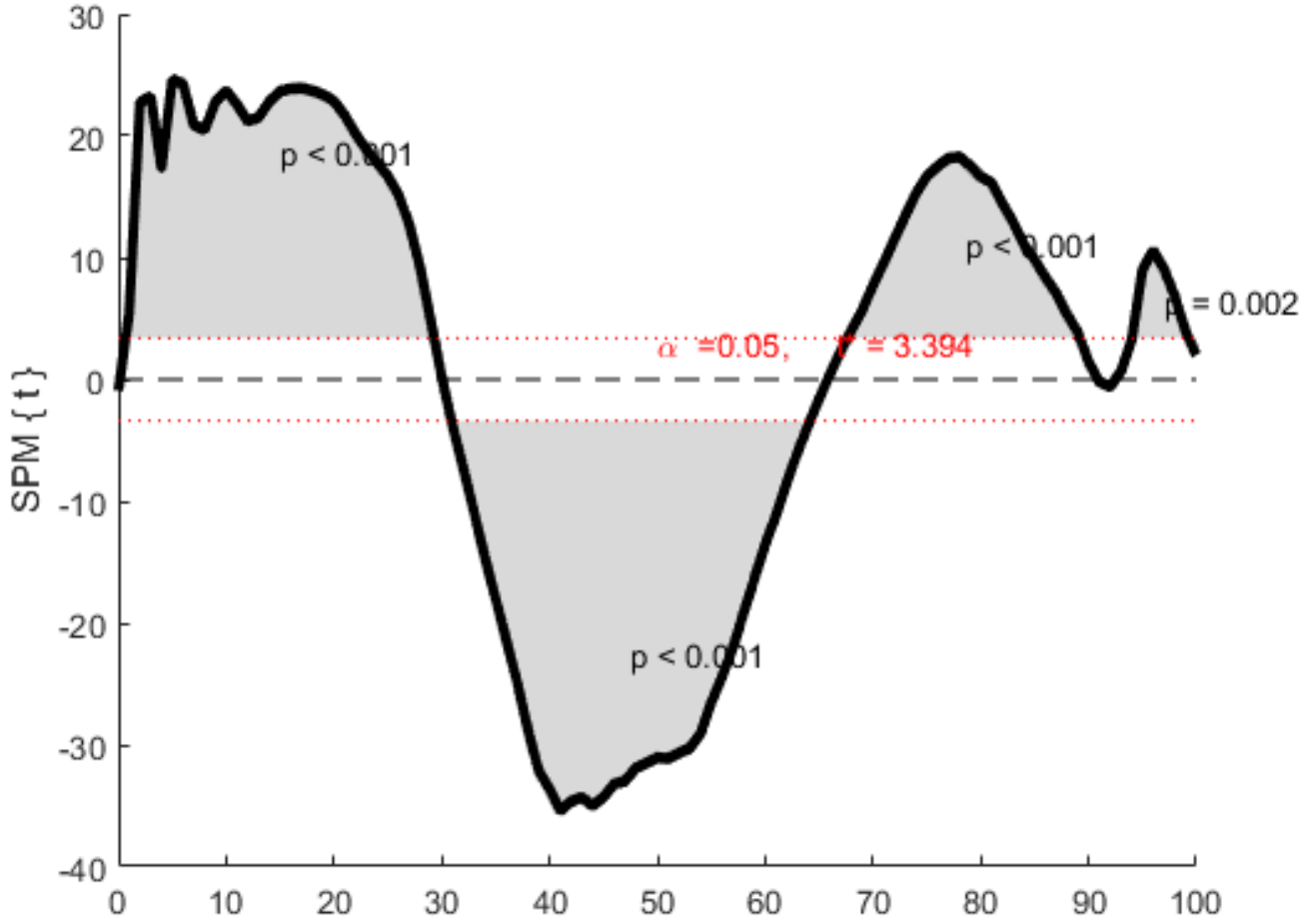


"x" independent variable
walking speed



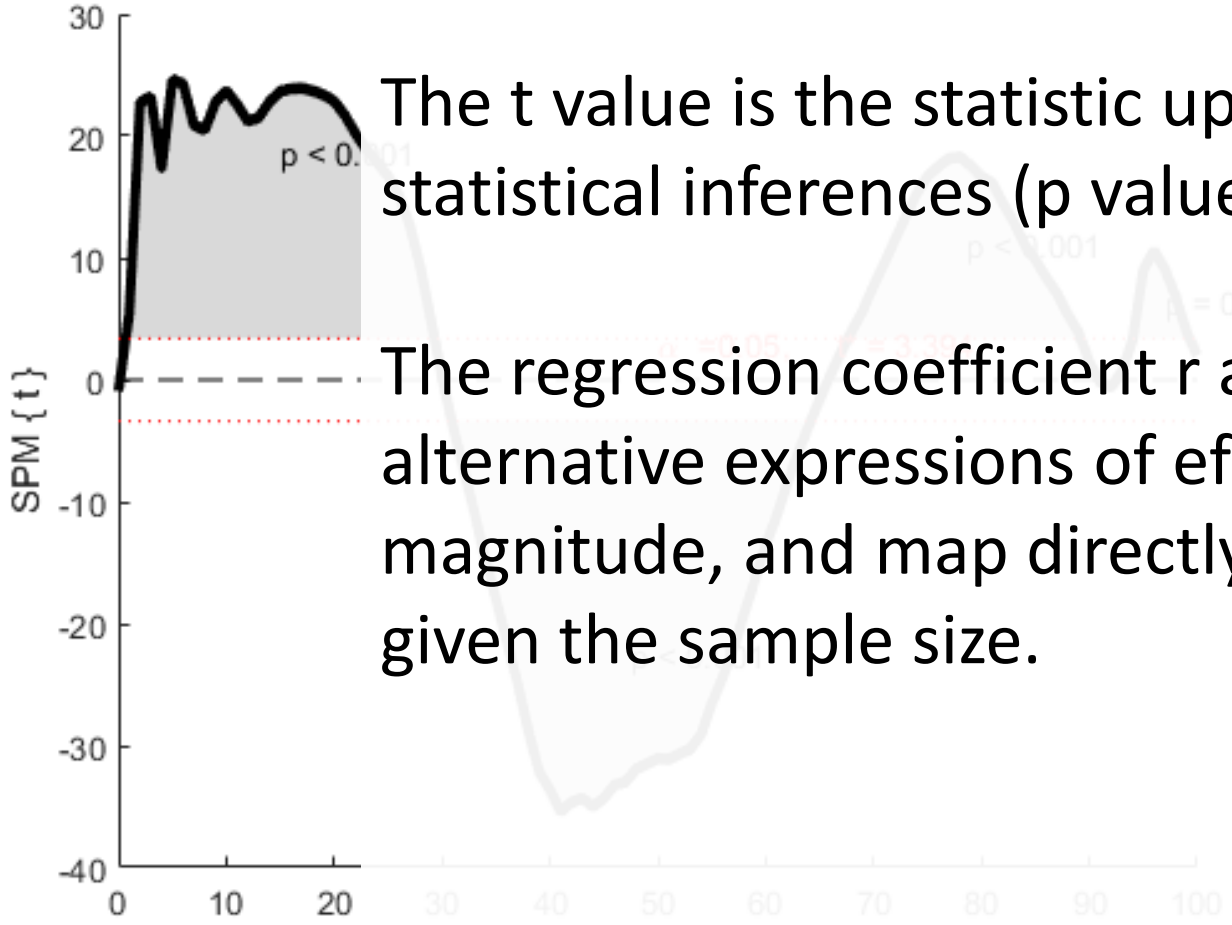
"Y" dependent variable
vertical GRF trajectories

SPM output



spm1D 0.4

SPM output



The t value is the statistic upon which statistical inferences (p values) are based.

The regression coefficient r and t value are alternative expressions of effect magnitude, and map directly to each other given the sample size.

ression interpretation

Critical threshold

Direction effect

There was a significant relationship between walking speed and vGRF. A greater walking speed significantly increased the vGRF during the first and last 30% stance but significantly reduced GRF from ~30-70% stance. As random data would produce this effect <5% time the null hypothesis was therefore rejected.

Null hypothesis

Example methods/results

- Pataky TC (2010). Generalized n-dimensional biomechanical field analysis using statistical parametric mapping. *Journal of Biomechanics* 43, 1976-1982.
- Pataky TC (2012) One-dimensional statistical parametric mapping in Python. *Computer Methods in Biomechanics and Biomedical Engineering*. 15, 295-301.
- Pataky TC, Robinson MA, Vanrenterghem J (2013). Vector field statistical analysis of kinematic and force trajectories. *Journal of Biomechanics* 46 (14): 2394-2401.

www.spm1d.org

Applications

- Vanrenterghem, J., Venables, E., Pataky, T., Robinson, M. (2012). The effect of running speed on knee mechanical loading in females during side cutting. *Journal of Biomechanics*, *45*, 2444-2449.
- De Ridder, R., Willems, T., Vanrenterghem, J., Robinson, M., Pataky, T., Roosen, P. (2013). Gait kinematics of subjects with chronic ankle instability using a multi-segmented foot model. *Medicine and Science in Sports and Exercise*, 45, 2129-2136.
- Robinson, M.A., Donnelly, C.J., Tsao, J., Vanrenterghem, J. (2014). Impact of knee modelling approach on indicators and classification of ACL injury risk. Medicine & Science in Sports & Exercise, 46 (7), 1269-1276.