The dynamics of Complex Morpholexical Processes revealed by Searchlight Representational Similarity Analysis of MEG/EEG Data

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Introduction

Although the neural basis of speech comprehension has been a growing focus for neuroimaging research, detailed neural models of morpho-lexical processing are notably absent.

Here we explore how the underlying properties of lexical constituents are computed in neural networks situated in bilateral fronto-temporal brain regions associated with speech comprehension [1,2]. In particular, we target the neurocognitive processes that are triggered as a regular inflectional morpheme is heard (the English past tense {*-ed*}).

A novel method that reveals the fine grained structure of neural computation (with centimetre and millisecond precision) has been developed based on the Representational Similarity Analysis (RSA, c.f. [3,4]) of combined MEG/EEG data in source space using spatio-temporal "searchlight" techniques.

RSA is a variation of Multivariate Pattern Analysis (MVPA), which has been successfully applied to fMRI data [3]. RSA is based on the pattern-information that is naturally embedded in multi-channel recording of neural activations. Specifically, we search the data in time and space for neurocomputational signatures that are correlated to theoretical models.

Methods

Participants
17 healthy, right-handed, native English speakers

Conditions	Examples	Phonological Cues	Inflection
Regular past tense	Played	Yes	Yes
Pseudo-inflection	Trend	Yes	No
Uninflected	Cream	No	No

Experimental Conditions
80 items in regular past tense and uninflected conditions,
40 items in pseudo-inflection condition matched on length, lemma and word form frequency, ngram frequency, and N size.

Procedure
Speech comprehension tasks with one-back memory in combined MEG/EEG to test the modulation of lexical complexity

MEG/EEG Acquisition
306-channel Vectorview MEG, 70-channel EEG and three-compartment boundary-element forward model using structural MRI (3T).

Multimodal Source Reconstruction
The source estimation of MEG/EEG data were performed using minimum-norm estimation [5], which computes a distributed-source solution combining both MEG and EEG scalp information.

Alignment to Inflectional Rhyme Pattern (IRP)
MEG/EEG time-series are aligned to the point of closure in the speech signal corresponding to the onset of the word-final coronal stop ([d] or [t] associated with a potential past tense morpheme (known as the Inflectional Rhyme Pattern or IRP), or to the onset of last phoneme in the uninflected condition. Epochs were analysed between -200 and +200ms.

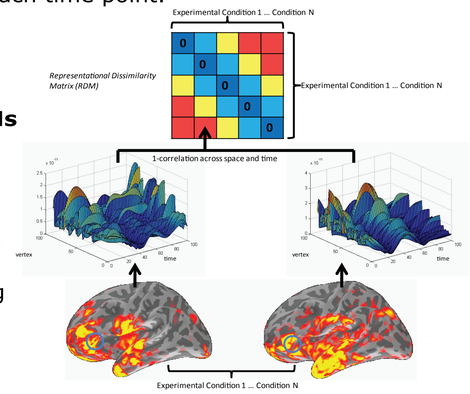
Searchlight Representational Similarity Analysis

First Level Analysis: Construct Representational Dissimilarity Matrix (RDM) for Individuals

The first level of RSA is the computation of similarity structures that express the dynamic patterns of neural activation over space and time. The primary data type that encodes such similarity structure is the representational dissimilarity matrix (RDM). Each entry in an RDM is the correlation-distance (e.g. one minus the correlation value) between activation patterns elicited by a pair of experimental conditions within a specific experimental design. The result of the first level analysis is a set of brain-based RDMs for each participant at each spatial location and each time point.

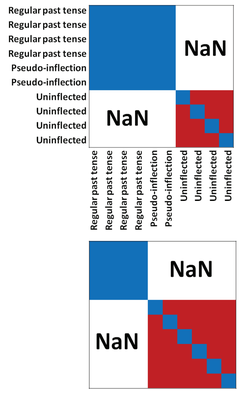
Second Level Analysis: Compare Brain-based RDMs to Theoretical Models and Group Statistics

Theoretical models can also be represented by RDMs (see below). In the second level of analysis, the resulting brain-based RDMs are compared to model RDMs.



A "searchlight" algorithm [3] is used to localise pattern information by searching across the entire brain. For MEG/EEG time-series, this combines with a temporal sliding window to separate effects in time [4]. The output indicates when and where in the brain each model fits to the patterns of neural activity.

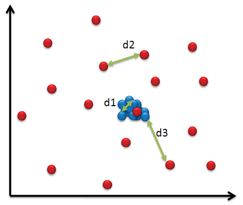
Group statistics are based on nonparametric methods, such as permutation testing, and cluster level statistics. This controls for false positive arised from multiple comparisons without making any assumptions about the distribution of the signal and noise.



Hypothesis and Model RDMs

Phonological model
predicts a pattern of neural activation that is more similar for words that share the same phonological cue (the IRP) than for words in uninflected conditions.

Morphosyntactic Model
predicts a pattern of neural activation that distinguishes 'real' inflected words from pseudo- and uninflected cases.

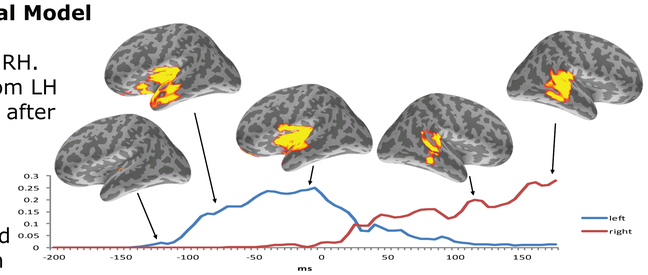


NaN = "not a number"

Results

Phonological Model

LH precedes RH. Switching from LH to RH occurs after the IRP.

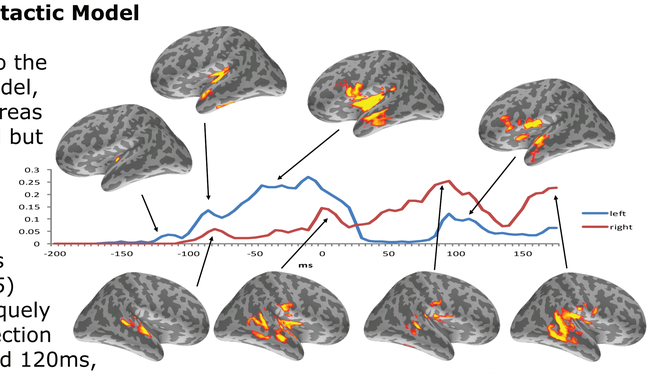


The time series plots are computed using PCA on the ($p<0.05$) thresholded T-map generated from the cluster level analysis described previously. The y-axis is the coefficients for the first component and the x-axis is time in ms with the IRP onset (stop closure) as time zero.

Morphosyntactic Model

Compared to the previous model, similar RH areas are engaged but with earlier onset.

Left inferior frontal areas (BA44, BA45) respond uniquely to 'real' inflection at -40ms and 120ms, suggesting that these regions distinguish real inflection from pseudo-inflection. The active regions in RH respond to both real inflection and pseudo-inflection.



Conclusions

* The left perisylvian area starts to engage with the phonological properties of inflection as early as 120ms prior to the IRP.

* RH effects are seen later and more posteriorly.

* The morphosyntactic model identifies a specific effect of inflection in left inferior frontal areas both early and late relative to the IRP.

* The two models reflect separable levels of processing of inflectional morphemes, engaging bilateral temporal and left lateralised frontal systems.

* Searchlight RSA and nonparametric statistics, applied to time resolved neuroimaging extracted from combined MEG and EEG, can rigorously integrate multiple neurocognitive components that participate in large-scale dynamic interactions in the brain.

References

[1] Bozic, M., Tyler, L.K., Ives, D.T., Randall, B., and Marslen-Wilson, W.D. (2010) PNAS, 107(45), 17439-17444. [2] Marslen-Wilson, W.D., and Tyler, L.K. (2007) Phil.Tran. of the Royal Society B: Biological Sciences, 362, 823-836. [3] Kriegeskorte, N., Goebel, R. and Bandettini, P. (2006) PNAS, 103, 3863-3868. [4] Su, L., Wingfield, C., Bozic, M., Fonteneau, E. Marslen-Wilson, W.D and Kriegeskorte, N. (2010) HBM 2010. [5] Hamalainen M.S. and Ilmoniemi, R.J. (1994) Med Biol Eng Comput, 32, 35-42.