

The optimum-1 as a new tool for developmentalists: a time efficient MMN paradigm



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Introduction

- ▶ The mismatch response (**MMR**) is an *event related potential (ERP)* triggered by the **perception of a change**.
- **Precious tool** to test **passively infants' auditory perception** of linguistic stimuli (see Cheour et al, 2000 for a review).
- ▶ ERPs require **large number of trials** **AND** MMN paradigm usually feature **80% of standards stimuli and only 20% of deviants stimuli**
- This result in a **high attrition rate** (up to 75% according to Hoehl & Wahl, 2012).
- ▶ The **optimum-1 paradigm** (Näätänen et al, 2004) **can solve this**

Method

In optimum-1 paradigm, standards and deviants are presented alternatively.

6 complex tones were made using the frequencies of English vowels of the en1 voices generated in MBROLA (Dutoit et al., 1996).

Tones can be found on <https://osf.io/8jcpy/>

Sound	Status	F1	F2	F3
ɒ	standard	827	2541.1	3445.1
e	deviant	1672.3	2343.5	3395.8
ʊ	deviant	1142.6	2077.1	3247.4
ʌ	deviant	1254.2	2343.1	3291.5
ɜ:	deviant	1380.6	2221.8	3321.6
ə	deviant	1289.6	2237.3	3321

Time

2 blocks of 85 standards and 17 deviants of each kind, presented in alternation with an ISI of 500 ms (2.3 minutes per block)

The optimum-1 is used as a **localizer** for our main task (see Fort et al., 2017). We plan to find **each participant's MMR using a cluster-based permutation**

Results

Pre-processing

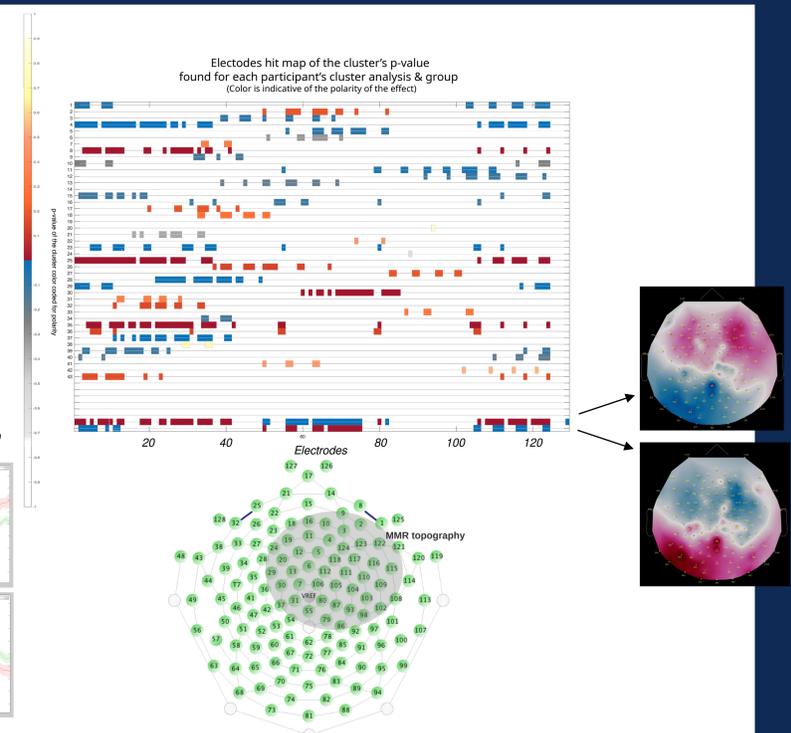
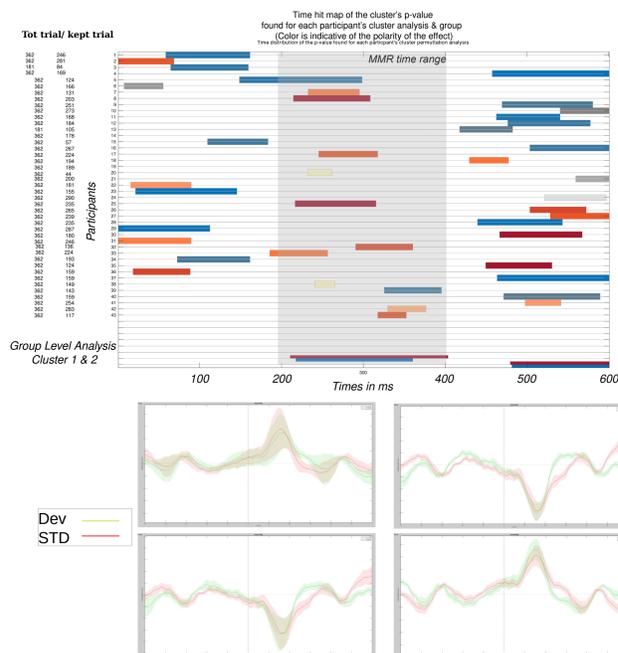
Data were segmented between **-500ms to 600ms** after stimulus onset
Contaminated channels by artefacts were rejected using custom functions based on EEGLAB toolbox (see Pena et al, 2012).
Channels presenting **local deviations > 80 µV** were excluded from trials
Trials with more than **40% contaminated channels** were rejected. Excluded channels were interpolated for each trial separately by using a linear interpolation (EEGLAB)

We conducted a **per participant cluster-based permutation analysis** comparing the **Standard tone** trials to the **Deviant tone** trials using the Fieldtrip toolbox (Oostenveld, et al., 2011) with 10,000 iterations.

We consider the **0-600 ms** time window in which the MMR should be observed if present where we excluded the electrodes at the edge of the scalp.

Results display THE cluster (positive or negative) featuring the largest **abs(t-value)**.

Another cluster-based permutation analysis was run using the group data to compare how the group analysis reflect the individual data.



Conclusion

- ▶ The **optimum-1 paradigm** was useful to trigger mismatch negativity (**MMR**) is a minimum amount of time (less than **5min for 362 trials**)
- **The fussiest baby end up with 40 clean trials to analyse.** (Avg trials 189)
- ▶ The amount of data collected allowed to run a **per-participants cluster analysis** and clusters appear significant
- This will allow us to run tailored individual analysis