## EEGLAB Bad Electrode Detection

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March 12, 2017

## 1 Joint Probability

- 1.1 Wrapper Function
- 1.2 Actual Function
- 1.3 Histogram Binning Function

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Algorithm 1 jointprob: wrapper function to apply joint probability detection for EEGLAB
function across the dataset.
Input: INEEG \in \mathbb{R}^{C \times T \times N} input EEG data, C = number of channels, N = number of time-
    points, T = number of trials. NOTE: the EEGLAB EEG object has other metadata
    objects attached to it
Input: icacomp \in [1|0], which type of data to run on: 1 = electrode data, 0 = ICA component
    activations. 1 is default
Input: elecrange \in \mathbb{R}^{j \leq C}, which electrodes to inspect for rejections
Input: locthresh \in \mathbb{R}, threshold for single electrode inspection
Input: globthresh \in \mathbb{R}, threshold for all electrode detection
Input: superpose and reject, other extra variables in EEGLAB that aren't relevant to the
    algo
Output: OUTEEG \in \mathbb{R}^{C \times N \times T} output EEG data, C = number of channels, N = number of
    timepoints, T = number of trials. The metadata has been updated, not the actual
    data.
 1: procedure POP\_JOINTPROB(INEEG, icacomp, electronge, locthresh, globthresh)
 2:
       if icacomp == 0 then
                                                              ▶ If running on ICA components
          Prompt running ICA on INEEG if not run vet
 3:
       if icacomp == 1 then
 4:
          tmpdata = strip\_metadata(INEEG)
 5:
 6:
          if empty(INEEG.jpE) then
                                                        ▶ If joint prob hasn't been done before
 7:
              This is for joint prob across each individual electrode
              INEEG.jpE, rejE = jointprob(tmpdata, locthresh, EEG.stats.jpE, 1) \triangleright Run
 8:
    it, get the prob distributions and the rejected electrodes
 9:
          This is for joint prob across all electrodes
10:
          tmpdata2 = permute(tmpdata, [312])
                                                       > switch the order of the dimensions to
    T \times C \times N
```

 $INEEG.jp, rej = jointprob(tmpdata, globthresh, EEG.stats.jp, 1) \triangleright Run it, get$ 

 $\triangleright$  combine into 2D  $T \times (C \times N)$ 

tmpdata2 = reshape(tmpdata2, size(tmpdata2, 1),

return (return nothing, EEG was directly modified)

size(tmpdata2, 2) \* size(tmpdata2, 3))

the prob distributions and the rejected electrodes

11:

12:

13:

14:

Algorithm 2 jointprob: histogram binning implementation of joint probability function.

**Input:**  $S \in \mathbb{R}^{C \times T \times N}$ ,  $\mathbb{R}^{T \times N}$ ,  $\mathbb{R}^{N}$ , S = signal, C = number of channels, N = number of time points, T = number of trials.

**Input:**  $threshold \in \mathbb{R}$ , Absolute threshold. If normalization is used then the threshold is expressed in standard deviation of the mean. 0 means no threshold.

**Input:**  $oldjp \in \mathbb{R}^{C \times T}$ , pre-computed joint probability (only perform thresholding). Default is the empty array [].

**Input:**  $normalize \in [0|1|2]$ , 0 = do not not normalize entropy. 1 = normalize entropy. 2 is 20% trimming (10% low and 10% high) proba. before normalizing. Default is 0.

**Input:**  $discret \in \mathbb{R}$ , discretization variable for calculation of the discrete probability density. Default is 1000 points.

**Output:**  $jp \in \mathbb{R}^{C \times T}$ , normalized joint probability of the single trials

Output:  $rej \in \mathbb{R}^{C \times T}$ , Only 1's and 0's, all rejected electrodes per trial

```
1: procedure JOINTPROB(S, threshold, jp, normalize, discret)
        jp = zeros(C, T)
        if exists(oldjp) then
 3:
            jp = oldjp
 4:
        else
 5:
            for c = 1 : C do
                                                                                ▶ Compute Density Function
 6:
                 prob, dist = realproba(S(c,:), discret)
 7:
                 for t = 1 : T do
                                                                                8:
                     tmp = prob((t-1) \times n + 1, t \times n + 1)
 9:
                     jp(c, t) = -\sum (\log(tmp))
                                                                                                 ⊳ log-likelihood
10:
        tmpip = ip
11:
12:
        if normalize == 2 then
            tmpjp = sort(jp)
13:
            tmpjp = tmpjp (round(length(tmpjp) \times 0.1):end-round(length(tmpjp) \times 0.1))
14:
            if ndims(S) = 2 then
jp = \frac{jp - \frac{1}{C \times T} \sum tmpjp}{\sigma(tmpjp)}
15:
16:
            if ndims(S) = 3 then
17:
                 \frac{jp - \sum_{C \times T} \sum_{T} tmpjp \times \text{ones}(1, \text{size}(jp, 2))}{\sigma(tmpjp, 0, 2) \times \text{ones}(1, \text{size}(jp, 2))}
18:
        if length(threshold) ; 1 then
19:
            rej = (threshold(1) > jp)|(jp > threshold(2))
20:
21:
        else
            rej = abs(jp) > threshold
22:
```

```
Algorithm 3 realproba: compute the effective probability of the value in the sample.
Input: D \in \mathbb{R}^{T \times N}, D = \text{data}, N = \text{number of timepoints}, T = \text{number of trials}.
Input: b \in \mathbb{R}, number of bins divided in histogram
Output: P \in \mathbb{R}^{C \times T}, normalized joint probability of the single trials
Output: P_{dist} \in \mathbb{R}^{C \times T}, Only 1's and 0's, all rejected electrodes per trial
 1: procedure REALPROBA(D, b)
          M = T \times N
                                                                                                    \triangleright size = trials x time
 2:
          zeros(1 dimension, b)
 3:
          min = \min(D)
 4:
         max = \max(D)

D = \text{floor}(\frac{D-min}{max-min} \times (b-1)) + 1

for i = 1 : M do
 5:
 6:
 7:
              P_{dist}(D(i)) = P_{dist}(D(i)) + 1
 8:
         P = \frac{P_{dist}(D)}{M}
P_{dist} = \frac{P_{dist}(D)}{M}
 9:
10:
```