

# EEGLAB Bad Electrode Detection

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## 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.

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**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.**

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1: procedure POP_JOINTPROB( $INEEG, icacomp, elecrange, locthresh, globthresh$ )
2:   if  $icacomp == 0$  then                                     ▷ If running on ICA components
3:     Prompt running ICA on  $INEEG$  if not run yet
4:   if  $icacomp == 1$  then
5:      $tmpdata = strip\_metadata(INEEG)$ 
6:     if  $empty(INEEG.jpE)$  then                               ▷ If joint prob hasn't been done before
7:       This is for joint prob across each individual electrode
8:        $INEEG.jpE, rejE = jointprob(tmpdata, locthresh, EEG.stats.jpE, 1)$  ▷ Run
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
 $T \times C \times N$ 
11:       $tmpdata2 = reshape(tmpdata2, size(tmpdata2, 1),$ 
12:         $size(tmpdata2, 2) * size(tmpdata2, 3))$               ▷ combine into 2D  $T \times (C \times N)$ 
13:       $INEEG.jp, rej = jointprob(tmpdata, globthresh, EEG.stats.jp, 1)$  ▷ Run it, get
the prob distributions and the rejected electrodes
14:   return (return nothing, EEG was directly modified)

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

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**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 timepoints,  $T$  = 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

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

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**Algorithm 3** realproba: compute the effective probability of the value in the sample.

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**Input:**  $D \in \mathbb{R}^{T \times N}$ ,  $D$  = data,  $N$  = number of timepoints,  $T$  = 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

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1: procedure REALPROBA( $D, b$ )
2:    $M = T \times N$  ▷ size = trials x time
3:   zeros(1 dimension,  $b$ )
4:    $min = \min(D)$ 
5:    $max = \max(D)$ 
6:    $D = \text{floor}(\frac{D-min}{max-min} \times (b-1)) + 1$ 
7:   for  $i = 1 : M$  do
8:      $P_{dist}(D(i)) = P_{dist}(D(i)) + 1$ 
9:    $P = \frac{P_{dist}(D)}{M}$ 
10:   $P_{dist} = \frac{P_{dist}(D)}{M}$ 

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