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Watershed-based visualization of high-density EEG coherence

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Abstract Synchronous electrical activity in different brain regions is generally assumed to imply functional relationships between these regions. A measure for this synchrony is electroencephalography (EEG) coherence. Recently, we developed a new method for data-driven visualization of high-density EEG coherence, avoiding the visual clutter of conventional data-driven methods. It uses the concept of maximal clique detection, having time complexity $O(3^{n/3})$ with n the number of vertices. Here, a more efficient clustering method is used with time complexity $O(n^2 \log n)$, based on a watershed algorithm which is modified to detect cliques in a greedy way. Here, it obtains a speedup of factor 400 while results are similar, making interactive visualization of high-density EEG coherence feasible.

Keywords: EEG, coherence, graph, watershed transform, medical data.

1. Introduction

Electroencephalography (EEG) measures the electrical activity of the brain using electrodes attached to the scalp at multiple locations. Synchronous electrical activity in different brain regions is generally assumed to imply functional relationships between these regions. A measure for this synchrony is EEG coherence [6,9]. Visualization of high-density EEG (at least 64 electrodes) is not always managed well [12–14]. For the analysis of high-density EEG coherence, EEG researchers often employ a hypothesis-driven definition of certain regions of interest (ROIs). In these ROIs, all electrodes are assumed to record similar signals, because of volume conduction effects [8]. As an alternative to the hypothesis-driven approach, we previously introduced a data-driven visualization of ROIs which shows less clutter than conventional data-driven methods [14]. It is based on a graph with vertices representing electrodes and edges representing significant coherences

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between electrode signals. The data-driven version of a ROI is called a functional unit (FU) and is represented in the graph by a clique consisting of spatially connected vertices [14].

Our existing maximal clique based (MCB) method clusters vertices into FUs using the concept of maximal clique detection [2], having time complexity $O(3^{n/3})$ with n the number of vertices [15], which we extended to find sets of spatially connected vertices [14]. With an interactive visualization of EEG coherence in mind, we here present a new method with time complexity $O(n^2 \log n)$, based on the concept of the watershed transform [11] which is adapted to detect cliques in a greedy way. We refer here to the more efficient new method as watershed based (WB) method.

2. Preliminaries

2.1 EEG data

EEG can be recorded using up to 512 electrodes attached to the scalp. A conductive gel is applied between skin and electrodes to reduce impedance. The electrical potential is measured at all electrodes simultaneously. The measured signals are amplified, resulting in one recording channel for every electrode. If there are many electrodes, the term 'multichannel' or 'high-density' EEG is used. As a result of volume conduction [8], multiple electrodes can record a signal from a single source in the brain. Therefore, nearby electrodes usually record similar signals. Because sources of activity at different locations may be synchronous, electrodes far apart can also record similar signals. A measure for this synchrony is coherence, calculated between pairs of signals as a function of frequency. The coherence c_λ as a function of frequency λ for two continuous time signals x and y is defined as the absolute square of the cross-spectrum f_{xy} normalized by the autospectra f_{xx} and f_{yy} [6], having values in the interval $[0, 1]$: $c_\lambda(x, y) = \frac{|f_{xy}(\lambda)|^2}{f_{xx}(\lambda) f_{yy}(\lambda)}$. An event-related potential (ERP) is an EEG recording of the brain response to a sensory stimulus. For L repetitive stimuli, the EEG data can be separated into L segments, each containing one brain response. A *significance threshold* for the estimated coherence is then given by [6]

$$\phi = 1 - p^{1/(L-1)}, \tag{1}$$

where p is a probability value associated with a confidence level α, such that $p = 1 - \alpha$. Throughout this paper, we use $p = 0.05$, unless stated otherwise.

2.2 Graph theory

A graph $G = (V, E)$ consists of a set of vertices V and a set of edges $E \subseteq V \times V$. The vertices u and v are called neighbors or adjacent if there

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is one edge between them. The neighborhood of vertex v is the collection of all neighbors of v. In a directed graph, the set E consists of ordered pairs of vertices from V. In an undirected graph, the pairs are not ordered. A directed edge is denoted as $e = (u, v)$, an undirected edge as $e = \{u, v\}$; u and v are called incident with e, and e is said to be incident with u and v. A walk between two vertices is a sequence of edges $(e_1, ..., e_n)$, with vertices $v_0, ..., v_n$ such that $e_i = \{v_{i-1}, v_i\}$. If a walk exists between two vertices, they are called connected. For a graph $G = (V, E)$ and $V' \subseteq V$, the set of all edges with both vertices in V' is denoted as $E|V'$. The graph $G' = (V', E|V')$ is called the (vertex-) induced subgraph on V'. If $V' \subset V$ and $E' \subset E|V'$, then $G' = (V', E')$ is called a subgraph. If any two vertices in $G = (V, E)$ are connected, G is called a connected graph. A maximal connected subgraph of G is a connected component. If all two-element subsets of V are edges, then $G = (V, E)$ is a complete graph. A clique is a set $V' \subseteq V$ such that the induced subgraph on V' is a complete graph. A maximal clique is a clique which is not a subgraph of a larger clique. For more background information on graphs, see, e.g., [7].

3. Data representation

3.1 Experimental setup

Here, brain responses from three young adults are studied, recorded using an EEG cap with 119 scalp electrodes. During a so-called P300 experiment, each participant was instructed to count target tones of 2000 Hz (probability 0.15), alternated with standard tones of 1000 Hz (probability 0.85) which were to be ignored. After the experiment, the participant had to report the number of perceived target tones. For each dataset, brain reactions to 20 target tones were recorded in $L = 20$ segments.

A procedure from Neurospec (`www.neurospec.org`) was adopted to compute the coherence. Frequencies between 1 and 30 Hz are typically studied clinically. We calculated the coherence within a lower (1-3 Hz) and a higher (13-20 Hz) EEG frequency band, because EEG synchrony behaves differently for lower and higher frequencies [9,10]. For 119 electrodes, in total 7021 coherence values were computed per frequency band. If the conductive gel accidentally connected two adjacent electrodes, very high coherences were measured. Coherences higher than 0.99 were therefore ignored.

3.2 EEG coherence graph

The data are represented by a *coherence graph* with vertices representing electrodes. Coherences above the significance threshold (Equation 1) are represented by edges, coherences below the threshold are ignored.

To determine spatial relationships between electrodes, a Voronoi diagram is employed which partitions the plane into regions with the same

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nearest vertex. For EEG data, the vertex set equals the set of electrode positions (Figure 1). The vertices are referred to as (Voronoi) centers, the boundaries as (Voronoi) polygons. The area enclosed by a polygon is called a (Voronoi) cell. We call two cells *Voronoi neighbors* if they have a boundary in common. A collection of cells C is called *Voronoi-connected* if for a pair $\phi_0, \phi_n \in C$ there is a sequence $\phi_0, \phi_1, ..., \phi_n$ of cells in C with each pair ϕ_{i-1}, ϕ_i consisting of Voronoi neighbors. We use the terms "Voronoi neighbor" and "Voronoi-connected" interchangeably for cells, vertices, and electrodes.

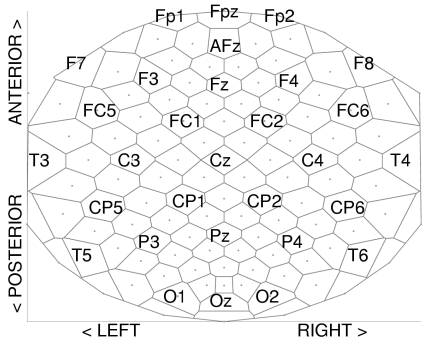

Figure 1. Voronoi diagram, with (a subselection of) all electrode labels in the corresponding cells (top view of the head, nose at the top). To improve the readability, the Voronoi diagram is stretched horizontally. The boundary is the convex hull of all electrodes. Because the coherence computation is independent of distance, distances between electrodes do not need to be preserved. However, spatial relationships between electrodes are maintained.

4. Vertex clustering

4.1 Existing maximal clique based (MCB) method

A *functional unit* (FU) is a clique consisting of Voronoi-connected vertices [14]. Consequently, an FU corresponds to a Voronoi-connected set of electrodes in which the electrodes record pairwise significantly coherent signals. Our existing FU clustering method for high-density EEG coherence [14] uses maximal clique detection [2], which we extended to find sets of Voronoi-connected vertices. Every vertex can be part of multiple (Voronoi-connected) maximal cliques. To assign a unique label to every vertex, a quantity *total strength* is defined for a (sub)graph $G = (V, E)$ as the sum of all edge values. This value is not normalized for the size of E. Consequently, if two graphs have an equal average coherence, the graph with more vertices has a higher total strength. Next, all cliques are queued in decreasing order by their total strength. Then the following labeling procedure is repeated, until there are no more cliques or until all vertices are labeled. The first clique is removed from the queue, and all its vertices are assigned a unique label and are removed from the other cliques. If necessary, the changed cliques are separated into Voronoi-connected components. For all changed cliques, the total strength is recomputed before they are put in the appropriate position in the sorted queue. After completion of the labeling procedure, every set of identically labeled vertices is an FU.

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The worst-case time complexity of maximal clique detections is $O(3^{n/3})$, with n the number of vertices [15]. In practice, performance of maximal clique detection strongly depends on graph structure [16].

4.2 New watershed based (WB) method

As an alternative to the MCB method, we present here a greedy method approximating maximal cliques on the basis of the watershed transform [11]. In the usual watershed algorithm, a subset of all local minima is selected as markers. Markers are labeled and are associated with basins. Basins contain vertices with the same label as the corresponding marker and are extended as follows, using the watershed implementation based on ordered queues [1]. The first vertex v is removed from a queue of vertices sorted in decreasing order of priority. Every unlabeled neighbor v' of v receives the same label as v and is put into the queue with a priority depending on the value of v', but not higher than the priority of v. This continues until the queue is empty.

Now we modify the usual watershed transform in order to obtain spatially connected sets of electrodes, where all electrodes in a given set have recorded mutually significantly coherent signals. This modification concerns two steps in the watershed transform: (i) choice of markers; (ii) use of an edge queue instead of a vertex queue. We explain these two points in more detail.

First, we define a marker as an electrode recording a signal that is locally maximally coherent with signals of its spatially neighboring electrodes. Because the EEG coherence graph has edge values instead of vertex values, we first assign a coherence value to each vertex by computing the average of the edge values between this vertex and all its Voronoi neighbors. Then, we select all vertices which are local maxima as markers to be associated with basins, because those vertices are locally maximally similar to their spatially neighboring vertices. Note that we choose *all* local maxima as markers, instead of a small subset as is usually done when the watershed algorithm is applied to digital images. In our case the over-segmentation problem is less severe, because the number of electrodes is an order of magnitude smaller than the number of pixels in an image. If the number of basins (i.e., clusters) found is still too large, we can suppress basins below a certain size in a post-processing step (see Section 6).

The second point concerns the type of queue we use. Whereas the usual queue-based implementation of the watershed transform uses a vertex queue sorted in increasing order of gray value, we use an edge queue sorted in decreasing order of coherence value. (The vertex values are only used for defining the markers, as indicated above.) In case the coherence graph has multiple identical edge values (which did not occur for our datasets), an ordered queue consisting of queues with identically valued elements can be used, as for digital images which usually contain multiple identically valued

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vertices [1].

This queue is initialized with edges (corresponding with a significant coherence) between markers and their Voronoi neighbors. The first edge (v, v') in the queue corresponds to the highest similarity (coherence) between any vertex v' outside and a Voronoi neighboring vertex v inside a basin. Therefore, vertex v' is the first candidate to be added to a basin.

The greedy WB method maintains the following dynamic vertex sets for the detection of Voronoi-connected cliques.

- bsn_i contains a sorted list of the vertices in basin i.
- $L(v)$ contains the basin label of vertex v.
- $adjCohBsn_i$ contains a list of vertices (sorted by vertex number) which are adjacent to *each* of the vertices in bsn_i in the coherence graph.
- *queue* contains edges in decreasing order. When vertex v receives a label, an edge $e = (v, v')$ is added to *queue* for each unlabeled Voronoi neighbor v' of v, provided that the corresponding edge value exceeds the significance threshold (Equation 1).

The main procedure consists of the following steps. Remove the first edge, say $e = (v, v')$ from *queue*. In case vertex v' was also labeled between the insertion and removal of $e = (v, v')$, nothing is done and the procedure continues with a new edge. Otherwise (v' is unlabeled), there are two cases. In case $v' \in adjCohBsn_{L(v)}$, v' receives label $L(v)$ and v' is added to $bsn_{L(v)}$; $adjCohBsn_{L(v)}$ is replaced by its intersection with the neighborhood of v' in the coherence graph; *queue* is extended with the edges between v' and its Voronoi-neighbors, provided that corresponding edge values exceed the significance threshold. In the other case, if $v' \notin adjCohBsn_{L(v)}$, v' is not labeled (yet). This procedure is repeated until *queue* is empty. Each basin then corresponds to an FU.

The WB vertex clustering procedure is described below in pseudocode. The operation *insertEdgeSort(e(v, v'),queue)* inserts edge $e(v, v')$ into the appropriate position in a decreasingly sorted edge queue *queue*; similarly, *insertVSort(v,vqueue)* inserts vertex v into the appropriate position in a decreasingly sorted vertex queue *vqueue*; *dequeue(queue)* returns and removes the first edge from an edge queue *queue*; *intersect(.,.)* gives the intersection of two sorted vertex sets. The size of a vertex set is denote by $|\ .\ |$.

The creation of the sorted edge queue (step 1) has time complexity $O(m \log m) = O(n^2 \log n)$, where n denotes the number of vertices and $m = \frac{n(n-1)}{2}$ the maximal number of edges. Then (step 2), for every edge $e = (v, v')$ in the queue with unlabeled v' (queue length $O(m) = O(n^2)$), the following steps are executed consecutively: (a) binary search ($O(\log n)$) is used to verify the presence of v' in the set $adjCohBsn_{L(v)}$, a sorted set of at most n vertices; (b) two sorted vertex sets (with maximum size n) are intersected ($O(n)$); (c) Voronoi-neighbors of v (at most n) are inserted

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Algorithm 1 WB pseudocode.

INPUT: V is the vertex set; *marker(i)* = marker i;
$c(v, v') = \text{coherence}(v, v') = c(v', v)$; ϕ = sign. threshold;
$adjCoh_v = \{v' \in V \mid c(v,v') \geq \phi\}$;
$adjVor_v = \{v' \in V \mid v' \in \text{Vor.-neighbors}_v \ \&\ v' \in adjCoh_v\}$;
$\{adjCoh_v,\ adjVor_v$ are both sorted by vertex number$\}$
OUTPUT: bsn_i is basin i (i.e., an FU) sorted by vertex number
INITIALIZATION:

```
queue ← ∅ {queue of edges}
for all v ∈ V do
    L(v) ← 0 {L(v) = label of vertex v}
end for
for i = 1 to |marker| do
    bsn_i ← marker(i); v ← marker(i); L(v) ← i
    adjCohBsn_L(v) ← adjCoh_v
    for all v' ∈ adjVor_v do
        insertEdgeSort(e(v,v'),queue)
    end for
end for
```

MAIN:

```
while queue ≠ ∅ do
    e(v, v') ← dequeue(queue)
    if L(v') = 0 then
        if v' ∈ adjCohBsn_L(v) then
            adjCohBsn_L(v) ← intersect(adjCohBsn_L(v), adjCoh_v')
            L(v') ← L(v); bsn_L(v) ← insertVSort(v', bsn_L(v))
            for all v* ∈ adjVor_v' do
                if L(v*) ≠ 0 then
                    insertEdgeSort(e(v', v*), queue)
                end if
            end for
        end if
    end if
end while
```

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into the edge queue ($O(n \log m) = O(n \log n)$). Step c has a higher time complexity than a and b. However, step b and c are only executed $O(n)$ times, because at most n vertices can be added to a basin. Thus, the time complexity for step 2 is $O(n^2 \log n)$, as for step 1, which is therefore the total time complexity.

5. FU map

In a so-called *FU map*, each FU is visualized as a set of identically colored Voronoi cells, with different colors for adjacent FUs [14]. Given the FUs, the *inter-FU coherence* c' at frequency λ between two functional units W_1 and W_2 is defined as the sum of the coherence values between one vertex in W_1 and the other vertex in W_2, scaled by the total number of edges between W_1 and W_2 [14]:

$$c'_\lambda(W_1, W_2) = \frac{\sum_{i,j}\{c_\lambda(v_i, v_j) \mid v_i \in W_1, v_j \in W_2\}}{|W_1| \cdot |W_2|}, \tag{2}$$

where, $|W_i|$ indicates the number of vertices in W_i. Note that coherences between *any* pair of vertices are taken into account, to normalize for the size of the FUs. A line is drawn between FU centers if the corresponding inter-FU coherence exceeds a threshold. We consistently choose this threshold to be equal to the significance threshold (Equation 1), because we already used this threshold to determine the coherence graph.

6. Results

We show FU maps for the MCB (Figure 2) and the WB (Figure 3) method, for three datasets and two frequency bands. Because FU maps including small FUs fail to give a good overview [14], only FUs larger than 5 cells are considered.

MCB FU maps (Figure 2) were previously shown to agree with earlier findings in the literature [14]. The number of connecting lines between FUs was lower for a higher EEG frequency, in accordance with [9, 10]. Furthermore, connections between anterior and posterior FUs were probably associated with the two most important sources of brain activity for this data type [3, 4]. Here, the WB FU maps (Figure 3) confirmed these findings.

Each WB FU map was compared to the corresponding MCB FU map (compare Figure 3 to Figure 2). From a visual inspection, the biggest dissimilarity appeared between the FU maps for *dataset 2* and frequency band *1-3 Hz* (Figure 2 and Figure 3: top row, middle). For this case, the WB method showed more FUs (at positions where the MCB method has no sufficiently large FUs) and more inter-FU connections than the MCB method. However, the six inter-FU connections with the highest value in the WB FU map corresponded to the six inter-FU connections in the MCB FU

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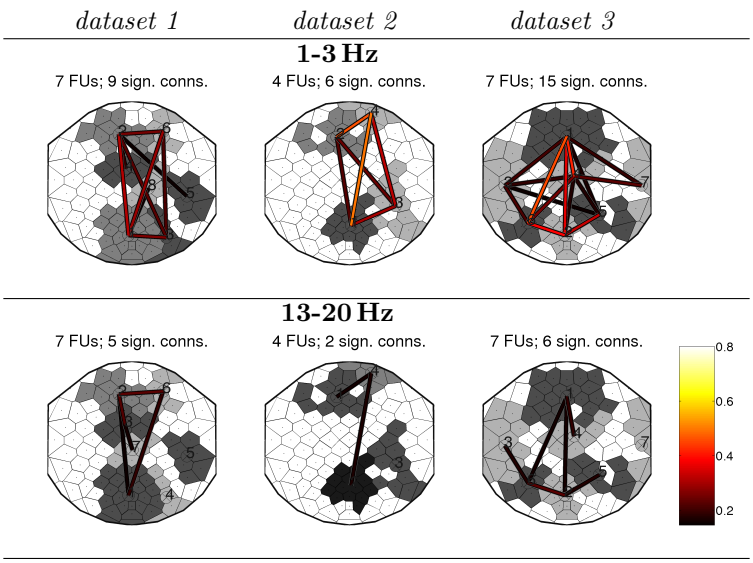

Figure 2. **MCB FU maps** (top view of the head, nose at the top) with FUs larger than 5 cells, for EEG frequency 1-3 Hz (*top row*) and 13-20 Hz (*bottom row*), for three datasets and $p = .05$. Each FU is visualized as a set of identically colored Voronoi cells, with different gray values for adjacent FUs. White Voronoi cells are part of FUs with $|\text{FU}| \leq 5$. Geographic centers of FUs are visualized as a circle with a cross inside, having a color corresponding to the FU. A line connects FUs if the inter-FU coherence exceeds the significance threshold (Equation 1), with its color depending on the value (see color bar, with minimum corresponding to the coherence threshold ≈ 0.15). Lines are drawn in the order from low to high inter-FU coherence values. Above each FU map the number of FUs and the number of connecting lines between FUs are displayed.

map. This became more clear by simultaneously increasing the significance threshold for both the coherence graph and the inter-FU connections in the WB FU map (i.e., decreasing the p-value). The result showed only the six highest inter-FU connections for $p = .001$ (Figure 4, right). Those six connecting lines completely connected two anterior and two posterior FUs for the WB method (Figure 4, right), which were in orientation very similar to the six connecting lines for the MCB method (Figure 4, left). The two anterior FUs in the MCB FU map did not correspond exactly with the two anterior FUs obtained with the WB method, because the latter is a greedy FU detection method. The same holds for the posterior FUs.

For the other cases, inter-FU connections between FUs which were no spatial neighbors were usually similar for the MCB and WB method. Further, the locations of the FUs were usually similar for the MCB and WB method, especially for FUs connected with another FU which was not a spatial neighbor. For example, anterior and posterior FUs connected by a

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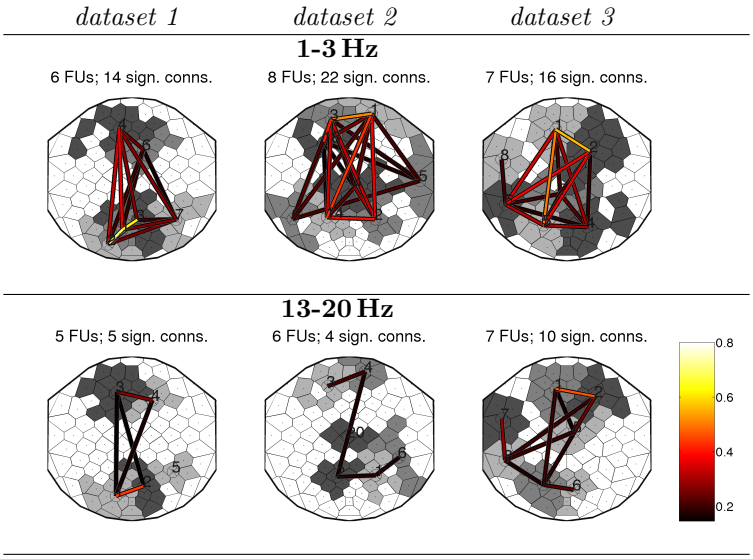

Figure 3. **WB FU maps**, with FUs larger than 5 cells, for the 1-3 Hz EEG frequency band (*top row*) and for 13-20 Hz (*bottom row*), for three datasets and $p = .05$.

line were similarly located for all cases.

Additionally, we compared the numbers of FUs obtained with both methods. In the range up to an FU size of 5 cells (not illustrated), the MCB method had on average 14 FUs and the WB method 6 FUs. In the range above an FU size of 5 cells, both methods had on average 6 FUs (Figure 2

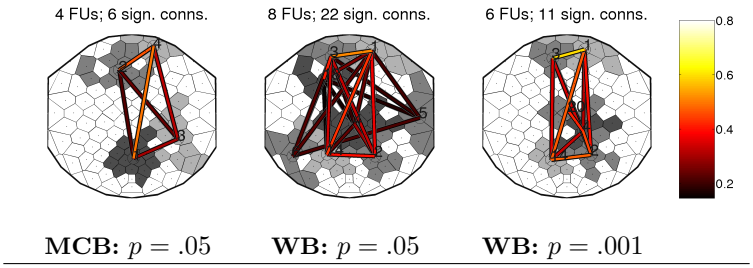

Figure 4. FU maps for *dataset 2* and frequency band *1-3 Hz*, $|FU| > 5$. **Left:** MCB, $p = .05$. **Middle:** WB, $p = .05$. **Right:** WB, $p = .001$. The WB FU map is more similar to the MCB FU map (left) when the the significance threshold (Equation 1) is increased (corresponding to decreasing p) for the WB method (right).

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and Figure 3). Thus, the maximal clique method detected relatively more small-size FUs.

For the FU maps created with both methods in Figure 2 and Figure 3, we determined the CPU time consumed by FU detection. On average, the (non-optimized) MCB and WB methods took 24 s and 0.06 s, respectively, meaning that a speedup of factor 400 was obtained by the new WB method.

7. Discussion and conclusions

EEG coherence analysis is defined as the study of coherence between functional units (FUs). We previously introduced the maximal clique based (MCB) method for data-driven visualization of high-density EEG coherence [14], avoiding the visual clutter of conventional data-driven visualizations. This MCB method makes use of the concept of maximal clique detection with time complexity $O(3^{n/3})$ for n electrodes. In practice, performance of maximal clique detection strongly depends on graph structure [16]. With an interactive visualization in mind, we have designed here a new watershed based (WB) method having time complexity $O(n^2 \log n)$, based on the watershed transform which is modified to detect cliques in a greedy way. The existing MCB and the new WB method both detect data-driven ROIs represented by cliques consisting of spatially connected vertices, referred to as FUs.

Comparing the MCB and the WB method, the greedy WB method directly results in uniquely labeled electrodes, contrary to the MCB method. The existing MCB method shows a relatively larger number of smaller FUs than the new WB method. The MCB and the WB method both depend on three thresholds. The first two thresholds concern the initial coherence graph and the inter-FU coherence. Both were chosen to be equal to the significance threshold. The third threshold concerns the minimal FU size. FUs and inter-FU connections were usually similar for the MCB and the greedy WB method. If not, systematically adapting the significance threshold revealed a strong similarity between FU maps obtained with both FU detection methods. Thus, both methods visualize similar information. Further, this information was found to agree with conventional findings [3, 4, 9, 10].

The watershed transform is generally known to suffer from over-segmentation, for which a solution may be based on the concept of dynamics [5]. However, dynamics are defined for vertex values, whereas the EEG coherence graph has edge values. For EEG coherence, there are two straightforward solutions for potential over-segmentation. First, two spatially neighboring FUs may be merged if the union of the two corresponding vertex sets is a clique. Second, determination of the markers can be based not only on (first degree) Voronoi neighbors, but also on (second degree) Voronoi neighbors of Voronoi neighbors.

Here, the new WB method is up to a factor 400 faster than the existing MCB method. The new method makes interactive visualization of

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high-density EEG coherence feasible for the intended users, including EEG researchers and clinical experts.

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