A MRF Based Random Graph Modelling the Human Cortical Topography

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Abstract. This paper presents a project aiming at the automatic detection and recognition of the human cortical sulci in a 3D magnetic resonance image. The two first steps of this project (automatic extraction of an attributed relational graph (ARG) representing the individual cortical topography, constitution of a database of labelled ARGs) are briefly described. Then, a probabilistic structural model of the cortical topography is inferred from the database. This model, which is a structural prototype whose nodes can split into pieces according to syntactic constraints, relies on several original interpretations of the inter-individual structural variability of the cortical topography. This prototype is endowed with a random graph structure taking into account this anatomical variability. The recognition process is formalized as a labelling problem whose solution, defined as the maximum a posteriori estimate of a Markovian random field (MRF), is obtained using simulated annealing.

1 Introduction

The current revival of the Talairach stereotactic proportional system applied to magnetic resonance (MR) images reflects the need for a precise identification of brain structures in a number of domains of neurology [6]. This need appears especially urgent in the field of human brain mapping, where several programs have been recently initiated in order to create an electronic database of human functional neuro-anatomy which can mediate data communication among a network of laboratories. This need appears also crucial in the current design of increasingly precise neuro-surgical operations. Indeed, the success of micro-surgical techniques depends upon utilizing natural sulcal pathways to gain access to pathologic structures within the brain, while preserving the integrity of healthy adjacent tissues [4, 5]. Unambiguous identification of internal brain structures is possible in high resolution MR images, when the neuro-anatomist is guided by a reference atlas, thanks to a relatively low variability [6]. In return, it turns out to be much more difficult to overcome the high variability of the human cortex, even with sophisticated 3D display interfaces. Indeed, the few studies dealing with this variability are only descriptive [6, 4] and therefore provide no real identification methodology.

This paper describes a project which aims at developing robust and reproducible methods to detect and identify automatically various cortical structures, mainly the sulci (cortical folds) and the dual gyri (cortical regions delimited by sulci). In the context of human brain mapping, main sulci are reliable landmarks to guide atlas deformation or individual definition of volumes of interest. This project consists of three main parts, the last one being addressed in this paper:

1. The design of a robust method allowing the construction of a high level representation (ARG) of the individual cortex topography [2].

2. The constitution of a large database of ARGs in which the main sulci are identified via the labelling of ARG nodes [1, 5].
3. The inference of a generic model of the cortex topography from this database and the design of a method matching this model and any individual cortex.

1.1 ARG Structure: An individual ARG is inferred from the segmentation in simple surfaces (SSs) of the 3D skeleton of the union of cerebrospinal fluid and gray matter. Hence ARG nodes represent mainly cortical folds. ARG relations are of two types: first, SS pairs connected in the skeleton (ρ_T); second, SS pairs delimiting a gyrus (ρ_C) (see Fig.1). An ARG is defined by the 6-tuple $\mathcal{G} = (\mathcal{N}, \mathcal{R}, \sigma_\mathcal{N}, \sigma_\mathcal{R}, \lambda_\mathcal{N}, \lambda_\mathcal{R})$, where: $\mathcal{N}$ and $\mathcal{R}$ are respectively node and relation sets; $\sigma_\mathcal{N} : \mathcal{N} \rightarrow \mathcal{S}_\mathcal{N} = \{\text{SS}, \mathcal{S}_{brain}, \mathcal{P}_{med}\}$ is a function called node syntactic interpreter ($\mathcal{S}_{brain}$ and $\mathcal{P}_{med}$ denote respectively brain surface and inter-hemispheric plane); $\sigma_\mathcal{R} : \mathcal{R} \rightarrow \mathcal{S}_\mathcal{R} = \{\rho_T, \rho_C\}$ is a function called relation syntactic interpreter; $\lambda_\mathcal{N} : \mathcal{N} \rightarrow E(At_\mathcal{N})$ and $\lambda_\mathcal{R} : \mathcal{R} \rightarrow E(At_\mathcal{R})$ are functions called respectively node and relation semantic interpreters; $At_\mathcal{N}$ and $At_\mathcal{R}$ are sets of semantic attributes describing respectively nodes and relations; $E(At_x)$ is the set of all semantic descriptions using semantic attributes of At_x. A semantic description of $E(At_x)$ is a set of couples (attribute, attribute value), each attribute of At_x appearing at most in one couple. A semantic attribute reserved to instances of only one syntactic type t is noted *t-name*: $At_\mathcal{N}$=\{*SS-size, SS-center, SS-orientation, SS-depth*\}; $At_\mathcal{R}$=\{ρ_T*-length*, ρ_T*-direction*, ρ_C*-size*\}.

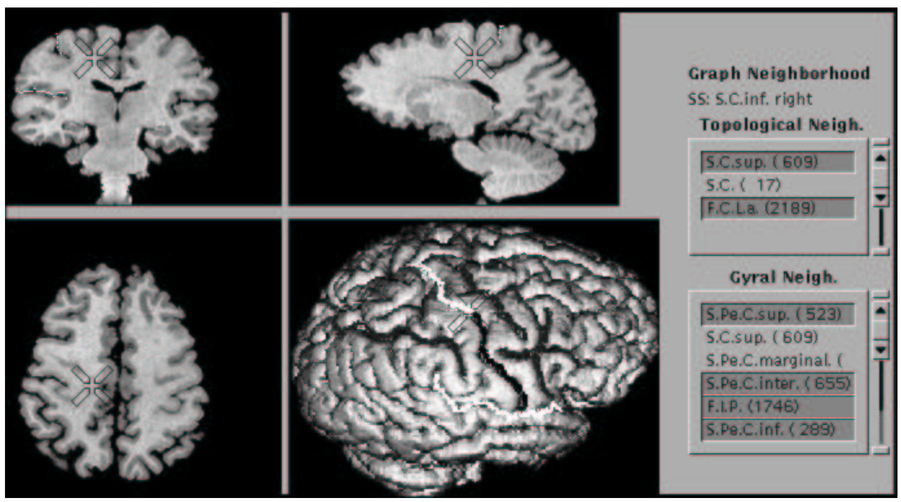

Fig. 1. *A glimpse of the interface allowing navigation in an ARG for the sulcus identification. The black SS (S.C.inf.right) neighborhood is explored. Topological neighbors are displayed in white and gyral neighbors are displayed in dark grey.*

1.2 Anatomical Variability: Unlike the case of monkey, the human cortical anatomy presents large pattern variations between individuals or even between brain hemispheres. Therefore, when trying to develop pattern recognition methods dedicated to cortical sulci, we have first to propose a coherent interpretation of this variability. Pratical results will show the validity or the weakness of this interpretation and will suggest modifications or improvements. The choice of cortical sulcus as landmarks, which may be criticized, relies on a number of anatomical and functional studies from the literature [5, 3]. An interpretation of these studies can be the following: the cortical surface may be viewed as a map of constant functional regions potentially separated by sulci. From this point of view, an individual sulcal topography is necessary a subset of the network of borderlines between these functional regions (the complete network of borderlines can be viewed as a skeleton by influence zones). This interpretation, which is clearly an abstract simplification of reality, will appear formally in our model through the notion of random graph. Another level of variability relies in potential sulcus interruptions. We think that a sulcus interruption occurs when a fiber bundle constituting a functional pathway between the two delimited gyri is especially developed. This variability aspect will be embedded in our model through a grammatical language describing usual sulcus forms in ARGs. Moreover, we have performed a first mapping of the main fiber bundles which leads to a new original description of the cortex anatomy of great help when identifying sulci [5]. We have begun the constitution of a database of labelled ARGs whose nodes are identified according to this description. A label corresponding to a brain structure of the hierarchical description introduced in Fig.2 is attached to each ARG node.

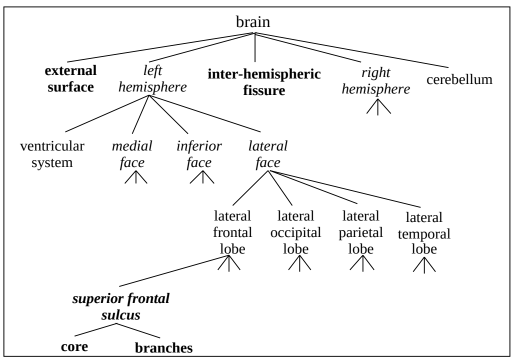

Fig. 2. *A glimpse of the hierarchical description of the cortex anatomy. The full tree will be noted $\mathcal{A}$. Bold fonts are used for elements involved in the web grammar describing usual sulcus patterns (see sect. 3). Italic fonts are used for nodes corresponding to random elements with empty realization (see sect. 2).*

2 Structural Framework

In an ideal case (no variability, perfect segmentation), sulcus recognition would just amount to finding an isomorphism between an ARG $\mathcal{G}$ and a structural prototype $\mathcal{P}$ whose nodes correspond to the leaves of tree $\mathcal{A}$ (see Fig.2). Because of all potential deformations of this prototype (node insertion and deletion, node split...), recognition amounts to finding a homomorphism between a subgraph of $\mathcal{G}$ and a subgraph of $\mathcal{P}$. For an accurate management of node insertion, the prototype $\mathcal{M}$ used in the following includes higher level structures of $\mathcal{A}$.

2.1 Random Graph: In order to formalize the different kinds of variabilities described previously, $\mathcal{M}$ is endowed with a structure of random graph (RG). This probabilistic framework provides then a natural adaptive similarity measure between any ARG $\mathcal{G}$ and $\mathcal{M}$: the maximum a posteriori (MAP) estimator. In order to allow node split (sulcus interruptions, branches...), the classical random graph definition proposed by Wong [7] is extended by substituting the monomorphism by a homomorphism (see Fig. 3). A random graph $\mathcal{M}$ is defined on a 4-tuple ($\mathcal{S}_\mathcal{N}$,$E(At_\mathcal{N})$,$\mathcal{S}_\mathcal{R}$,$E(At_\mathcal{R})$) by the couple ($\mathcal{N}^A$,$\mathcal{R}^A$) with:

$\mathcal{N}^A$ is a set $\{\alpha_1, \alpha_2, ..., \alpha_n\}$ where each α_i, called a random vertex (RV), is a random variable whose realizations are sets of couples $(s,d) \in \mathcal{S}_\mathcal{N} \times E(At_\mathcal{N})$;

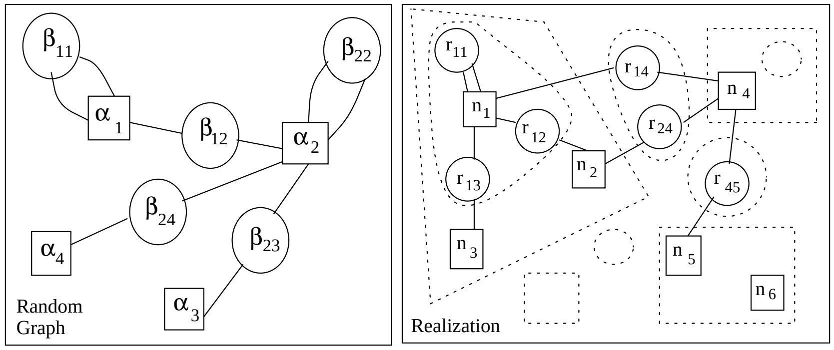

Fig. 3. *RG realization* ($h_{\mathcal{N}}(n_1)=h_{\mathcal{N}}(n_2) = h_{\mathcal{N}}(n_3)=\alpha_1$; $h_{\mathcal{N}}(n_4)=\alpha_2$; $h_{\mathcal{N}}(n_5)=h_{\mathcal{N}}(n_6)=\alpha_3$).

$\mathcal{R}^A$ is a set $\{\beta_{i_1j_1}, \beta_{i_2j_2}, ..., \beta_{i_mj_m}\}$ where each β_{ij}, called a random arc (RA), is a random variable whose realizations are sets of relations between elements of the realizations of the RVs α_i and α_j, each relation being described by a couple $(s, d) \in \mathcal{S_R} \times E(At_{\mathcal{R}})$.

A realization of the random graph $\mathcal{M}$ is a couple ($\mathcal{G}$,$h_{\mathcal{N}}$), where $h_{\mathcal{N}}$ is a graph homomorphism between the ARG $\mathcal{G}$ and $\mathcal{M}$.

2.2 Random Graph and Set Hierarchy: Given an ARG $\mathcal{G}$, let e_i be the subset of nodes of $\mathcal{N}$ belonging to the brain structure i (element of the tree $\mathcal{A}$ defined in Fig. 2). The set hierarchy described in $\mathcal{A}$ induces naturally a partition of $\mathcal{N} = \bigcup \mathcal{N}_i$, where $\mathcal{N}_i$ is the complementary in e_i of the union of the e_j strictly included in e_i. This partition is composed by two kinds of $\mathcal{N}_i$: those corresponding to leaves of $\mathcal{A}$ and those corresponding to other elements of $\mathcal{A}$. This last subsets of $\mathcal{N}$ regroup nodes that cannot be identified according to the brain structure nomenclature defined by $\mathcal{A}$ leaves. These nodes can only be associated to higher structures in the hierarchy. In the following, we consider each set $\mathcal{N}_i$ as the realization of a RV α_i. The RA set is defined by endowing the underlying random graph $\mathcal{M}$ with a complete graph structure. Hence, we define a RA β_{ii} for each RV α_i, and a non-oriented RA β_{ij} for each pair $\{\alpha_i, \alpha_j\}$ of distinct RVs. A homomorphism $h_{\mathcal{N}}$ between $\mathcal{G}$ and $\mathcal{M}$ induces a mapping $h_{\mathcal{R}}$ between $\mathcal{R}$ (relation set of $\mathcal{G}$) and $\mathcal{R}^A$. The labelled ARGs of the database $\mathcal{B}$ are naturally considered as realizations of the random graph $\mathcal{M}$.

3 Markovian Framework

The recognition process is formalized as a labelling problem. A label l_i is associated with each RV α_i of $\mathcal{M}$, the label set being noted $\mathcal{L}$. A labelling l of $\mathcal{N}$ is equivalent to a homomorphism $h_{\mathcal{N}}$. The recognition will be achieved using the MAP estimator: arg $\max_l p(l|\mathcal{G})$. This estimator is constructed from a Markovian random field (MRF) model. The main reasons which motivate this choice, which is a key feature of our model, are the following:

1. The contextual information used by a neuro-anatomist to identify a sulcus derives from a confined neighborhood of the sulcus in the brain.
2. The equivalence between MRFs and Gibbs random fields (GRFs) gives a very flexible way to introduce syntactic constraints in a MRF based discrete relaxation sheme which has not been exploited yet.
3. It has been proven that stochastic relaxation schemes like simulated annealing (SA) applied to a Gibbs distribution based MAP have very good

convergence properties.

3.1 Random Field: Let us introduce a few notations:

$\mathcal{L}_\mathcal{B} = \{l_i \in \mathcal{L} \mid p(h_\mathcal{N}^{-1}(\alpha_i) = \emptyset) \neq 1\}$. Related elements of $\mathcal{A}$ are its leaves, lobes and brain (see Fig. 2). Indeed, during database $\mathcal{B}$ constitution, an ARG node is either identified (leaves) or associated to one lobe (lobes make up a cortex partition) or to the brain (segmentation error, pathology);

l_0, $l_{\mathcal{S}_{brain}}$ and $l_{\mathcal{P}_{med}}$ denote respectively labels bound to brain, $\mathcal{S}_{brain}$ and $\mathcal{P}_{med}$.

$\mathcal{L}_m = \mathcal{L}_\mathcal{B} - \{l_{\mathcal{S}_{brain}}, l_{\mathcal{P}_{med}}\}$; $\mathcal{L}_p = \mathcal{L}_m - \{l_0\}$ and $\mathcal{L}_t = \mathcal{L}_\mathcal{B} - \{l_0\}$;

$\mathcal{N}_x^A$ and $\mathcal{R}_{xy}^A$ denote respectively the set of RVs related to $\mathcal{L}_x$ and the set of RAs connecting a RV of $\mathcal{N}_x^A$ and a RV of $\mathcal{N}_y^A$ (x and $y \in \{m, p, t\}$);

$S = \{n \in \mathcal{N} \mid \sigma_\mathcal{N}(n) = \text{SS}\}$.

Since $h_\mathcal{N}^{-1}(\alpha_{\mathcal{S}_{brain}})$ and $h_\mathcal{N}^{-1}(\alpha_{\mathcal{P}_{med}})$ are known, $p(l|\mathcal{G}) = p(l_{|S}|\mathcal{G})$. $l_{|S}$ is considered as the realization of a random field defined on the set of sites S. For $n \in S$, $l(n)$ is a random variable whose realization set is $\Omega_n \subset \mathcal{L}_m$.

3.2 State Space of the Random Field: Introduction of constraints on the localization in a reference frame $\mathcal{D}_\mathcal{M}$ (similar to Talairach one [6]) of the realization nodes of the RVs of $\mathcal{N}_p^A$ endowes the random field with the Markovian property. These constraints rely on the attachment of an influence domain $\mathcal{D}_i^{inf}$ to each RV $\alpha_i \in \mathcal{N}_m^A$. The state space Ω of the random field is then defined by: $\Omega = (\Omega_n)_{n \in S}$, where $\forall n \in S, \Omega_n = \{l_i \in \mathcal{L}_m \mid \lambda_{SS}^c(n) \in \mathcal{D}_i^{inf}\}$, (λ_t^n denotes the function which gives the value of the semantic attribute t-*name*; hence λ_{SS}^c refers to the *SS-center* attribute). The $\mathcal{D}_i^{inf}$ of the RVs of $\mathcal{N}_p^A$ are parallelepipedic boxes of $\mathcal{D}_\mathcal{M}$ inferred from the database $\mathcal{B}$, and $\mathcal{D}_0^{inf} = \mathcal{D}_\mathcal{M}$.

3.3 Markovian Random Field: The random field is a MRF defined on $(S, \Omega, \mathcal{C})$ where $\mathcal{C}$ is the set of cliques involved in the distribution of the equivalent GRF: $p(l_{|S}|\mathcal{G}) = \frac{1}{Z}\exp\{-U(l)\}$, where $U(l)$ is the energy (or Hamiltonian) of the GRF defined by $U(l) = \sum_{c \in \mathcal{C}} V[c](l)$, and Z is a normalization constant. $V[c](l)$ is a potential attached to clique $c \in \mathcal{C}$ whose value depends only on $l_{|c}$.

The set $\mathcal{C}$, defined for a given ARG $\mathcal{G}$, is constituted by five kinds of cliques:

1. Topological cliques, inferred from the graph structure of $\mathcal{G}$:
   (a) $\mathcal{C}_1$ is the set of order one cliques, noted c_n for $n \in S$.
   (b) $\mathcal{C}_2$ is the set of order two cliques, noted $c_{nn'}$ for $(n, n') \in S^2 \cap \mathcal{R}$.
2. Influence cliques, inferred from the RV influence domains:
   (a) $\mathcal{C}_p^{inf}$ is the set of RV influence cliques c_i^{inf} defined by $\forall \alpha_i \in \mathcal{N}_p^A, c_i^{inf} = \{n \in S \mid l_i \in \Omega_n\}$.
   (b) $\mathcal{C}_{pt}^{inf}$ is the set of RA influence cliques, noted c_{ij}^{inf} for $\beta_{ij} \in \mathcal{R}_{pt}^A$ when it exists. RA influence cliques are naturally induced by RV influence cliques. We point out that c_{ij}^{inf} exists only if $p(h_\mathcal{R}^{-1}(\beta_{ij}) = \emptyset \mid \Omega) \neq 1$, which holds for a very restricted number of RAs. Otherwise, the random field would not really be Markovian.
3. Grammatical cliques (set $\mathcal{C}^G$) associated to each cortical sulcus. For a sulcus s of the sulcus set $\mathcal{A}_s$, the grammatical clique c_s^G is the union of the two influence cliques bound to the core and to the branches of s (note that a sulcus itself is associated to a RV with empty realization (see Fig. 2)).

3.4 Gibbs Distribution: The random field distribution is estimated from the following decomposition: $p(l|\mathcal{G}) = p(l|\mathcal{G}, \Omega) = p(l|\mathcal{N}, \mathcal{R}, \sigma_\mathcal{N}, \sigma_\mathcal{R}, \lambda_\mathcal{N}, \lambda_\mathcal{R}, \Omega)$ $\propto p(\lambda_\mathcal{N}, \lambda_\mathcal{R}|l, \mathcal{N}, \mathcal{R}, \sigma_\mathcal{N}, \sigma_\mathcal{R}, \Omega)p(l|\mathcal{N}, \mathcal{R}, \sigma_\mathcal{N}, \sigma_\mathcal{R}, \Omega) = p_1 p_2$. Probability p_2 is considered as the probability of a first MRF defined on $(S, \Omega, \mathcal{C})$. The energy $U_{str}(l)$ of this MRF will constitute the "structural energy" of the whole random field. In order to estimate probability p_1, the notion of indivisible random graph (IRG) is introduced. An IRG is a RG whose RVs and RAs have realizations of cardinal one or zero [7]. We assume that this "a posteriori" probability of semantic attribute values of a realization of $\mathcal{M}$ is equivalent to the "a posteriori" probability of the semantic attribute values of $\mathcal{M}$ if $\mathcal{M}$ were an IRG. Hence, we attach a set $\mathcal{A}t[\alpha_i]$ of new semantic attributes to each RV of $\mathcal{N}_m^A$ and a set $\mathcal{A}t[\beta_{ij}]$ to each RA of $\mathcal{R}_{pt}^A$ [3]. The values of this new semantic attributes are synthesized from the values of the semantic attributes of $\mathcal{G}$ using semantic rules similar to semantic rules of an attributed grammar. We assume that the respective values taken by all these synthesized attributes are independent, which allows to express p_1 as a sum of potentials attached to influence cliques of $\mathcal{C}$ which will constitute the "semantic energy" $U_{sem}(l)$ of the whole random field. Hence the product $p_1 p_2$ has the form of a Gibbs distribution of energy $U(l) = U_{str}(l) + U_{sem}(l)$. Therefore, the whole random field is a MRF defined on $(S, \Omega, \mathcal{C})$. $U_{str}(l)$ is the sum of an occurrence energy and a syntactic energy. $U_{sem}(l)$ is the sum of a recognition energy and an identification energy.

3.5 Occurrence and Recognition Potentials: These potentials are attached to cliques of $\mathcal{C}_p^{inf}$ and $\mathcal{C}_{pt}^{inf}$. They constitute three kinds of potential families. The first kind is associated to RVs of $\mathcal{N}_p^A$, and the two other kinds are associated to sub-RAs of RAs of $\mathcal{R}_{pt}^A$ defined by the following partitions: $\forall \beta_{ij} \in \mathcal{R}_{pt}^A,\ h_{\mathcal{R}}^{-1}(\beta_{ij}) = h_{\mathcal{R}}^{-1}(\beta_{ij}^{\rho_T}) \cup h_{\mathcal{R}}^{-1}(\beta_{ij}^{\rho_C})$, where $h_{\mathcal{R}}^{-1}(\beta_{ij}^t) = \{r \in h_{\mathcal{R}}^{-1}(\beta_{ij}) \mid \sigma_{\mathcal{R}}(r) = t\}$. All the families are constructed according to the same principle. We briefly describe, for instance, the potential family related to a sub-RA $\beta_{ij}^{\rho_T}$, whose contribution to $U(l)$ is weighted by the frequence of occurrence $f_{\rho_T}^{oc}[i,j]$ of a non empty realization of $\beta_{ij}^{\rho_T}$ in the database $\mathcal{B}$. If $h_{\mathcal{R}}^{-1}(\beta_{ij}^{\rho_T}) \neq \emptyset$, occurence potential $V_{\rho_T}^{oc}[c_{ij}^{inf}](l)$ is equal to $-K_{\rho_T}^{oc} f_{\rho_T}^{oc}[i,j]$, where $K_{\rho_T}^{oc} > 0$; otherwise this potential is zero. For each synthesized semantic attribute ρ_T-*Name* of $\mathcal{A}t[\beta_{ij}^{\rho_T}]$, if this attribute can be synthesized from $h_{\mathcal{R}}^{-1}(\beta_{ij}^{\rho_T})$, the recognition potential $V_{\rho_T}^{N}[c_{ij}^{inf}](l)$ is a positive function of the attribute value ranging from zero to $K_{\rho_T}^N[i,j] f_{\rho_T}^{oc}[i,j]$, where $K_{\rho_T}^N[i,j] > 0$; otherwise this potential is zero. This function has a basin shape centered around a mean parameter, and with a declivity depending on a variance parameter. These two parameters are estimated from the database $\mathcal{B}$. Constants are chosen according to the following constraint: $\Sigma_{\mathcal{A}t[\beta_{ij}^{\rho_T}]} K_{\rho_T}^N[i,j] = K_{\rho_T}^{oc}$. Hence, contribution to the global energy of the family constituted by $V_{\rho_T}^{oc}[c_{ij}^{inf}]$ and the different $V_{\rho_T}^{N}[c_{ij}^{inf}]$ is negative and varies from $-K_{\rho_T}^{oc} f_{\rho_T}^{oc}[i,j]$ to zero.

3.6 Syntactic and Identification Potentials: The global energy includes three other kinds of potentials with positive values. Two kinds introduce syntactic constraints and the last kind manages recognition failure cost.

A. Grammatical potentials: At any step of the relaxation, a sulcus is represented by a subgraph $\mathcal{G}_s$ possibly empty. This subgraph is made up of nodes labelled as belonging to sulcus core or sulcus branches, and of relations between these nodes and with $\mathcal{S}_{brain}$ and $\mathcal{P}_{med}$. In order to favour sulcus patterns which respect our interpretation of variability, potentials are attached to grammatical cliques of $\mathcal{C}^G$. A context-free web grammar $G_{\mathcal{G}_s}$ whose terminal set is $\mathcal{S}_{\mathcal{N}} \cup \mathcal{S}_{\mathcal{R}}$

describes usual patterns of subgraphs corresponding to sulci [3]. For each sulcus s, the grammatical potential $V_G[c_s^G](l)$ is zero if the subgraph $\mathcal{G}_s(l)$ can be parsed by $G_{\mathcal{G}_s}$, otherwise this potential is a rough distance to the language generated by $G_{\mathcal{G}_s}$, namely $K^G n_{cc}(\mathcal{G}_s(l))$, where $K^G > 0$ and $n_{cc}(\mathcal{G}_s(l))$ is the number of connected components of $\mathcal{G}_s(l)$. Since the node set of a subgraph $\mathcal{G}_s$ is already partitioned in two subsets, one for the core and one for branches, the parsing is unambiguous and can be performed with an efficient algorithm.

B. Potts model: A higher level constraint, induced from the hierarchical description of Fig. 2, intends to act on the realization structure of RVs and RAs which are not taken into account by the grammar $G_{\mathcal{G}_s}$. This is achieved using a Potts model (n-class Ising model) whose classes C_i^P are inferred from the partition of the brain in lobes and out of lobes leaves of $\mathcal{A}$. The class C_i^P associated with a lobe is the subset of $\mathcal{L}$ corresponding to RVs whose realizations belong anatomically to this lobe (see Fig. 2). The model expresses itself with potentials attached to cliques of $\mathcal{C}_2$: $\forall (n, n') \in S^2$, if $\exists C_i^P$ with $l(n) \in C_i^P$ and $l(n') \in C_i^P$, then $V^P[c_{nn'}] = 0$, otherwise the potential is equal to K^P ($K^P > 0$).

C. Identification Potentials: Thanks to the linearity of the semantic production yielding the single synthesized semantic attribute of the RV brain (α_0), contribution of this attribute can be decomposed in potentials attached to cliques of $\mathcal{C}_1$. $\forall n \in S$, if $l(n) = l_0$, $V^{int}[c_n] = K^{int} \lambda_{SS}^s(n)$, where $K^{int} > 0$; otherwise the potential is zero. Hence the cost of a full failure of the recognition process for a given SS increases linearly with the *SS-size* attribute value.

4 Conclusion

First recognition experiments using SA (Gibbs sampler) have been performed with the five first ARGs of database $\mathcal{B}$ with very satisfying results as regard the main sulci identification. The increase of $\mathcal{B}$ size will allow the study of the model hyper-parameter influence. This paper shows that the MRF framework provides an appealing way to combine syntactic and semantic constraints in a relaxation based recognition process relying on a structural prototype potentially subject to various kinds of deformations. The flexibility of the proposed construction principle with regard to the modelling of anatomical variability calls for adaptations to other similar recognition problems in the field of medical imaging.

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