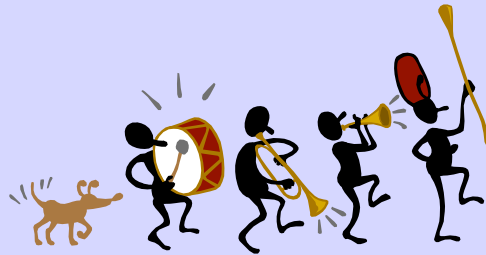


Computational models of biological systems



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Complexity in biology

- **Molecular level**
 - Regulatory gene networks
 - Protein folding
- **Cellular level**
 - Cell physiology
- **Organism level**
 - Immune system
 - Nervous system
- **Population level**
 - Population dynamics
 - Ecological systems

Does Neural Communication Grow on Trees?

Analysis of interspike intervals
sequences to learn and generalize
correlations among neurons

The Goals

- To search for discriminating parameters between neural substrates sottending different perceptive states
- To develop analysis strategies applicable to spontaneous neural activities
- To understand neural code
- To infer (thalamocortical) networks of neurons from simultaneous record of their firing activity
- To study the neurophysiology of (cronic) pain

State of the art

- **Gerstein, Aertsen 1985: Crosscorrelograms to study cooperative firing activity in simultaneously recorded populations of neurons**
- **Knierim, McNaughton 2001: analysis of records of hippocampal place-cells firing through embedding in a vector space**
- **Victor, Purpura 2001: metric space based on edit distance**

State of the art

- **Rieke et al. 1997; Borst, Theunissen 1999; Johnson et al 2001: Information theoretical analysis of neural coding**
- **Panzeri et al. 1999: study of the capacity of neural channels**

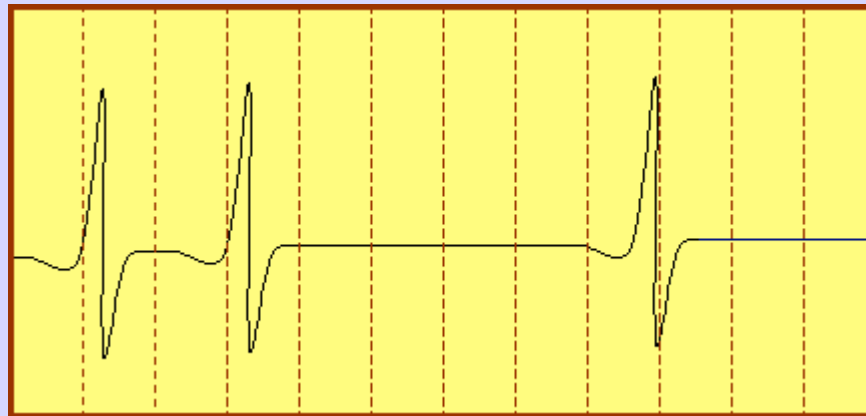
The tools

- **Longest Common Subsequence**
- **Lempel-Ziv complexity and LZ-Trees**
- **Tree Compression**

Encoding neuron's activity

Time Diagram

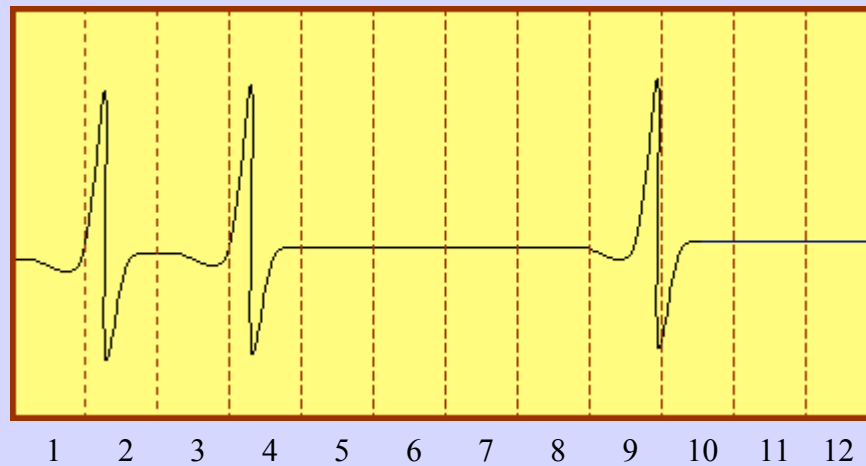
Record



Encoding neuron's activity

Time discretization

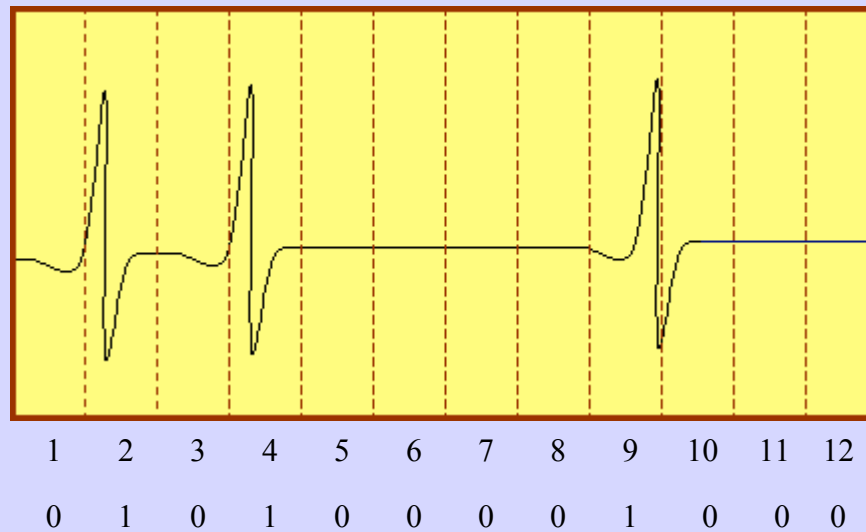
Record



Encoding neuron's activity

Binary encoding

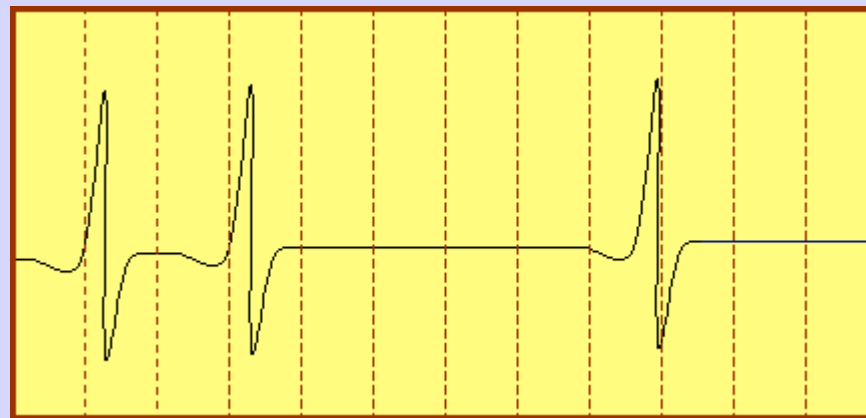
Record



Encoding neuron's activity

Encoding through interspike intervals

Record



Spike Times

2	4	9
---	---	---

Interspike Intervals

1	1	4	3
---	---	---	---

Alphabets, words, languages

Alphabet

=

finite set Σ of elements called *letters, characters or symbols*

Examples

$$\Sigma = \{0, 1\}$$

$$\Sigma = \{a, b, c, \dots, v, z\}$$

$$\Sigma = \{A, C, G, T\}$$

$$\Sigma = \{GLY, ALA, VAL, LEU\}$$

Alphabets, words, languages

Word, string or sequence over Σ

=

function w from $\{1, \dots, n\}$ to Σ

- We write $w = a_1 a_2 \dots a_n$ where $a_i = w(i) \in \Sigma$
- n is the **length** of the sequence, denoted by $|w|$
- Σ^* denotes the set of words over Σ

EX: $w = \text{AATGCA}$

$|w| = 6$

Empty word ϵ

$|\epsilon| = 0$

Alphabets, words, languages

Concatenation of w and v ,

=

word consisting of the characters from w , followed by the characters from v

- **ES:** $w = \text{AATGCATAGGC}$
 $v = \text{GGCTACT}$
 $wv = \text{AATGCATAGGCGGCTACT}$

Alphabets, words, languages

Prefix of w

=

string v such that $w = vt$ for some $t \in \Sigma^*$

Suffix of w

=

string v such that $w = tv$ for some $t \in \Sigma^*$

Longest Common Subsequence

Let S_1 and S_2 be two sequences over Σ .

S_2 is a subsequence of S_1 if it can be obtained from S_1 by removing some of its symbols

$S_1 =$	T	A	T	A	G	C	G	C	A	A	T	C	G
$S_2 =$	T	A	T		G	C			A		T		G

S_2 is subsequence of S_1

Longest Common Subsequence

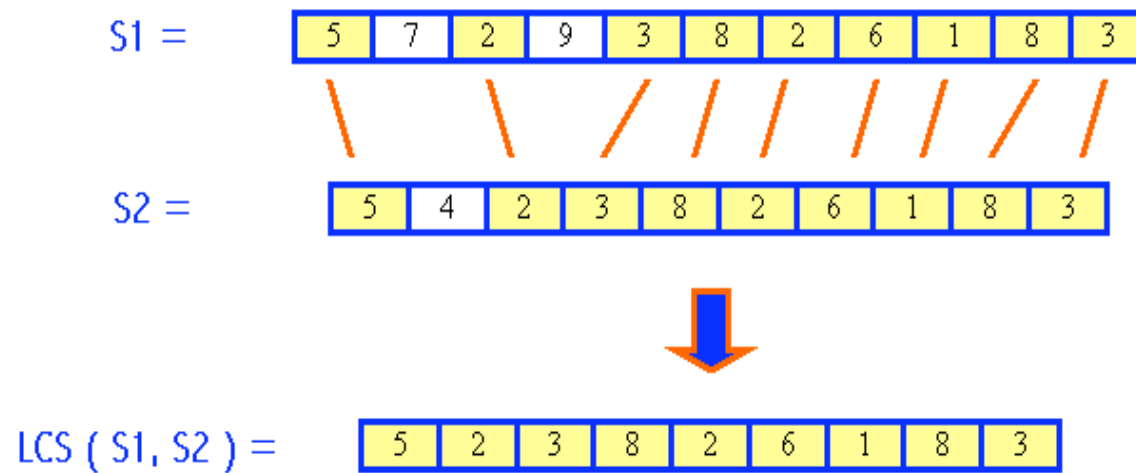
Let $\mathcal{S}$ be a set of sequences.

S is a *common subsequence* of $\mathcal{S}$ if it is a subsequence of every sequence in $\mathcal{S}$

Problem (LCS):

Given a set $\mathcal{S}$ of sequences, compute a longest common subsequence $lcs(\mathcal{S})$

Longest Common Subsequence, an example



Longest Common Subsequence

Def: Given an alphabet Σ and sequences $S_1, S_2 \in \Sigma^*$, $\text{lcs}(S_1, S_2)$ is a sequence W such that:

- 1) $\forall i, 1 \leq i \leq |W|-1,$
 $\exists j, j': 1 \leq j < j' \leq |S_1|, \exists k, k': 1 \leq k < k' \leq |S_2|$ such that:

$$W[i] = S_1[j] = S_2[k],$$

and

$$W[i+1] = S_1[j'] = S_2[k'];$$

- 2) $\neg \exists W' \in \Sigma^*: (1) \text{ and } |W'| > |W|.$

LCS in sequence analysis

The lcs is able to:

- Measure the similarity among a set of sequences through its length
- Exhibit the nature of the similarity through the symbols it contains

Applications in:

- data compression
- syntactic pattern recognition
- file comparison
- bioinformatics

Complexity of LCS

- Many polynomial time algorithms for LCS on two sequences
- Maier 78: LCS among k sequences is NP-hard
- Jiang, Li 95: nonapproximability results
- Jiang, Li 95: Long Run, approximation algorithm over a fixed alphabet
- Bonizzoni, Della Vedova, Mauri 98: better approximation ratio on the average

LCS, Relaxed

Def: Given an alphabet Σ , Σ^* , sequences $S_1, S_2 \in \Sigma^*$, $\epsilon \geq 0$,

$\text{LCS}_\epsilon(S_1, S_2)$ is a sequence W such that:

1) $\forall i, 1 \leq i \leq |W|-1,$

$\exists j, j': 1 \leq j < j' \leq |S_1|, \exists k, k': 1 \leq k < k' \leq |S_2|$ such that:

$$W[i] = S_1[j] = S_2[k] \pm \epsilon,$$

and

$$W[i+1] = S_1[j'] = S_2[k'] \pm \epsilon,$$

with $0 \leq \epsilon \leq 1$;

2) $\neg \exists W' \in \Sigma^*: (1) \text{ and } \ell(M_{W'}, S_1, S_2) > \ell(M_W, S_1, S_2),$

where:

LCS, Relaxed

$\square S_1, S_2, W \square \square^*,$

$M_w(S_1, S_2) := \{(j, k) \mid 1 \leq j \leq |S_1|, 1 \leq k \leq |S_2|, \exists i: 1 \leq i \leq |W| \text{ st:}$
 $W[i] = S_1[j] = S_2[k] \pm \square, \text{ with } 0 \leq \square \leq \square\};$

and

if $1 \leq i \leq |W|-1,$

then $\exists j': 1 \leq j' \leq |S_1|, \exists k': 1 \leq k' \leq |S_2|$ such that:

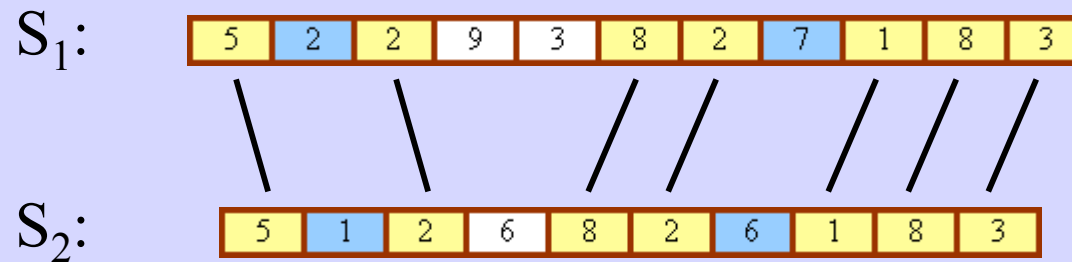
$(W[i+1] = S_1[j'] = S_2[k'] \pm \square) \wedge (j' > j) \wedge (k' > k),$

$\text{with } 0 \leq \square \leq \square; \}$

and where: $\square(M, S_1, S_2) := \max_{(j, k) \in M} \text{cost}(S[j], S[k]);$

and $\text{cost}(a, b) := 1 - |a - b|, \text{ with } a, b \in \Sigma.$

LCS (Relaxed), an example



$LCS(S_1, S_2)$:

5	2	2	8	2	7	1	8	3
---	---	---	---	---	---	---	---	---

Lempel-Ziv complexity

- L. & Z. propose as a complexity measure of a sequence the minimum number of steps needed to produce it from its prefixes using copy and paste operations
- L. & Z. give an algorithm to compute the above measure
- The complexity notion defined by L. & Z. is compatible with the algorithmic complexity theory (Kolmogorov, Chaitin)

Lempel-Ziv Algorithm

INPUT: $S \in \Sigma^*$; OUTPUT: $w = \{Q \in \Sigma^* \mid \exists i, j: S[i:j] = Q\}$;

$w := \epsilon$;

$w := w \cup \{\epsilon\}$;

$\text{curr} := 1$;

while $\text{curr} \leq |S|$ do

begin

$S' := S[\text{curr}:n]$ s.t. $S' \in w$ and $S' \circ S[n+1] \notin w$;

$w := w \cup \{S' \circ S[n+1]\}$;

$\text{curr} := n+2$;

end

NOTE: $S[i:j] = \epsilon$ for $j < i$

Lempel-Ziv -Trees

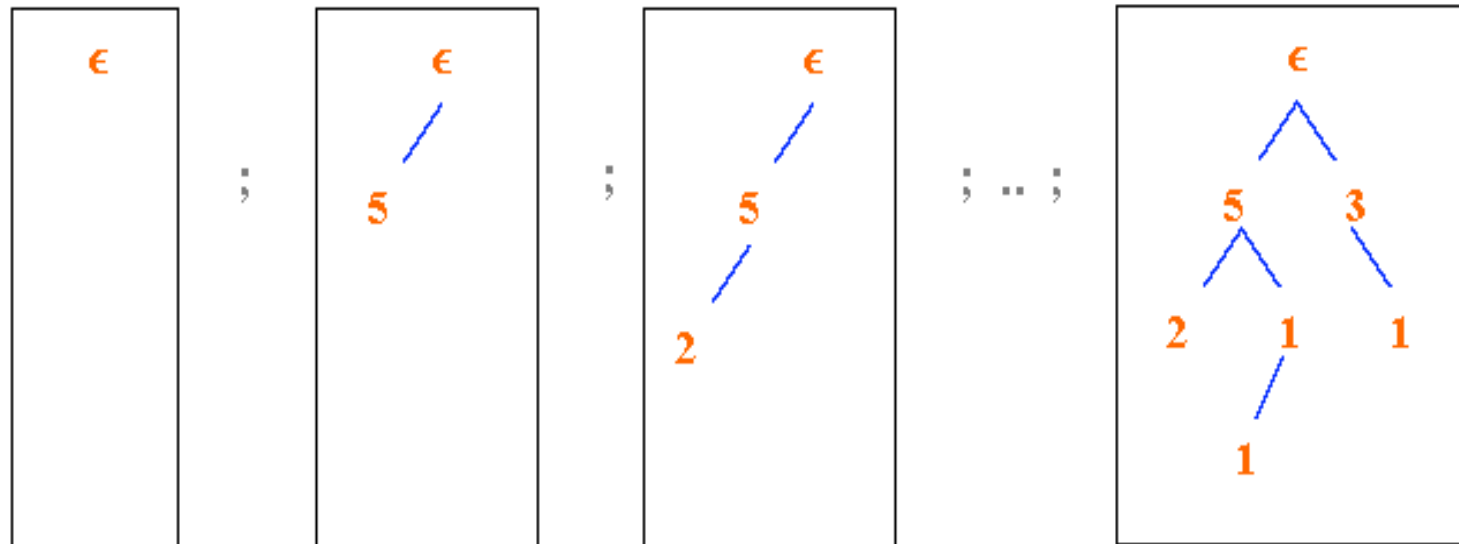
- The vocabulary w obtained can be organized in a hierarchical (tree) structure through the **prefix** relation:

$$\text{prefix} := \{ (u, v) \mid u, v \in w \text{ and } \exists i: u=v[1:i] \};$$

- Every word in w (except ϵ) can be obtained by adding a single symbol to another word in w ; hence, it can be encoded through a pointer to its maximal prefix, plus the last symbol
- $\text{LZCompl}(S) := |w| / |S|$

Lempel-Ziv-Trees, an example

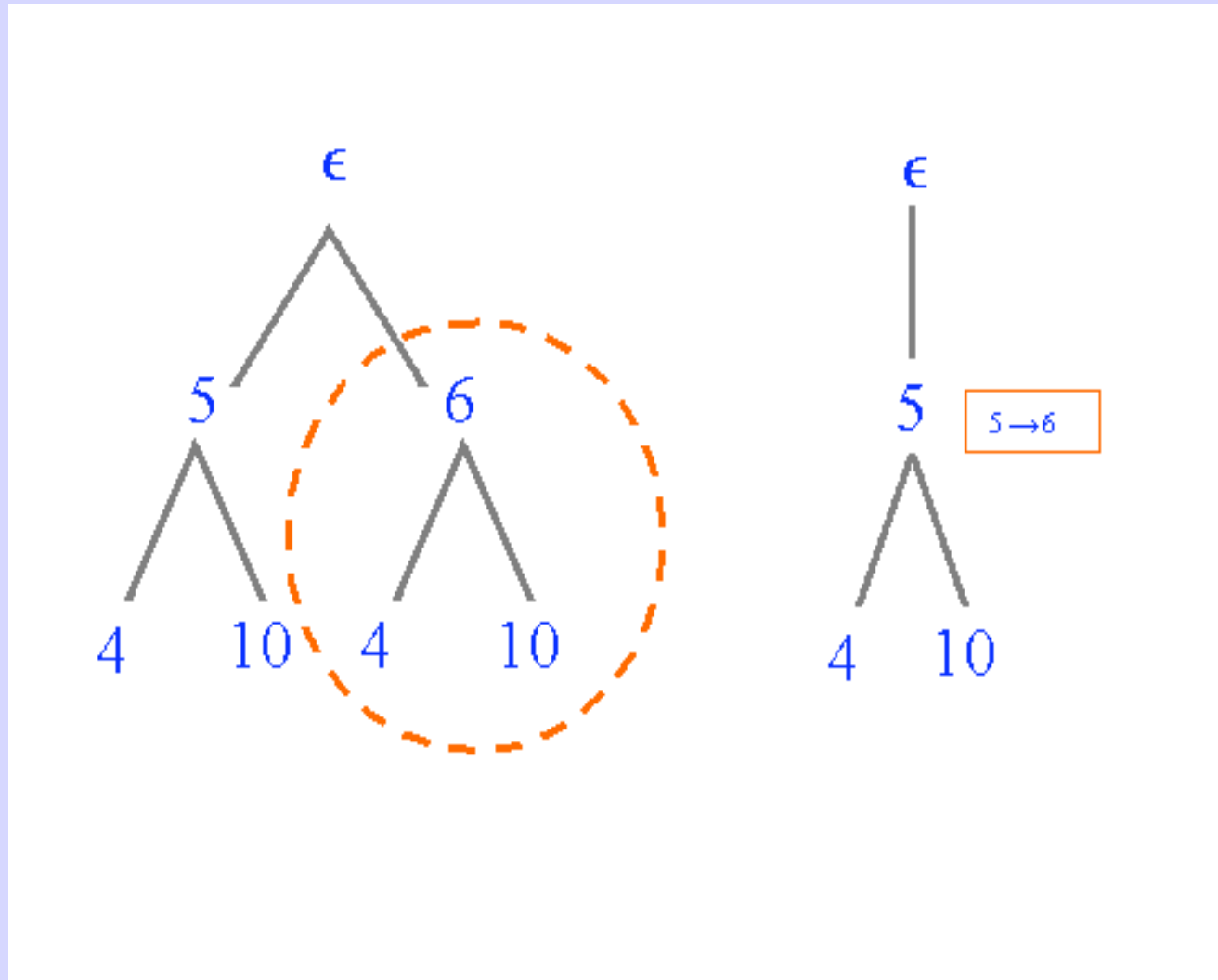
$S = 5 \cdot 52 \cdot 3 \cdot 51 \cdot 31 \cdot 511 \cdot$



Lempel-Ziv-Trees, meaning

- Acquisition of knowledge about the regularity of occurrence of symbol patterns in the sequence
- Structuring of knowledge so as to give a representation of the sequence shortest than the list of its symbols.

Tree Compression, an example



Tree Compression, meaning

- Reduction of redundancy in the tree structure
- Minimization of hierarchical knowledge representations
- Abstraction and generalization of the knowledge empirically acquired

Edit Distance between trees

Let T be a rooted labeled tree over a given alphabet Σ :

$$T = \langle V, E, r, \text{lab}: V \rightarrow \Sigma \rangle$$

and let have the following operations on it :

- Insertion of an element: $\Sigma^* a, a \Sigma^*$;
- Deletion of an element: $a \Sigma^* \rightarrow a \Sigma^*$;
- Substitution of the label of an element: $a \Sigma^* b, a, b \Sigma^*$;

Edit Distance between trees

$\text{EditOps} := \{a \mapsto b \mid a, b \in \text{Nodes} \setminus \{\text{root}\}\};$

Given the (metric) cost function :

$$\text{cost} : \text{EditOps} \rightarrow \mathbb{R}^+;$$

We define the cost of a sequence $\text{Sop} \in \text{EditOps}^*$ as

$$\text{cost}(\text{Sop}) = \sum_{i=1, \dots, |\text{Sop}|} \text{cost}(\text{Sop}[i]).$$

Edit Distance between trees

Def: Given two labeled trees T e T' , the **edit distance** between them is defined by:

$\text{Edist}(T, T') :=$

$$\min_{\text{Sop} \in \text{EditOps}^*} \{ |\text{Sop}| \mid T' = \text{Sop}(T) \}.$$

Tree Compression, Algorithm

```
proc TreeCompr( tot  $\square$  R, < &T, &Sop > ) :  
  
  if (  $V_T \neq \square$  ) {  
    if ( Edist(Tdx( $r_T$ ), Tsx( $r_T$ )) < threshold ) {  
      Prune(Tdx( $r_T$ ));  
      TreeCompr( tot, < Tdx, Sop $\circ$ SopEdist(Tdx( $r_T$ ), Tsx( $r_T$ )) > );  
    } else {  
      TreeCompr( tot, < Tdx, Sop > );  
      TreeCompr( tot, < Tsx, Sop > );  
    }  
  }  
}
```

Tree Complexity

Def: given a tree T , let T' and $Sop \subseteq EditOps$ the results of the compression of T through TreeCompr; the **Tree Complexity** of T is:

$$TC(T) := (|T'| / |T|) + \alpha \cdot \beta(Sop)$$

where $0 \leq \alpha \leq 1$

Tree Complexity

Teorema: The computation of the tree complexity of a tree T based on an Edit Distance *Structure Respecting* has time complexity :

$$O(D^3 \cdot |T|^2),$$

where D is the maximum degree of nodes in T .

Application

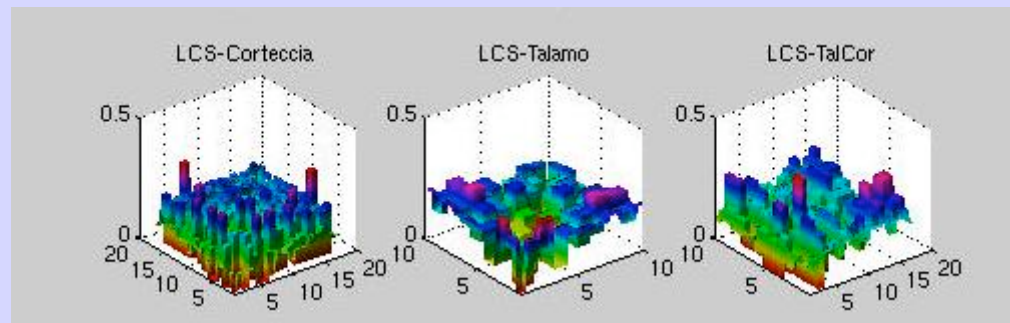
Analysis of sequences of *Interspike Intervals* from simultaneous recordings of thalamic and cortical cells populations.

Motivation: key role of thalamocortical areas in the elaboration of somatosensorial stimuli.

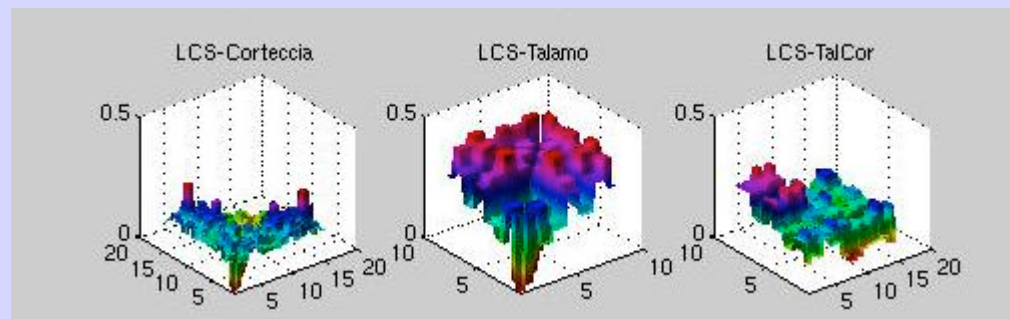
Goal: to discover rhythmic correlations among cells activities.

Application, LCS

NORM:

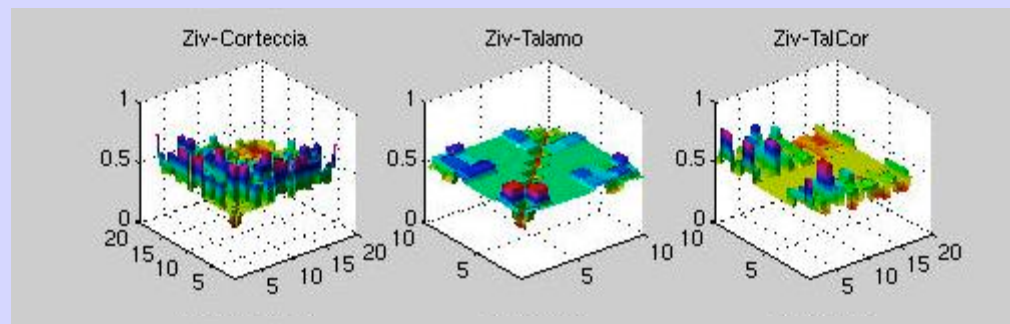


CCI:

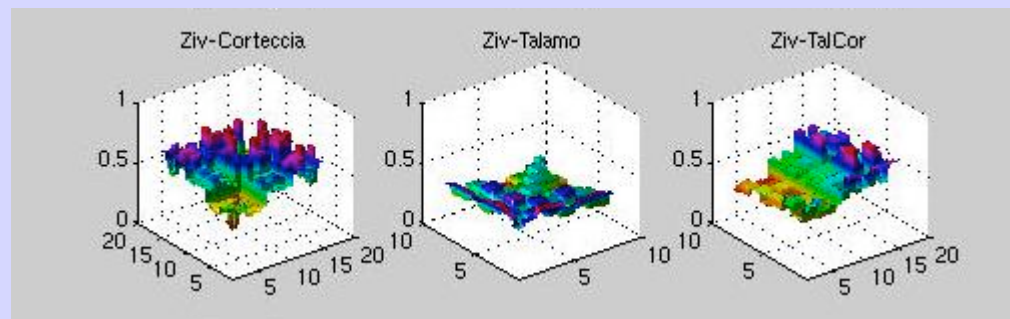


Application, LZ-Complexity

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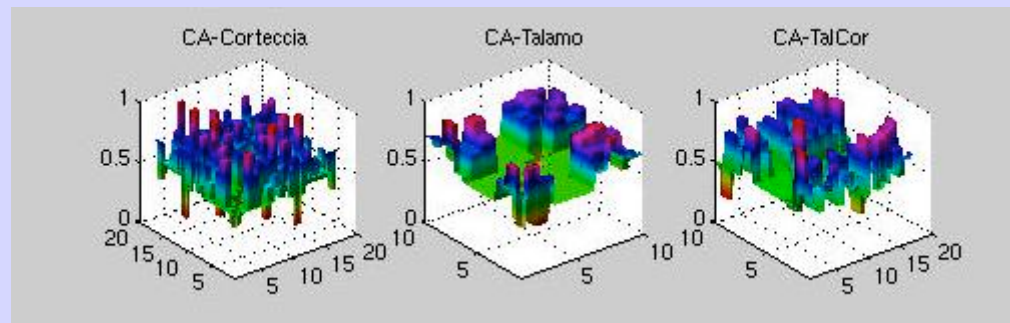


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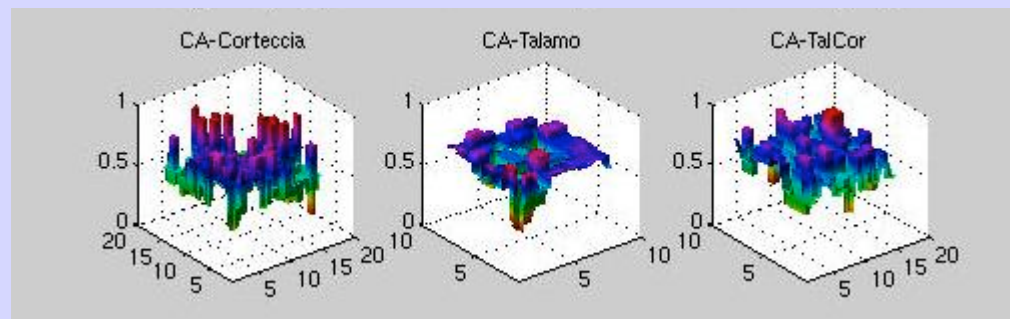


Applicazione, CplArb

NORM:



CCI:



Application, conclusions

The three kinds of di analysis help us to enlightening different aspects of the process we are observing:

- LCS

Omogeneity

- Ziv-Tree

Monotonicity

- Tree compression

Fault Tolerance