Homological Processing of Biomedical digital images: automation and certification

Jónathan Heras, Gadea Mata, María Poza and Julio Rubio

Department of Mathematics and Computer Science
University of La Rioja
Spain

June 27, 2011

1Partially supported by Ministerio de Educación y Ciencia, project MTM2009-13842-C02-01, and by European Commission FP7, STREP project ForMath, n. 243847
Table of Contents

1 Motivation

2 Automating the process

3 Main problems

4 Conclusions and further work
Table of Contents

1 Motivation
2 Automating the process
3 Main problems
4 Conclusions and further work
Motivation: Synapses counting

- **Synapses** are the points of connection between neurons
- **Relevance**: Computational capabilities of the brain
- The different number of synapses may be an important asset in the treatment of neurological diseases
Manual processing to count synapses

- Apply two different antibody markers, bassoon and synapsin
Manual processing to count synapses

- Process the images in order to count the synapses (*ImageJ*)
Manual processing to count synapses

- Overlap both images
Manual processing to count synapses

- The synapses are manually counted one by one
Goal to count synapses

Goal

Provide a reliable and automatic method for counting synapses in a neuron
Table of Contents

1 Motivation

2 Automating the process

3 Main problems

4 Conclusions and further work
Count synapses automatically

- New ImageJ plugin called *SynapCountJ*
- Improve the interaction with the *ImageJ* system
Count synapses automatically

- New ImageJ plugin called SynapCountJ
- Improve the interaction with the ImageJ system
- Steps
  - Determine the neuron morphology from one of those pictures (*NeuronJ plugin*)
Count synapses automatically

- New ImageJ plugin called *SynapCountJ*
- Improve the interaction with the *ImageJ* system
- Steps
  - Determine the neuron morphology from one of those pictures (*NeuronJ plugin*)
  - Overlap the images with the two markers with the one with the structure (*SynapCountJ*)
Motivation
Automating the process
Main problems
Conclusions and further work

Preprocessing the image
Algebraic Topology for digital images analysis
General method

Count synapses automatically

- New ImageJ plugin called *SynapCountJ*
- Improve the interaction with the *ImageJ* system
- Steps
  - Determine the neuron morphology from one of those pictures (*NeuronJ plugin*)
  - Overlap the images with the two markers with the one with the structure (*SynapCountJ*)
  - Invert the colors to show the synapses as black points

J. Heras, G. Mata, M. Poza and J. Rubio
Homological Processing of Biomedical digital images
The method

Digital Image
The method

Digital Image

\[ \text{algebraic structure} \]

Chain Complex
The method

Digital Image

\rightarrow \text{algebraic structure}

\rightarrow \text{Chain Complex}

\rightarrow \text{computing}

\rightarrow \text{Homology}
The method

Digital Image → Chain Complex → Homology

interpreting → algebraic structure → computing
Image to Chain Complex

Digital Image \rightarrow \text{Chain Complex} \rightarrow \text{Homology}
Image to Chain Complex

Digital Image → Chain Complex → Homology

interpretation

$C_0 = \mathbb{Z}\left[\text{vertices}\right]$  
$C_1 = \mathbb{Z}\left[\text{edges}\right]$  
$C_2 = \mathbb{Z}\left[\text{triangles}\right]$
Image to Chain Complex

Preprocessing the image

Algebraic Topology for digital images analysis

General method

Image to Chain Complex

Digital Image $\rightarrow$ Chain Complex $\rightarrow$ Homology

interpretation

triangulation

J. Heras, G. Mata, M. Poza and J. Rubio

Homological Processing of Biomedical digital images
Motivation

Automating the process

Main problems

Conclusions and further work

Preprocessing the image

Algebraic Topology for digital images analysis

General method

Image to Chain Complex

Digital Image \rightarrow \text{Chain Complex} \rightarrow \text{Homology}

\[
\begin{align*}
C_0 &= \mathbb{Z} \left[ \text{vertices} \right] \\
C_1 &= \mathbb{Z} \left[ \text{edges} \right] \\
C_2 &= \mathbb{Z} \left[ \text{triangles} \right]
\end{align*}
\]

J. Heras, G. Mata, M. Poza and J. Rubio

Homological Processing of Biomedical digital images
Image to Chain Complex

Digital Image $\xrightarrow{\text{triangulation}}$ Chain Complex

$C_0 = \mathbb{Z}[\text{vertices}]$  
$C_1 = \mathbb{Z}[\text{edges}]$  
$C_2 = \mathbb{Z}[\text{triangles}]$  

$0 \xleftarrow{\mathbb{Z}^{16}} \xrightarrow{d_1} \mathbb{Z}^{32} \xrightarrow{d_2} \mathbb{Z}^{16} \xleftarrow{0}$

J. Heras, G. Mata, M. Poza and J. Rubio  
Homological Processing of Biomedical digital images
Compute Homology

- Problem of diagonalizing matrices
- Compute the Smith Normal Form
Interpretation from Homology to Image

- $H_0$ measures the number of connected components
- $H_1$ measures the number of holes

In our case, $H_0$ counts the number of synapses
General method

Preprocessing the image
Algebraic Topology for digital images analysis

General method

Motivation
Automating the process
Main problems
Conclusions and further work

General method

Biomedical Image
Digital Image
Chain Complex
Homology

interpretation
General method

Biomedical Image → Digital Image → Chain Complex → Homology

interpretation
General method

Biomedical Image → Digital Image → Chain Complex → Homology

interpretation
General method

Biomedical Image → Digital Image → Chain Complex → Homology

- **properties**
- **interpretation**
Table of Contents

1 Motivation

2 Automating the process
   - Preprocessing the image
   - Algebraic Topology for digital images analysis
   - General method

3 Main problems
   - Reduce the size: Discrete Morse theory
   - Safety of the results: Certification of the programs

4 Conclusions and further work
Problems

- Size of the images
- Safety of the results
Problems

- Size of the images $\rightarrow$ Discrete Morse theory
- Safety of the results $\rightarrow$ Certification of the programs
The method

Digital Image → Chain Complex

interpreting

algebraic structure → computing

Homology

J. Heras, G. Mata, M. Poza and J. Rubio

Homological Processing of Biomedical digital images
The method

Digital Image → Chain Complex

interpreting

algebraic structure → reduction

computing

Homology
The method

Digital Image → interpreting → Chain Complex → reduction → Homology

Digital Image → algebraic structure → computing

J. Heras, G. Mata, M. Poza and J. Rubio

Homological Processing of Biomedical digital images
Reduction of chain complex

- Reduce information keeping the homological properties
- Discrete Morse Theory
  - Vector fields are a tool to cancel “useless” information
Reduction of chain complex

- Reduce information keeping the homological properties
- Discrete Morse Theory
  - Vector fields are a tool to cancel “useless” information
Reduction of chain complex

- Reduce information keeping the homological properties
- Discrete Morse Theory
  - Vector fields are a tool to cancel “useless” information

Digital Image → Chain Complex → Homology

0 ← ℤ ← ℤ ← 0 ← 0
Discrete Morse Theory

Definition

Let $C_* = (C_p, d_p)_{p \in \mathbb{Z}}$ be a free chain complex with distinguished $\mathbb{Z}$–basis $\beta_p \subset C_p$. A $(p-1)$-cell $\sigma$ is a face of a $p$-cell $\tau$ if the coefficient of $\sigma$ in $d\tau$ is non-null. It is a regular face if this coefficient is $+1$ or $-1$.

Definition

A discrete vector field on $C_*$ is a collection of pairs $V = \{(\sigma_i, \tau_i)\}_{i \in \beta}$ satisfying the conditions:

1. Every $\sigma_i$ is some element of $\beta_p$, in which case the other corresponding component $\tau_i \in \beta_{p+1}$. The degree $p$ depends on $i$ and in general is not constant.

2. Every component $\sigma_i$ is a regular face of the corresponding component $\tau_i$.

3. A generator of $C_*$ appears at most one time in $V$. 

J. Heras, G. Mata, M. Poza and J. Rubio

Homological Processing of Biomedical digital images
Discrete Morse Theory

**Definition**

A *V-path of degree* $p$ is a sequence $\pi = ((\sigma_{i_k}, \tau_{i_k}))_{0 \leq k < m}$ satisfying:

1. Every pair $((\sigma_{i_k}, \tau_{i_k}))$ is a component of $V$ and the cell $\tau_{i_k}$ is a $p$-cell
2. For every $0 < k < m$, the component $\sigma_{i_k}$ is a face of $\tau_{i_{k-1}}$, non necessarily regular, but different from $\sigma_{i_{k-1}}$

**Definition**

A *discrete vector field* $V$ is admissible if for every $p \in \mathbb{Z}$, a function $\lambda_p : \beta_p \rightarrow \mathbb{Z}$ is provided satisfying the property: every $V$-path starting from $\sigma \in \beta_p$ has a length bounded by $\lambda_p(\sigma)$.
Discrete Morse Theory

**Definition**

A cell \( \chi \) which does not appear in a discrete vector field \( V = \{(\sigma_i, \tau_i)\}_{i \in \beta} \) is called a *critical cell*.

**Vector-Field Reduction Theorem**

Let \( C_* = (C_p, d_p, \beta_p)_p \) be a free chain complex and \( V = \{(\sigma_i, \beta_i)\}_{i \in \beta} \) be an admissible discrete vector field on \( C_* \). Then the vector field \( V \) defines a canonical reduction \( \rho = (f, g, h) : (C_p, d_p) \Longrightarrow (C_p^c, d'_p) \) where \( C_p^c = \mathbb{Z} \left[ \beta_p^c \right] \) is the free \( \mathbb{Z} \)-module generated by the critical \( p \)-cells.

---


J. Heras, G. Mata, M. Poza and J. Rubio

Homological Processing of Biomedical digital images
Discrete vector field over matrices

- 2D-images
- Chain complex associated with an image is finite
  \[ 0 \xleftarrow{d_0} C_0 \xleftrightarrow{d_1} C_1 \xleftrightarrow{d_2} C_2 \xrightarrow{} 0 \]
- Differential maps can be represented by integer matrices
- Reduction chain complex $\rightarrow$ Reduction matrices
A *vector field* \( V \) for a matrix \( M \in \text{Mat}_{m,n}(\mathbb{Z}) \) is a set of integer pairs \( \{(a_i, b_i)\}_i \) satisfying these conditions:

1. \( 1 \leq a_i \leq m \) and \( 1 \leq b_i \leq n \)
2. The entry \( M[a_i, b_i] \) is \( \pm 1 \)
3. The indices \( a_i \) (respectively \( b_i \)) are pairwise different
**Goal**

- Let $M_n$ be a finite matrix which represents the differential map $d_n$ of $C_*$
  - Compute an admissible discrete vector field $V$ from $M_n$
  - Obtain a new matrix $\hat{M}_n$ from $M_n$ and $V$
Goal

- Let $M_n$ be a finite matrix which represents the differential map $d_n$ of $C_*$
  - Compute an admissible discrete vector field $V$ from $M_n$
  - Obtain a new matrix $\hat{M}_n$ from $M_n$ and $V$

In our case, we have to reduce two matrices $M_1$ and $M_2$. Compute the homology groups of $C_*$ with $\hat{M}_1$ and $\hat{M}_2$ can be much faster.
Reduction of Chain Complex

- Implemented in Haskell

**Algorithm 1**

*Input:* an integer matrix $M_n$

*Output:* an admissible discrete vector field $V$

**Algorithm 2**

*Input:* an integer matrix $M_n$

*Output:* a reduced matrix $\hat{M}_n$
The method

Digital Image → algebraic structure → Chain Complex → reduction → computing → Homology
The method

Digital Image → algebraic structure → Chain Complex → reduction → computing → Homology

J. Heras, G. Mata, M. Poza and J. Rubio

Homological Processing of Biomedical digital images
Coq/SSReflect

- **Coq**
  - Theorem prover assistant
  - High logic order

- **SSReflect**
  - Extension of Coq
  - Introduce new tactics and libraries
  - Used to formalize of the Four Colour Theorem
Steps

1. Translate our *Haskell* code into the *Coq* language
2. Define the test functions to specify the properties which our programs must satisfy
3. State and prove the lemmas which ensure the correctness of our programs
Steps

1. Translate our Haskell code into the Coq language
2. Define the test functions to specify the properties which our programs must satisfy
3. State and prove the lemmas which ensure the correctness of our programs

Example: Let $M$ be an integer matrix, $(\text{vectorCvd } M)$ builds an admissible discrete vector field

\begin{verbatim}
Lemma admissible-vf:
forall M, (int-matrix M) -> (admissible (vectorCvd M))
\end{verbatim}
# Table of Contents

1. **Motivation**
2. **Automating the process**
3. **Main problems**
4. **Conclusions and further work**

---

J. Heras, G. Mata, M. Poza and J. Rubio

Homological Processing of Biomedical digital images
Conclusions

- Methodology to study Biomedical images
- Programs partially verified with Theorem Prover tools
- Application to count synapses
Further work

- Verification of our Haskell programs by means of Coq/SSReflect is still an ongoing work
- Verification of Smith Normal Form of a matrix
- Find other applications of our homological tools in the Biomedical imaging context
Homological Processing of Biomedical digital images: automation and certification

Jónathan Heras, Gadea Mata, María Poza and Julio Rubio

Department of Mathematics and Computer Science
University of La Rioja
Spain

June 27, 2011

2Partially supported by Ministerio de Educación y Ciencia, project MTM2009-13842-C02-01, and by European Commission FP7, STREP project ForMath, n. 243847