Computational Homology Project (CHomP)

Paweł Pilarczyk

Department of Mathematics
Kyoto University
Kyoto, Japan

Mathematical Software and Free Documents 4
Saitama University, Tokyo, March 26, 2007

Talk Outline

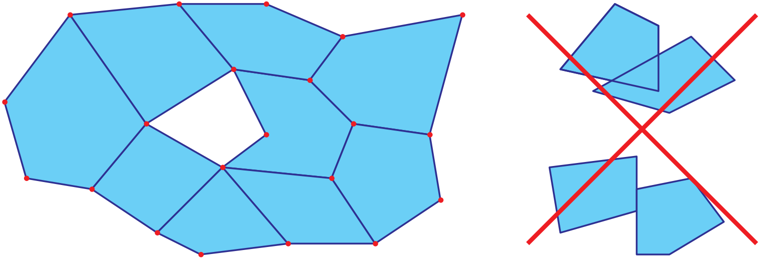
1. What is Homology?
   - The Homology Functor
   - Geometric Interpretation of Homology
   - Relative Homology
2. How can it be computed?
   - An Algebraic Algorithm
   - Geometric Reduction
   - Maps Induced in Homology by Continuous Maps
3. Software and Applications
   - Computational Homology Project
   - Entertainment
   - Serious Applications

CHomP

Algebraic Topology

TOPOLOGY	⟶	ALGEBRA
topological space	⟶	abelian group
continuous map	⟶	homomorphism
homeomorphism	⟶	group isomorphism
“similar” spaces	⟶	isomorphic groups
“similar” maps	⟶	the same homomorphisms
substantially different spaces	⟵	different groups
substantially different maps	⟵	different homomorphisms

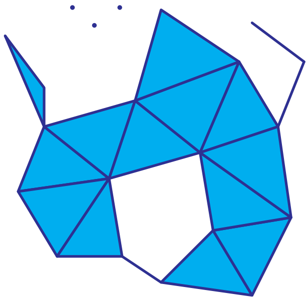
Cellular Complexes (Polyhedra)

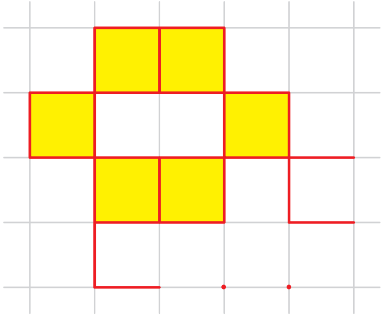


The topological space is built of cells:

- Each cell is homeomorphic with an *n*-dimensional ball.
- The intersection of two cells is a lower-dimensional cell.
- The “boundary” of a cell is a union of cells.

Simplicial Complexes and Cubical Complexes

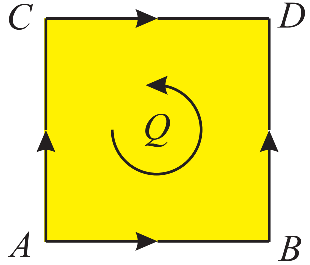




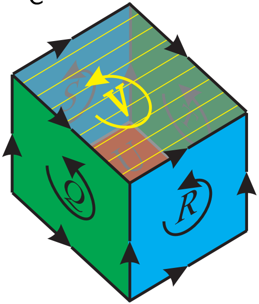
Each k-dimensional cell is a simplex with $k+1$ vertices. A k-dimensional simplex is the convex hull of a set of $k+1$ affinely independent points.

Each k-dimensional cell is a product of unit intervals $[i, i+1]$ or degenerate intervals $[i, i] = \{i\}$ with respect to the uniform rectangular grid.

Algebraic Boundaries of Cells



$$\partial(\overrightarrow{AB}) = B - A$$
$$\partial(\overrightarrow{BD}) = D - B$$
$$\partial(\overrightarrow{AC}) = C - A$$
$$\partial(\overrightarrow{CD}) = D - C$$



$$\partial Q = \overrightarrow{AB} + \overrightarrow{BD} - \overrightarrow{CD} - \overrightarrow{AC}$$
$$\partial A = \partial B = \partial C = \partial D = 0$$
$$\partial Z = Q - T + R - S + U - V$$

Note: $\partial(\partial Q) = \partial(\overrightarrow{AB} + \overrightarrow{BD} - \overrightarrow{CD} - \overrightarrow{AC}) =$
$(B - A) + (D - B) - (D - C) - (C - A) = 0.$

CHomP

Homology Groups

C_k — the group of k-dimensional **chains**: free abelian group generated by all the k-dimensional cells, defined for $k \in \mathbb{Z}$; note: $C_k = \{0\}$ if there are no cells of dimension k

$\partial_k \colon C_k \to C_{k-1}$ — the **boundary operator**; note: $\partial_0 \equiv 0$

$B_k := \operatorname{im} \partial_{k+1} \subset C_k$ — the group of **boundaries**

$Z_k := \ker \partial_k \subset C_k$ — the group of **cycles**

Note: $\partial \circ \partial \cong 0$*; therefore,* B_k *is a subgroup of* Z_k*.*

$H_k := Z_k / B_k$ — the k-th **homology group**

CHomP

The Classification Theorem for Abelian Groups

Theorem

If G is a finitely generated commutative group, then

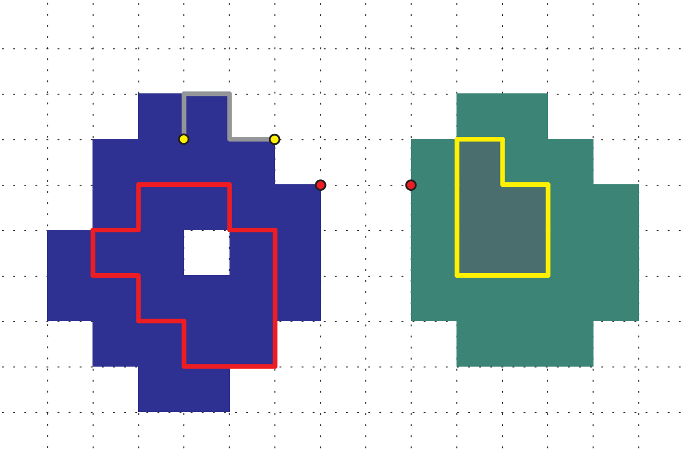
$$G \cong \mathbb{Z}_{p_1^{n_1}} \oplus \cdots \oplus \mathbb{Z}_{p_k^{n_k}} \oplus F,$$

where $p_1, \ldots, p_k$ are primes, $n_1, \ldots, n_k$ are positive integers, and $F = \mathbb{Z} \oplus \cdots \oplus \mathbb{Z}$ is a free group. This factorization is unique (up to the order of factors).

$\beta_q := \operatorname{rank} F$ (in H_q) — q-th **Betti number**

$p_i^{n_i}$ (for $i = 1, \ldots, k$) — torsion coefficients

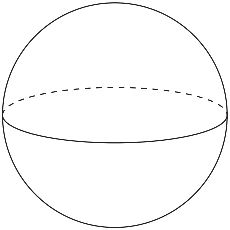
Cycles and Boundaries



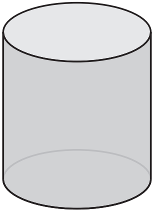
Cycles indicated in red are not boundaries.
Cycles drawn in yellow are boundaries of grey chains.

Connected Components, Tunnels and Cavities

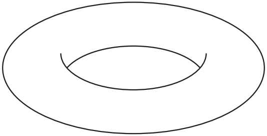
β_0 equals the number of connected components
β_1 indicates the number of holes (tunnels in 3D)
β_2 represents the number of cavities



$\beta_0 = 1$
$\beta_1 = 0$
$\beta_2 = 1$



$\beta_0 = 1$
$\beta_1 = 1$
$\beta_2 = 0$



$\beta_0 = 1$
$\beta_1 = 2$
$\beta_2 = 1$

Relative Homology

X — cellular complex

$A \subset X$ — cellular subcomplex of X

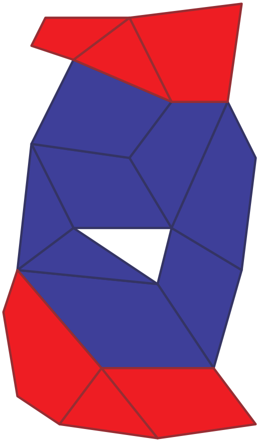
$C(A), C(X)$ — chain complexes of A and X

$C(X, A) := C(X)/C(A)$ — quotient group

$C(X, A) = \langle \{ \widehat{Q} \mid Q \subset X \text{ and } Q \not\subset A \} \rangle$

$\partial_q \colon C_q(X, A) \to C_{q-1}(X, A)$

$H_q(X, A) := Z_q(X, A)/B_q(X, A)$



The Main Idea of the Homology Algorithm

In order to compute the homology of the chain complex

$$C_n \xrightarrow{\partial_n} C_{n-1} \xrightarrow{\partial_{n-1}} \cdots \xrightarrow{\partial_1} C_0 \xrightarrow{\partial_0} \{0\}$$

take all the matrices D_q of the boundary homomorphisms ∂_q with respect to the same bases in each C_q, $q = 0, \ldots, n$.

1. Change the bases of each C_q to make the matrices D_q as simple as possible.
2. Determine the Betti numbers and torsion coefficients from the matrices D_q.

Smith Normal Form of ∂_q

$$
\begin{array}{c c}
 & \begin{array}{ccc|ccc} e_1 & \dots & e_l & e_{l+1} & \dots & e_n \end{array} \\
\begin{array}{c} e'_1 \\ \vdots \\ e'_l \\ e'_{l+1} \\ \vdots \\ e'_m \end{array} &
\left[\begin{array}{ccc|ccc}
b_1 & & & 0 & \dots & 0 \\
 & \ddots & & \vdots & & \vdots \\
 & & b_l & 0 & \dots & 0 \\
\hline
0 & \dots & 0 & 0 & \dots & 0 \\
\vdots & & \vdots & \vdots & & \vdots \\
0 & \dots & 0 & 0 & \dots & 0
\end{array}\right]
\end{array}
$$

where $b_i \geq 1, \quad b_1 \mid b_2 \mid \cdots \mid b_l$

$\{e_{l+1}, \dots, e_n\}$ is a basis for Z_p

$\{e'_1, \dots, e'_l\}$ is a basis for W_{p-1} such that $\partial_p(C_p) \subset W_{p-1}$

$\{b_1 e'_1, \dots, b_l e'_l\}$ is a basis for B_{p-1}

$b_i > 1$: torsion coefficients of H_{p-1}

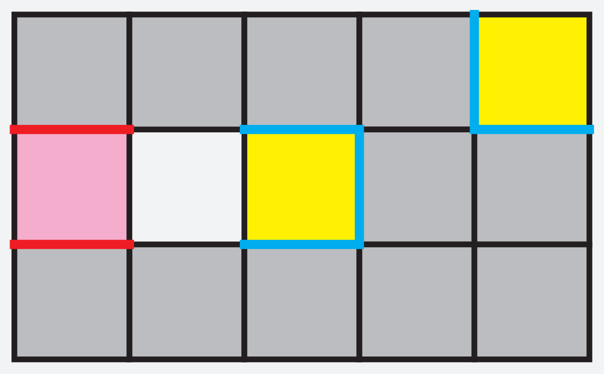
Betti numbers:
$\beta_p = \text{rank}\, Z_p - \text{rank}\, W_p$

Acyclic Sets

Definition

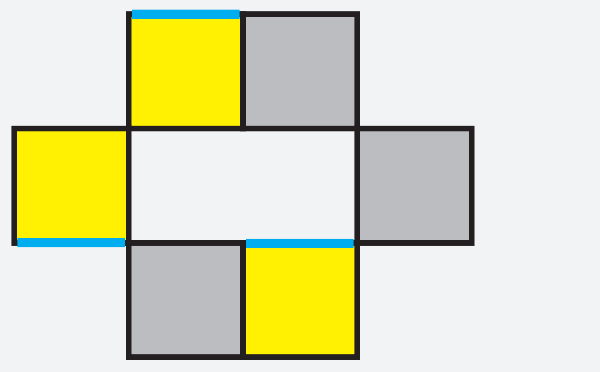
A set is **acyclic** if its homology is the same as the homology of a single point, i.e., $H_0 \cong \mathbb{Z}$ and $H_q \cong \{0\}$ for $q \neq 0$.

Acyclic Intersection



If the intersection of a cell with the remainder of the cellular polyhedron is acyclic, then this cell can be removed without affecting the homology.

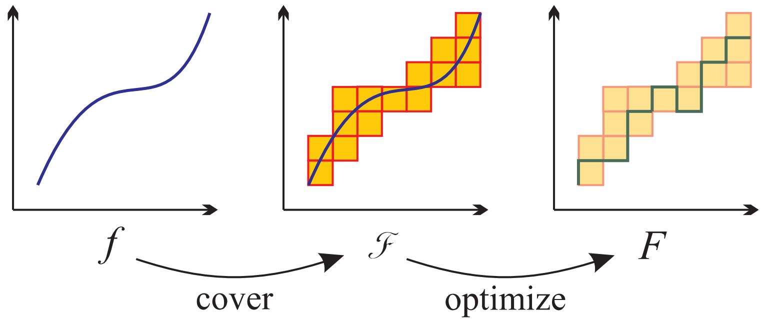
Free Face Collapses



A **free face** is a cell which is in the boundary of exactly one cell. Free faces can be removed together with the interior of the corresponding cell.

CHomP

Computing the Maps Induced in Homology

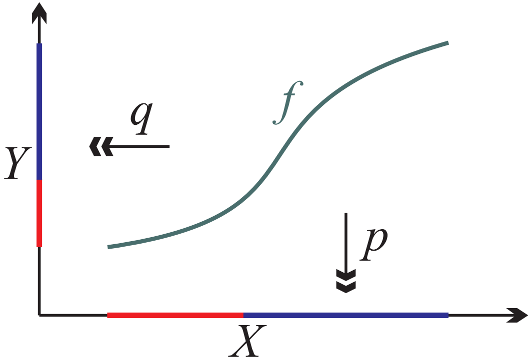


Use cubical cells to cover the graph of a continuous map:

K. Mischaikow, M. Mrozek, P. Pilarczyk, *Graph approach to the computation of the homology of continuous maps*, Foundations of Computational Mathematics (2005), Vol. 5, No. 2, 199–229.

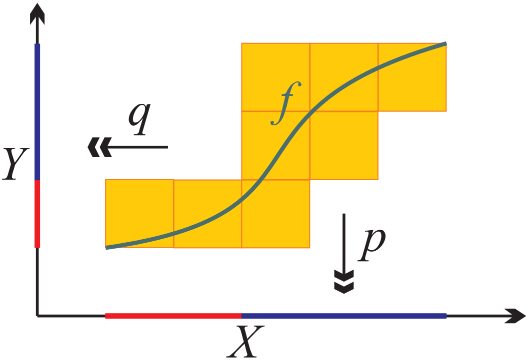
CHomP

Graph Approach to the Homology of Continuous Maps



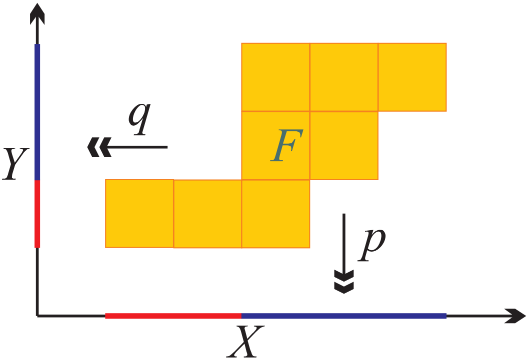
p is a homeomorphism, so $f = q \circ p^{-1}$, and $f_* = q_* \circ (p_*)^{-1}$.

Graph Approach to the Homology of Continuous Maps



Cover the graph of the map f with cubical cells.

Graph Approach to the Homology of Continuous Maps



Unfortunately, the projection $p\colon \Gamma_F \to X$ is not a homeomorphism.

Vietoris Maps

Definition

$X \subset \mathbb{R}^n$, $Y \subset \mathbb{R}^m$ — compact ENRs. A continuous map $f : X \to Y$ is a Vietoris map if:

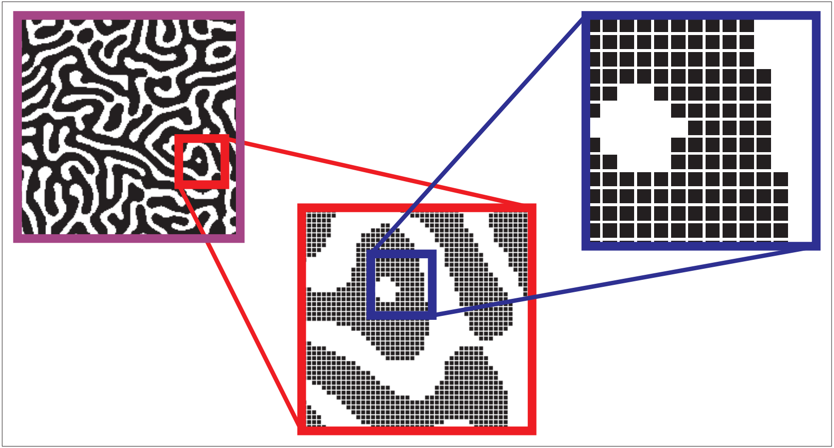
- $C \subset Y$ is compact $\implies f^{-1}(C)$ is compact,
- $f^{-1}(y)$ is acyclic for every $y \in Y$.

Theorem (Vietoris-Begle Mapping Theorem)

If $f : X \to Y$ is a Vietoris map and X, Y are compact, then the map induced in homology $f_* : H_*(X) \to H_*(Y)$ is an isomorphism.

If our $F : X \multimap Y$ is acyclic, then $p : \Gamma_F \to X$ is a Vietoris map, and we can define $F_* := q_* \circ (p_*)^{-1} : H_*(X) \to H_*(Y)$.

Pixel Images as Sets of Cubical Cells

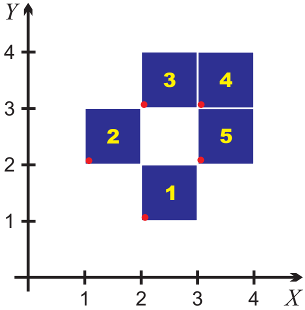


CHomP and CAPD

- Computational Homology Project (CHomP)
  - `http://chomp.rutgers.edu/`
  - M. Allili, Z. Arai, M. Gameiro, T. Kaczynski, W. Kalies, K. Mischaikow, M. Mrozek, P. Pilarczyk, T. Wanner, ...
  - cubical/simplicial homology (also chain complexes), including relative homology, and homomorphisms induced by continuous maps on cubical sets
- Computer Assisted Proofs in Dynamics (CAPD)
  - `http://capd.wsb-nlu.edu.pl/`
  - Z. Galias, T. Kapela, M. Mrozek, P. Pilarczyk, D. Wilczak, M. Zalewski, P. Zgliczyński, M. Żelawski, and others
  - interval arithmetic, integration of ODEs, new cubical homology algorithms based on bitmaps

Cubical Sets

Cubes are represented by vertices with minimal coordinates.



(2,1)		2 1
(1,2)		1 2
(2,3)	or	2 3
(3,3)		3 3
(3,2)		3 2

Computing the Homology of a Set of Cubes

- homcubes setofcubes.txt

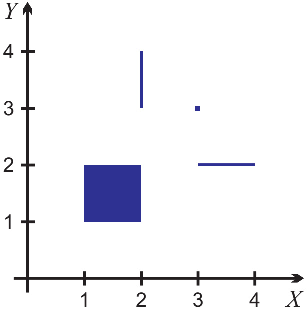
```
HOMCUBES, ver.  3.06, 12/20/05.  Copyright (C) 1997-2006 by Pawel Pilarczyk.
This is free software.  No warranty.  Consult 'license.txt' for details.
Reading cubes to X from 'setofcubes.txt'...  5 cubes read.
300 bit fields allocated (0 MB) to speed up 2-dimensional reduction.
Reducing full-dim cubes from X...  1 removed, 4 left.
Transforming X into a set of cells...  4 cells created.
Collapsing faces in X...  16 removed, 16 left.
Note:  The dimension of X decreased from 2 to 1.
Creating the chain complex of X...  Done.
Vertices used:  12 of dim 2.
Time used so far:  0.00 sec (0.000 min).
Computing the homology of X over the ring of integers...
Reducing D_1:  0 + 7 reductions made.
H_0 = Z
H_1 = Z
Total time used:  0.00 sec (0.000 min).
```

- chomp setofcubes.txt

```
1 1
```

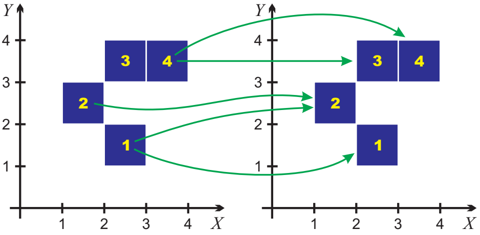
Elementary Cubical Cells

Lower-dimensional cells are either represented as products of intervals, or by the two opposite vertices (min & max).



[1,2] x [1,2]		[(1,1) (2,2)]
[3,4] x [2]	or	[(3,2) (4,2)]
[2] x [3,4]		[(2,3) (2,4)]
[3] x [3]		[(3,3) (3,3)]

Multivalued Cubical Maps



$$F : X \to 2^Y$$

$$F(q) \subset Y$$

```
(2,1) -> {(2,1) (1,2)}
(1,2) -> {(1,2)}
(2,3) -> {}
(3,3) -> {(2,3),(3,3)}
```

The Multi-Engine Program chomp

- Handling of multiple data formats
  - 2-dimensional Bitmap Images (BMP)
  - *n*-dimensional Bitmap Images
  - lists of full cubes or cubical cells
- Many algorithms (a.k.a. *engines*) to choose from
  - BK (the original Bill Kalies' algorithm)
  - BK_LT (with lookup tables)
  - MM_AR (algebraic reductions—Marian Mrozek)
  - MM_ASLT (acyclic subset with lookup tables)
  - MM_CR (coreductions)
  - PP (the old algorithms by P.P.)

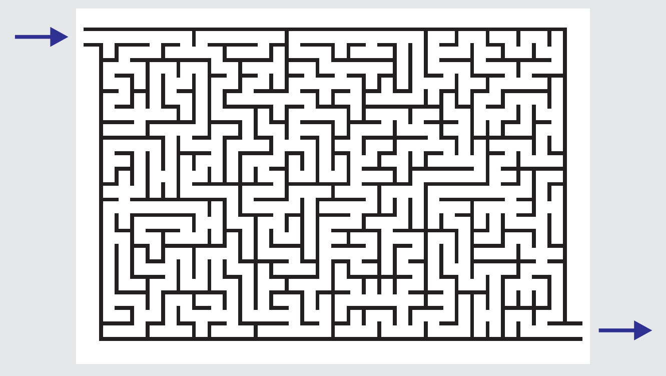
Example Computation with chomp

```
chomp --verbose kleinbot.cub
Start time:  Tue Jun 06 01:57:37 2006
This is CHomP, version 1.00 beta4, 04/28/06.  Copyright (C) 1997-2006
by William Kalies, Marian Mrozek, Pawel Pilarczyk, and others.
This is free software.  No warranty.  Consult 'license.txt' for details.
Analyzing the type of 'kleinbot.cub'...  text list of cubes.
Determining the most appropriate homology engine...
     - BK does not support dimension 4.
     - BK_LT does not support dimension 4.
     - MM_ASLT does not support dimension 4.
The engine(s) upon consideration are:  PP MM_CR MM_AR.
     + PP is the first choice.
Scanning 'kleinbot.cub'...
204 cubes of dim 4 in [-4,7]x[-5,6]x[-1,3]x[-1,2].
     + MM_CR is faster.
     - MM_AR would be slower.
Using the homology engine 'MM_CR'.
Time used so far:  0.00 sec (0.000 min).
Reading cubes from 'kleinbot.cub'...
Time used so far:  0.00 sec (0.000 min).
Computing homology...
The computed homology is (Z, Z + Z_2).
Betti numbers:  1 1 0 0 0
Total time used:  0.01 sec (0.000 min).
```

Other Programs in the CHomP Package

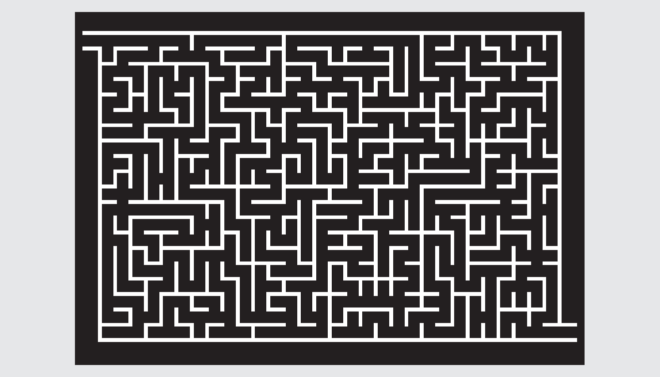
- `homsimpl`—homology computation of simplicial complexes
- `homchain`—homology computation of chain complexes and chain maps
- converting cubical sets (BMP / binary format / bitcode)
- programs for manipulating with cubical sets (cubdiff, cubslice, psetconn, ...)
- visualization of cubes (`showcubes`)
- other programs (`cubtop`, ...)

Solving a Maze



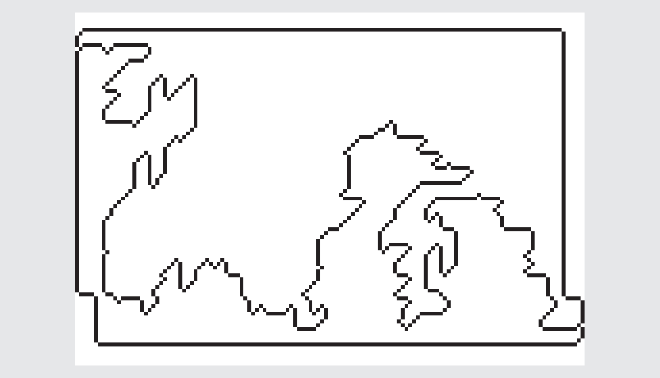
- Is there a way through the maze?
- If so, then is it unique?
- How to find the way if it exists?

Solving a Maze



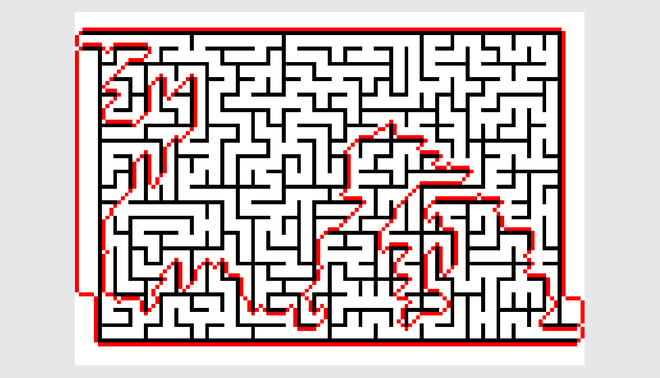
- Invert the picture.
- Compute the homology of the black area.
- Find the generators of H_1.

Solving a Maze



- The picture of the generators of H_1.
- $H_0 \cong \mathbb{Z} \implies$ no isolated areas inside the maze.
- $H_1 \cong \mathbb{Z} \oplus \mathbb{Z} \implies$ exactly one way through the maze.

Solving a Maze



- The way through the maze.
- The same algorithm works for higher-dimensional mazes.
- Computation time: < 1s.

Serious Applications

- Quantification of complexity of patterns obtained from numerical simulations:
  M. Gameiro, K. Mischaikow and W. Kalies, *Topological Characterization of Spatial-Temporal Chaos*, Physical Review E 70, no. 3, 035203, (2004).
- Analysis of patterns obtained in physical experiments:
  K. Krishan, M. Gameiro, K. Mischaikow and M. Schatz, *Homological Characterization of Spiral Defect Chaos in Rayleigh-Benard Convection.*
- Dynamical Systems:
  Computation of the Conley Index
- Medicine:
  Analysis of blood vessel topology (Marc Niethammer et al.)
- Computer Science:
  Optical character recognition (Marcin Żelawski)

Useful References

- Paweł Pilarczyk (Kyoto University)
  `http://www.pawelpilarczyk.com/`
- **C**omputational **Hom**ology **P**roject (CHomP)
  http://chomp.rutgers.edu/
- T. Kaczynski, K. Mischaikow, M. Mrozek, *Computational Homology*, Appl. Math. Sci. Vol. 157, Springer Verlag, NY 2004