



ELSEVIER

Contents lists available at ScienceDirect

Journal of Symbolic Computation

www.elsevier.com/locate/jsc



Reducing complexes in multidimensional persistent homology theory



Madjid Allili ^{a,1}, Tomasz Kaczynski ^{b,2}, Claudia Landi ^{c,2}

^a Bishop's University, Mathematics Department, Sherbrooke (Québec) J1M 1Z7, Canada

^b Université de Sherbrooke, Département de Mathématiques, Sherbrooke (Québec) J1K 2R1, Canada

^c Dipartimento di Scienze e Metodi dell'Ingegneria, Università di Modena e Reggio Emilia, Reggio Emilia, Italy

ARTICLE INFO

Article history:

Received 30 January 2015

Accepted 19 November 2015

Available online 25 March 2016

Keywords:

Multidimensional persistent homology

Discrete Morse theory

Acyclic partial matchings

Matching algorithm

ABSTRACT

Forman's discrete Morse theory appeared to be useful for providing filtration-preserving reductions of complexes in the study of persistent homology. So far, the algorithms computing discrete Morse matchings have only been used for one-dimensional filtrations. This paper is perhaps the first attempt in the direction of extending such algorithms to multidimensional filtrations. An initial framework related to Morse matchings for the multidimensional setting is proposed, and a matching algorithm given by King, Knudson, and Mramor is extended in this direction. The correctness of the algorithm is proved, and its complexity analyzed. The algorithm is used for establishing a reduction of a simplicial complex to a smaller but not necessarily optimal cellular complex. First experiments with filtrations of triangular meshes are presented.

© 2016 Elsevier Ltd. All rights reserved.

1. Introduction

The *persistent homology* has been intensely developed in the last decade as a tool for studying problems of two kinds. One is the topological analysis of discrete data, e.g. *point-cloud data*, where the chosen framework is a discrete linear filtration of simplicial complexes. The first contributions in this

E-mail addresses: mallili@ubishops.ca (M. Allili), t.kaczynski@usherbrooke.ca (T. Kaczynski), claudia.landi@unimore.it (C. Landi).

¹ Tel. +1 (819) 822 9600 (2740); fax: +1 (819) 822 9661.

² This work was partially supported by the following institutions: INdAM-GNSAGA (C.L.), NSERC Canada Discovery Grant (T.K.).

<http://dx.doi.org/10.1016/j.jsc.2015.11.020>

0747-7171/© 2016 Elsevier Ltd. All rights reserved.

direction given by Edelsbrunner et al. (2002), and later by Zomorodian and Carlsson (2005) opened a new direction in research. The other one is the study of shape similarity by *shape-from-function* methods, where the framework is the filtration of a topological triangulable space by the values of a continuous function called *measuring function*. The 0-dimensional persistent homology case, where the topological invariants are based on the number of connected components, were known under the name of the *size function* theory since the paper by Frosini (1991). The applications of persistent homology to shape similarity are studied by Verri et al. (1993), Carlsson et al. (2005), Di Fabio and Landi (2012). The two frameworks, discrete and continuous, have been extended to the multiparameter filtration case called *multidimensional persistence*, where the filtration is set up with respect to a parameter space that is no longer ordered linearly (Carlsson and Zomorodian, 2007; Biasotti et al., 2008; Cagliari et al., 2010; Cerri et al., 2013). In the continuous setting this gives rise to *multidimensional measuring functions*, that is functions with values in \mathbb{R}^k . In Cavazza et al. (2013) the relation between the discrete and continuous settings is established.

In parallel, another mathematical theory which became increasingly popular in computational sciences is Forman's discrete Morse theory (Forman, 1998). We will not elaborate on all possible applications of this theory in visualization, imaging, computational geometry and other fields but just point out the one to computing persistence. The effective computation of the persistent homology is a challenge due to a huge size of complexes built from data, for instance, via meshing techniques. Discrete Morse theory enables algorithms reducing a given complex (simplicial, cubical, or cellular) to a much smaller cellular complex, homotopically equivalent to the initial one, by means of *Morse matching*, also called *Morse pairing*. An ultimate goal is often to reduce the complex to an optimal one, where all remaining cells are topologically significant. If a reduction by Morse pairings can be performed in a filtration-preserving way, that leads to a faster persistent homology computation. This goal motivated the contributions of King et al. (2005), Mischaikow and Nanda (2013), Robins et al. (2011), and Dłotko and Wagner (2014).

Given a complex and a partial pairing of its cells, the paired cells form a discrete vector field in the language of discrete Morse theory and can be reduced in pairs so to obtain at each step a new complex homotopically equivalent to the previous one. The final complex consists of unpaired cells that are also called critical cells. First, we give an algorithm that constructs a Morse matching for a given complex and we prove its correctness and analyze its complexity. Then, we go on proving that given a multifiltration on the initial complex, the reduction process yields a new multifiltration consisting of smaller complexes and which has the same persistent homology as the initial one. As pointed out in Mischaikow and Nanda (2013) for the one dimensional case, the complexity of computing multidimensional persistent homology of a filtration is essentially determined by the sizes of its complexes. This motivates this approach of reducing the initial complexes for achieving a low computational cost in the persistent homology computation. Our matching algorithm can be considered as an extension to the multidimensional setting of the algorithms given in King et al. (2005) and Cerri et al. (2011). The multidimensionality is symbolized by the function defined on the vertices of the complex. The algorithm is of iterative and recursive nature. It considers every vertex of the complex and builds a partial matching recursively on its lower link before extending it to the entire complex. When the dimension is fixed and the number of cofaces of every cell in the complex is bounded above by a fixed constant, we prove that the computational complexity of the algorithm is linear in the number of vertices of the initial complex.

So far, the algorithms for discrete Morse pairings have only been used for one-parameter filtrations. There does not yet exist a systematic extension of Forman's discrete Morse theory to the multiparameter case, and this goal offers challenges on both theoretical and computational levels. This paper is the first attempt in this direction.

The paper is organized as follows. In Section 2, we recall definitions and some known facts about the structure of S -complexes, multidimensional persistent homology, acyclic matchings, and an S -complex reduction. Although our main algorithm takes simplicial complexes as an input, in order to make use of it for the computation of persistent homology, one shall need a more general class of complexes introduced in Mrozek and Batko (2009) under the name of S -complexes. This structure is equivalent to the structure of a *complex* introduced by Lefschetz (1942) and currently called *Lefschetz complex*. Roughly speaking, an S -complex is a convenient combinatorial framework for

Download English Version:

<https://daneshyari.com/en/article/570560>

Download Persian Version:

<https://daneshyari.com/article/570560>

[Daneshyari.com](https://daneshyari.com)