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Cell structures and topologically complete spaces

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ABSTRACT

The authors [5] defined cell structures to be inverse sequences of graphs with some mild convergence conditions and they defined cell maps between cell structures. They showed how to obtain from these all complete metric spaces and continuous mappings between such spaces. In this paper that work is extended to the class of topologically complete spaces. This shows that topologically complete spaces and their continuous functions are determined by discrete approximations.

1. Introduction

P.S. Alexandroff [1], [2] approximated spaces by polyhedra in order to extend algebraic topology to compact metric spaces. Representation of continuous mappings between spaces by systems of mappings between inverse spectra came later. These ideas were not fully successfully developed until the 1980's as inverse limits were replaced first by approximate inverse limits, then by resolutions and finally by approximate resolutions.

The problem is that in general it is impossible to construct commutative diagrams in inverse spectra using the desired types of approximating polyhedra. This problem was eventually solved by replacing commutative diagrams in inverse spectra by diagrams which were only approximately commutative. The approximation to commutativity becomes better and better as one goes deeper and deeper into the inverse spectrum. However, the required machinery is formidable.

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The idea behind both this paper and [5] is that the commutativity problem originates in the attempt to preserve too much information via the bonding maps of inverse spectra. The commutativity problem disappears if one restricts one's attention to inverse spectra of discrete spaces. We show that to represent topologically complete spaces and their mappings it suffices to use only the information contained in graphs, i.e. in the 1-skeletons of polyhedra approximating the space or spaces involved.

A (combinatorial) graph is a discrete set of vertices together with a set of edges. To us an edge simply indicates a pair of adjacent vertices. We define cell structures to be inverse systems of graphs (hence, an inverse system of discrete spaces) with mild convergence conditions and we define cell maps between cell structures. The inverse limit of a cell structure is, therefore, a closed subset of a product of discrete spaces. The adjacency conditions in the graphs define an upper semi-continuous equivalence relation with compact equivalence classes on the inverse limit space. Hence, there is a perfect quotient map of the inverse limit onto a Tychonoff space which we call the space determined by the cell structure. We define cell maps between cell structures which determine the continuous mappings between the spaces determined by those cell structures.

Properties of topological spaces depend on both geometry and set theory. We study spaces which are obtainable as images of closed subsets of products of discrete spaces under perfect mappings (i.e. continuous closed functions which have compact point preimages). This class of spaces is large and includes topologically complete spaces (i.e. spaces which admit a complete uniformity), paracompact Hausdorff spaces, compact Hausdorff spaces and metric spaces.

Each such space X admits a defining family of locally finite closed covers. The family of 0-skeletons of the nerves of these covers (i.e. the sets of elements of these covers with the discrete topology) naturally forms an inverse system [7] of discrete sets with bonding maps defined by inclusions. We call this inverse system a cell structure. The inverse limit G_∞ of this cell structure is a closed subset of a product of discrete spaces. Using the 1-skeletons of the nerves of these covers (i.e. using whether or not two elements of a cover intersect) we define an equivalence relation with compact equivalence classes on G_∞ whose quotient space is homeomorphic to the original space X.

Alexandroff [2] was first to approximate compact metric spaces by simpler spaces-namely by finite polyhedra. Freudenthal [9] (see also [13]) considered inverse sequences of polyhedra and showed that if X is a compact metric space then it is homeomorphic to the inverse limit of an inverse sequence of polyhedra whose dimension is bounded by the dimension of X. In the 1950's Mardešić [14] and Pasynkov [20] showed independently that Freudenthal's Theorem fails for compact Hausdorff spaces.

Mioduszewski [19] (see also Brown [3]) showed that mappings between inverse limits of inverse sequences of compact polyhedra were induced by sequences of mappings between the coordinate spaces in the inverse sequences. These mappings between coordinate spaces in general commute only approximately with bonding mappings. For non-compact spaces such inverse systems did not work well.

In 1981 Mardešić [15] (see also [16], [17] and [4]) introduced approximate inverse systems and resolutions to deal with mappings of arbitrary spaces. Later Mardešić and Watanabe [18] introduced approximate resolutions of arbitrary spaces and mappings. The limit of an approximate resolution of a topologically complete space yielded a homeomorphic copy of that space.

In [5] we defined cell structures as inverse limits of inverse sequences of graphs and we defined cell maps between cell structures. We showed that these defined all complete metric spaces and all continuous maps between such spaces. In this paper we extend the work in [5] to inverse systems of graphs. The only really new difficulties in this paper arise in extending results from inverse sequences to inverse systems. For that reason the reader may wish to at least scan [5] before reading this paper.

It is worth noting that there are choices to be made in defining bonding maps and cell maps. However, unlike in inverse systems or resolutions cell maps induce functions of the inverse limit spaces which do commute with bonding maps.