TITLE: Parallel Setup for computing the Homological Region Adjacency Tree of a 3D binary image

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ABSTRACT: Being \$I\_D\$ a 3D binary digital image, and using the \$6\$-adjacency relationship for the set of black voxels \$D\$ and \$26\$-adjacency relationship for the set of white voxels, an almost fully parallel algorithm for computing a topological model called {\em Homological Region Tree} (Hom-Tree, for short) of \$I\_D\$ is designed and implemented here. This model is an edge-weighted version of the classical representation of the Adjacency Tree of \$I\_D\$. It is obtained from an Homological Spanning Forest representation (HSF, for short) of \$I\_D\$ in which each constant-value set of voxels (node of the Hom-Tree) is a sub-tree of this hierarchical graph-based structure (the HSF).

If  $I_D$  has  $m_1 \times m_2 \times m_3$  voxels, the theoretical time complexity order of the algorithm for computing the Hom-Tree is near  $O(\log(m_1+m_2+m_3))$ , under the assumption that a processing element is available for each voxel. An implementation of the Hom-Tree structure has been written in MATLAB/OCTAVE and well-composed three-dimensional digital images have been used to test and validate its correctness. The experiments allow us to assert that the number of iterations in which the homological information is found varies only to a small extent from the theoretical computational time.