Bioimage informatics

DiversePathsJ: diverse shortest paths for bioimage analysis

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Abstract

Motivation: We introduce a formulation for the general task of finding diverse shortest paths between two end-points. Our approach is not linked to a specific biological problem and can be applied to a large variety of images thanks to its generic implementation as a user-friendly ImageJ/Fiji plugin. It relies on the introduction of additional layers in a Viterbi path graph, which requires slight modifications to the standard Viterbi algorithm rules. This layered graph construction allows for the specification of various constraints imposing diversity between solutions.

Results: The software allows obtaining a collection of diverse shortest paths under some user-defined constraints through a convenient and user-friendly interface. It can be used alone or be integrated into larger image analysis pipelines.

Availability and implementation: http://bigwww.epfl.ch/algorithms/diversepathsj

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Supplementary information: Supplementary data are available at Bioinformatics online.

1 Introduction

A large number of problems in image analysis and computer vision can be formulated as search for the shortest path. Given an edge-weighted graph, the optimal shortest path between two nodes can be found efficiently using dynamic programming (Bellman, 1952). The Viterbi algorithm is a popular example of the latter. A solution is, however, always only optimal with respect to its associated cost function or energy. In practice, due to discrepancies between the model associated with an objective function and reality, it is common for the optimal solution to differ from what would be the best one from a human perspective. For this reason, obtaining a collection of good solutions instead of a single one is often desirable.

The design of algorithms for obtaining the M most probable solutions to combinatorial problems has been extensively studied in the context of probabilistic random field models and is known as the M-best maximum a posteriori (MAP) problem (Batra, 2012; Lawler, 1972). Further works aimed at introducing supplementary constraints to ensure that the M-best solutions are sufficiently diverse (Batra et al., 2012; Kirillov et al., 2015). In Straehle et al. (2013), these very general formulations were adapted for bioimage segmentation in the context of exploring various watershed solutions by searching for the K-smallest spanning trees. Most similar to our approach is the one from Fujita et al. (2003) in the context of robot motion planning, which could also be viewed as a two-layers-graph construction.

We make two contributions: first, we propose a more general formulation for the diversity constraint and second, we provide the first freely available, readily usable and general purpose open source implementation of a diverse shortest path tool for bioimage analysis.

2 Materials and methods

The search for a diverse collection of M-diverse best solutions using a layered-graph construction is implemented efficiently by modifying the Viterbi algorithm. The construction of the additional layers is done on-the-fly as the search for the M-diverse best paths is being performed. The software is designed as an ImageJ/Fiji plugin and integrates seamlessly into existing pipelines.

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rules of the standard Viterbi algorithm. The mathematical formulation of
our approach is inspired from our more general work (Haubold et al.,
2017) and is provided in the Supplementary Material. Here, we
give an intuitive description of the algorithm.

To find the shortest path, the standard Viterbi algorithm is per-
formed from a source point $s$ to a target point $t$ by computing the
cost to all intermediate nodes. We refer to this collection of costs as
the forward derived cost map (Fig. 1a). The shortest path is found
by backtracking the minimal cost from $t$ to $s$ (Fig. 1b). For the se-
cond shortest path, another pass of Viterbi algorithm is first per-
formed, this time from the target $t$ to the source $s$, to obtain the
backward derived cost map (Fig. 1c). The forward and backward
derived cost map are then summed (Fig. 1d) and all nodes laying
within an exclusion corridor around the shortest path are assigned
an infinitely large cost (represented as white area in Fig. 1e). The ex-
clusion corridor aims at enforcing that the second shortest path dif-
ers from the first one. The node corresponding to the new minimal
cost in the summed map, denoted as $(v^*, x^*_r)$, is identified. Finally,
the second diverse shortest path is obtained by joining the two sub-paths obtained by backtracking from $(v^*, x^*_r)$ to $s$ and from
$(v^*, x^*_s)$ to $t$. This amounts to performing the Viterbi algorithm on
a two-layers graph constructed by copying the original graph and
introducing layer-jump-edges (Fig. 1f).

The next $M-2$ diverse best solutions can be computed efficiently
by updating the exclusion corridor to be the union of the exclusion
corridors built from previously found solutions, and searching for
the next minimum in the remaining available nodes of the summed
cost map. The $M$ shortest paths are thus computed at the cost of two
standard Viterbi algorithm passes plus $M$ backtrackings. A possible
refinement is to enforce in addition that the new solution accum-
ulates a given amount of diversity. Formally, this requires the
introduction of a supplementary input cost map on the lower graph
layer encoding the discrepancy between the new solution and previ-
ous ones, referred to as the diversity map. It can be combined with
the exclusion corridor to enhance diversity in the set of shortest
paths. Layer-jump-edges are then allowed only when the integrated
diversity over the path exceeds a threshold.

Our approach is implemented as a Java-based plug-in for ImageJ
and Fiji. The plug-in is designed to be generic and readily usable.
A full description of the GUI and all available settings is provided
in the Supplementary Material. The required input consists in two
end-points provided by the user or by custom automated pre-
processing steps. The collection of resulting (diverse) paths can then
either be swiftly browsed and displayed on the image using the arrow
keyboard keys, or exported in generic formats for further processing.

3 Results
Bioimages often feature several instances of the same object in a single
image (e.g. cells). Due to small differences between the appearance
and neighborhood of these individual objects, it is practically impos-
sible to find a cost function whose minimum always corresponds to
the desired output. Exploring several shortest paths, however, allows
to analyze multiple instances of the same objects exhibiting slight vari-
ations without the need for fine-tuning of the cost function.

We illustrate the usefulness of searching for several shortest
paths in bioimage analysis with identification of the medial axis of
mycobacteria (phase contrast microscopy images) and of C.elegans
nematodes (brightfield microscopy images). The original images,
their characteristic, experimental protocols and plugin settings can
be found in the Supplementary Material. We use our approach with
the same parameters to analyze two similar objects in the same
image. For one of the objects (Fig. 1g and j), the shortest path is the
desired medial axis. Conversely, for the second one, the shortest
path does not correspond to a correct medial axis (Fig. 1h and k).
The desired solution can, however, be found in the set of additional
diverse shortest path (Fig. 1i and l), the exploration of which is
made easy through the interface of our ImageJ/Fiji plugin. A full de-
scription of the software is provided in the Supplementary Material.

Medial axis outline serves as the first step for quantitative esti-
nation of shape features such as length and bending. The proposed
approach is however not restricted to this use-case and covers every
problem in which a path is to be searched between two end-points.
Our implementation only requires the specification of the source
and target locations as ImageJ points and of the input cost map spe-
cifying the cost associated to each pixel in the image, in addition to
data-independent parameters (number of desired shortest paths and
minimum amount of diversity between paths). Ridge detectors
and algorithms estimating probability distributions for the identifi-
cation of principal curves such as subspace constrained mean shift
(Ozertem et al., 2011) are good examples of relevant input cost
maps. DiversePathsJ can be used alone in an interactive way or inte-
grated as a module in larger automated image analysis pipelines.

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References


