A Bayesian Approach to Inferring Vascular Tree Structure from 2D Imagery

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Abstract
We describe a method for inferring tree-like vascular structures from 2D imagery. A Markov Chain Monte Carlo (MCMC) algorithm is employed to sample from the posterior distribution given local feature estimates, derived from likelihood maximization for a Gaussian intensity profile. A multiresolution scheme, in which coarse scale estimates are used to initialize the algorithm for finer scales, has been implemented and used to model retinal images. Results are presented to show the effectiveness of the method.

Introduction

The Problem

• Infer vascular structure from medical image data. Important for surgical planning.
• Likelihood techniques tend to give oversegmentation of vessels.
• Bayesian methods are expensive computationally.

The Solution

• Local likelihood maximisation reduces data volume.
• Global optimisation uses prior model to constrain inference.
• Markov Chain Monte Carlo (MCMC) approach avoids local minima at acceptable cost computationally.

A Statistical Model of Vascular Structure

• The data are modelled as a random tree-like structure.
• We use an MCMC algorithm [1] to sample from the posterior distribution. The sampling distribution is an approximate equilibrium of a random process whose state space is the space of tree-like structures.
• The prior distribution defines the global structure as a forest of a random number of binary trees.
• Vertex location is specified by an autoregressive model to approximate local structure (left hand figure 1). AR(1) process leads to clear tree (right hand figure 1).
• Each vertex has a Gaussian kernel to approximate the spatial grey level profile of the corresponding vessel segment.
• The posterior distribution for a random number N of trees is given by

\[ \pi(t_1, t_2, \ldots, t_N) = \mathcal{P}(N = n) \prod_i \mathcal{P}(x_i | t_i, \theta_i) \times \mathcal{L}(t_1, t_2, \ldots, t_N) \]  

– \( f \) is the image.
– \( \mathcal{P}(N = n) \) penalises the number of trees; in the example a Poisson distribution was used.
– \( \mathcal{P}(x_i | t_i, \theta_i) \) are the probabilities defining the degree of the branching process.
– \( \nu \) is the degree of the vertex.
– \( \omega \) is the probability of edge.
– \( \mathcal{L}(t_1, f) \) is the likelihood function.

The observation model is based on the approximation of linear structures by a sum of Gaussian kernels:

\[ t(s) = \sum_k a_k \mathcal{N}(s - s_k, \Sigma_k) \]  

where \( a_k \) is a magnitude scale factor and \( s_k, \Sigma_k \) the mean and covariance parameters of the kernel.

Likelihood computation uses a normal model of the observations within a region

\[ f(s) = \sum x_i \mathcal{N}(s - x_i, \Sigma_i) \]  

where \( x_i \) represents the noise in the observations, which again is assumed to be normally distributed, with zero mean and independent at each pixel.

The posterior distribution for a random number of (binary) trees.

\[ \mathcal{P}(N = n) \prod_i \mathcal{P}(x_i | t_i, \theta_i) \times \mathcal{L}(t_1, t_2, \ldots, t_N) \]  

where the data \( f(s) \) are windowed with a cosine window, whose size is twice the block width at a given scale, to give the data \( f_N(s) \) used in the estimator.

The index \( t \) denotes iteration number, typically 4–5 iterations are sufficient to give accurate estimates. Figures 3(b)–(c) show reconstructions using the 2D Gaussians in each block (at corresponding block sizes) based on the ML feature estimates at block sizes of 64 × 64 and 16 × 16 respectively. Clearly, at lower spatial resolutions, the model cannot easily describe the presence of multiple vessels within the window, such as occur at bifurcations, and the resulting low-amplitude, isotropic Gaussians are locally the ‘best’ description of these regions. However, these blocks can be modelled accurately at higher spatial resolutions.

Figure 2. Moves used in MCMC simulation on trees.

Figure 3. A summary of the moves currently implemented for forest estimation. The Markov Chain Monte Carlo (MCMC) algorithm is used to sample from the posterior distribution given local feature estimates, derived from likelihood maximization for a Gaussian intensity profile. A multiresolution scheme, in which coarse scale estimates are used to initialize the algorithm for finer scales, has been implemented and used to model retinal images. Results are presented to show the effectiveness of the method.

Conclusions

• We have demonstrated that a Bayesian approach to infer vascular structure is feasible.
• We have obtained encouraging preliminary results.
• Further work is needed to establish the correct parameter values and move probabilities for particular datasets in 2-D and 3-D.

References