

Bayesian analysis of vascular structure

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1 Introduction

The detection of artery and vein structure is of interest in both medical diagnosis and surgical planning. Here we examine vascular structure in the eye which is important for example to diagnose abnormal vessel growth due to diabetic retinopathy. The results presented here focus on retinal blood vessels; however all methods can be applied to general artery/vein structure. For example, in future we plan to investigate the three dimensional vascular structure in a human brain.

As the images of interest are large, we first use a multi-resolution approach to summarise the image. All inference is then based on the image summarisation rather than the original image. We develop a prior model for vascular structure and use Markov Chain Monte Carlo (MCMC) to sample from the posterior distribution describing the global artery/vein structure in the image.

2 Image summarisation

Vascular structures can be viewed as binary spatial trees. We assume that a forest \mathcal{F} of binary trees τ describing vascular structure f is given by $f = \sum_{\tau \in \mathcal{F}} \sum_{e \in \tau} k_e$ where k_e describes the shape and illumination of the vessel segment e . In the following we choose k_e to be proportional to a bivariate Gaussian kernel, that is

$$k_e(x) = A_e \exp\left(-\frac{1}{2}(x - \mu_e)^T \Sigma_e^{-1}(x - \mu_e)\right). \quad (1)$$

If the standard deviation of the first principal component is chosen to be much larger than the standard deviation of the second, then k_e has an elongated shape similar to that of a vessel segment. The choice of a Gaussian kernel for the elongated shape of a blood vessel is one of convenience. As we will explain later, it leads to substantial computational savings.

The image is a noisy, discretized observation of f in a sampling window W . If we assume independent, additive, pixelwise noise then the evaluation of the resulting likelihood function entails a summation over the pixels of the image. However, this is computationally very expensive if, as in our application, the image is large. Instead we aim to simplify computations using a local description of the image in terms of a Gaussian mixture. More formally, we use a *treed model* to summarize the data. Treed models, as in Chipman et al. (2002), are extensions to Classification and Regression Trees (CARTs) which partition data into more homogeneous

groups, see Breiman et al. (1984). However, rather than summarizing each partition member by a mean or a proportion, treed models fit a model to each subset. In our setting as a model for the data in subset \mathcal{R}_i we use a multivariate Normal distribution whose mean is specified by a Gaussian function k_i which is concentrated on \mathcal{R}_i as defined in (2).

As the number of possible partitions is prohibitively large, fitting a treed model to an image can be a computationally daunting task. To allow for efficient computation we restrict our partition to follow a quadtree, that is, the partition is produced by successively splitting the image or a subset of the image into four equal sized subregions. For each subset we now fit the Gaussian model given in (2). Details of the fitting procedure can be found in Bhalerao et al. (2001) and Thönnies et al. (2002). We then evaluate a model fit criterion for the subregion. If the model fits sufficiently well then the subregion is no longer subdivided. Figure 1 (b) shows the mean of the treed model fitted to the retinal image in Figure 1 (a) using a model fit criterion based on the mean squared error. Alternatively one can use for example Aikake’s information criterion (AIC) to evaluate the model fit, see Li and Bhalerao (2003).

3 Prior model

While the approach in the previous section provides us with a good *local* description, the image summarisation given by the fitted treed model needs to be further analyzed if we wish to detect *global* vascular structure. We therefore take a Bayesian approach and specify a prior model for global vascular structure. As described earlier we assume that the functional form of a network of vessels is given by $f = \sum_{\tau \in \mathcal{F}} \sum_{e \in \tau} k_e$ and so we need to specify our distributional assumptions on \mathcal{F} and k_e . The prior model specifies that the forest \mathcal{F} contains a Poisson distributed number of trees. Each tree is obtained as an independent realisation of a subcritical, binary, spatial branching process. Finally, the parameters of k_e follow an AR(1) process along connected sequences of edges.

Consider the vascular structure $\tilde{f} = \sum_{\tau \in \mathcal{F}} \sum_{e \in \tau} k_e$ and let $\phi = \sum_{i \in M} k_i$ be the fitted treed model. (Note that M is a simple index set for the subregions in the image summarisation and does not specify any tree structure). We can now write down the log-likelihood of \tilde{f} given our fitted treed model:

$$l(\tilde{f}|\phi) = -\frac{1}{2} \sum_{i \in M} \sum_{x \in \mathcal{R}_i} \frac{(\tilde{f}(x) - k_i(x))^2}{\sigma_i^2} \approx -\frac{1}{2} \sum_{i \in M} \int \frac{(\tilde{f}(x) - k_i(x))^2}{\sigma_i^2} dx.$$

Thus, the evaluation of $l(\tilde{f}|\phi)$ requires pixelwise summation but can be approximated by a sum of integrals. The integrand is a simple quadratic function of Gaussian kernels for which we can derive an analytical expression. Thus we can replace pixelwise summation over a subregion \mathcal{R}_i by a closed form expression. This leads to substantial computational savings when evaluating the log-likelihood function.

4 Posterior model and inference

The prior model together with the likelihood function specify a posterior model describing the global vascular structure in the image. We sample from the posterior model using Markov Chain Monte Carlo (MCMC). As the model allows a variable number of random trees we use a reversible jump MCMC algorithm, see Green (1995). Each transition of this algorithm is a two-step procedure: 1) a proposal to move from the current state to a new state which may

lie in a space of different dimension and 2) an acceptance or rejection which ensures that the resulting Markov chain has the correct equilibrium distribution. All moves of the algorithm are geometric operations such as growing or deleting of branches or the joining and splitting of trees. All transitions maintain the binary tree condition.

A common problem when using MCMC in imaging applications is to find an adequate proposal mechanism that has a sufficiently high acceptance rate. However, in our setting the image summarisation provides a good local description of the image in terms of vessel segments. This description is exploited such that proposals lie close to local modes in the likelihood function. This not only achieves sufficiently high acceptance rates and but also ensures that the algorithm works efficiently for a range of different images without further fine-tuning. Convergence appears to be achieved rather rapidly. For the 400×400 pixel image shown below convergence is believed to be reached at about 50000 iterations resulting in samples such as the one shown in Figure 1(c). Branches of the same tree are displayed in the same colour.

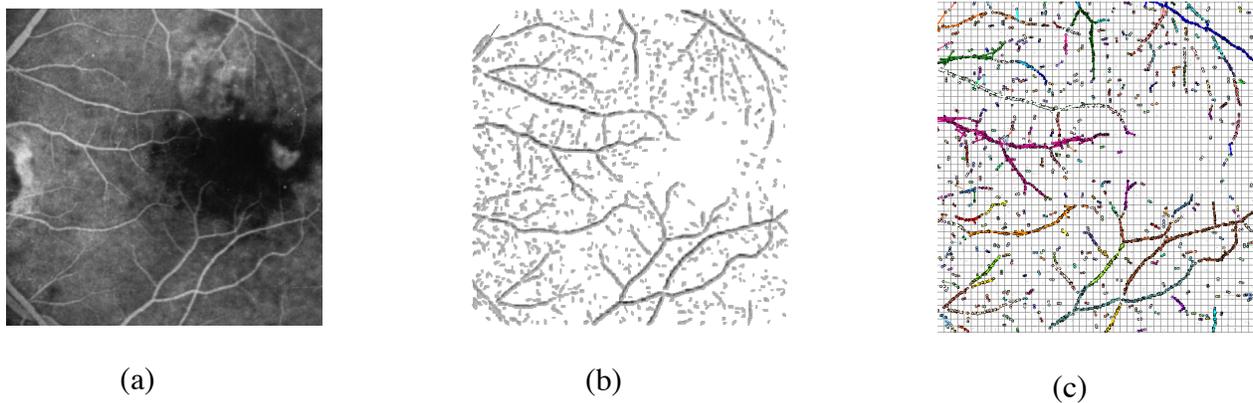


Figure 1: (a) Retinal image. (b) Image summarisation.(c) Posterior sample.

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