The Variational Approach to Phase Retrieval in Endoscopes

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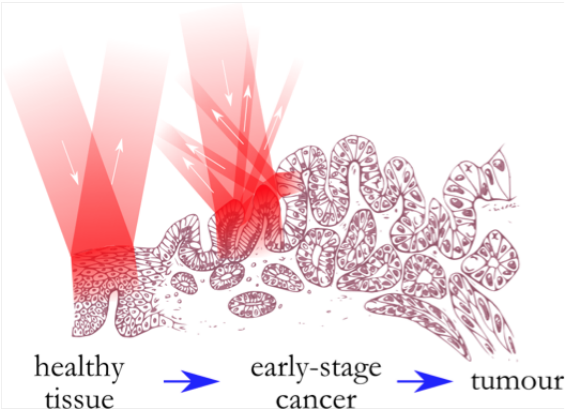
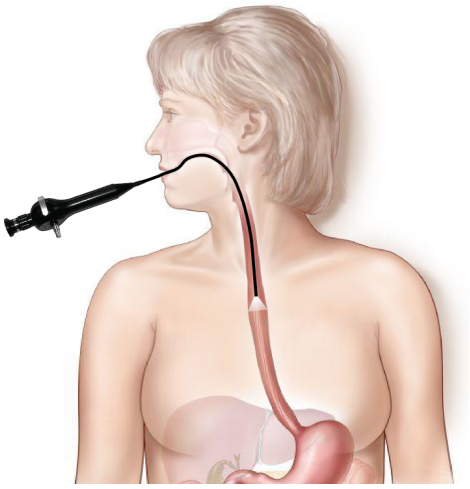


I spent my summer working with the biological and soft systems group in the Cavendish laboratory. The purpose of my project was to find, investigate and apply algorithms that would be useful in the early diagnosis of esophageal cancer. As it stands the main method of diagnosis is using endoscopes which allow doctors to see the inside the esophagus and hence identify malignant lesions. Unfortunately in early stage cancer it is very difficult to identify such lesions with an ordinary camera. To overcome this it has been suggested that the increased scattering caused by the roughness of cancer cells might be exploited. This scattering can be detected by considering the phase and polarization of reflected light. This in turn requires knowledge of the full complex transfer matrix of the endoscope, which depends on the curvature of the endoscope and conditions such as temperature; hence measurements used in characterising the endoscope must be done whilst it is inside the patient.



My goal was to find an algorithm capable of finding the (complex) transfer matrix of an endoscope based on the received images of a number of known (complex) test messages. The complicating factor was that the received images were taken with a conventional camera; hence we only had the moduli of the full complex images...

Our model for the relationship between an input message $\mathbf{x} \in \mathbb{C}^N$, an output message $\mathbf{y} \in \mathbb{R}^M$, for a transfer matrix A and hidden variables $\boldsymbol{\theta} \in [0, 2\pi]^M$ is:

$$y_\mu = e^{i\theta_\mu}(A_{\mu j}x_j + n_\mu)$$

Where $n_\mu \sim \mathbb{C}\mathcal{N}(0, \sigma_n^2)$. We seek to maximise the following probability:

$$p(\mathbf{x}|\mathbf{y}) = \int_{\boldsymbol{\theta}} p(\mathbf{x}, \boldsymbol{\theta}|\mathbf{y})\, d\boldsymbol{\theta}$$

Where we have the following: $p(\mathbf{x}, \boldsymbol{\theta}|\mathbf{y}) \propto p(\mathbf{y}|\mathbf{x}, \boldsymbol{\theta})p(\boldsymbol{\theta})p(\mathbf{x})$ Maximising the above expression proves rather tricky, hence we resort to approximating:

$$p(\mathbf{x}, \boldsymbol{\theta}|\mathbf{y}) \qquad \text{by} \qquad q(\mathbf{x}, \boldsymbol{\theta}) = \prod_{j=1}^{N} \hat{q}_j(x_j) \prod_{\mu=1}^{M} \bar{q}_\mu(\theta_\mu)$$

Where the factors of q are constrained so that they each integrate to 1. We then minimise the following measure of the similarity of the two distributions with respect to each factor of q in sequence:

$$D_{KL}\big(q(\mathbf{x}, \boldsymbol{\theta})||p(\mathbf{x}, \boldsymbol{\theta}|\mathbf{y})\big) = \int_{\mathbf{x}, \boldsymbol{\theta}} q(\mathbf{x}, \boldsymbol{\theta}) \log(q(\mathbf{x}, \boldsymbol{\theta})/p(\mathbf{x}, \boldsymbol{\theta}|\mathbf{y}))\, d\mathbf{x}\, d\boldsymbol{\theta}$$

This gives the VBEM algorithm.

To solve this problem I attempted two different Bayes methods of phase retrieval, and had varying degrees of success with both. The first method is called the variational Bayes expectation maximization algorithm (VBEM), and the basic mathematical idea is described in the panel opposite. The second method is an application of an algorithm called generalised approximate message passing (GAMP). The mathematics of this algorithm is somewhat more complicated, and hence I will omit any in depth discussion of how it works.

Whilst both algorithms worked when naively applied to simulated data based on the transfer matrix of a real endoscope, the message passing proved considerably quicker, as it could exploit the sparsity of the transfer matrix. Furthermore GAMP required fewer test messages to run. I concluded the project by proposing hardware changes that would allow the implementation of an algorithm that would achieve the aims of the project using a very small number of test messages and in an acceptable computational time.