Solving Probabilistic Inverse Problems Using Factor Graph Analysis

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Abstract

Many formulations in biosensing and communications can be modeled as an equivalent inverse problem involving parameters which are random variables with partially known distributions. For communication systems, the objective for the inverse formulation is to estimate the transmitted data given the noisy measurements obtained from the communication channel. For biosensors, the objective of the inverse formulation is to estimate the concentration of pathogens present in a sample given the multi-dimensional measurements obtained from biomolecular circuits. In this regard factor graph serves as an important analysis and visualization tool that can produce probabilistic estimates of the parameters of interest. In its general form, a factor graph is a graphical representation that graphically captures the interdependencies between different independent random variables. The syntax of a factor graph uses two kinds of nodes as shown in Fig. 1: (a) variable nodes which represent the parameters to be estimated and (b) check nodes which represent the functional model between different variable nodes. The dependencies between different check and variable nodes are represented using edges which facilitate efficient representation of large scale inverse problems in a distribution manner. Solving an inverse problem on a factor graph entails distributed message passing between the variable and check nodes and the steady-state solution of this procedure is indicative of the solution of the inverse problem (represented by the factor graph). In this paper we also present a density evolution technique as one of the methods that is used to visualize the convergence properties of factor-graph methods. Some representative examples are discussed to demonstrate how factor-graph based inverse analysis can be used for reliable communications and for biomolecular circuit analysis.



Fig. 1. The factor graph model representing an inverse problem which consists of variable nodes, check nodes and the edges which capture the dependencies between different nodes