

Design and Iterative Decoding of Networks of Many Small Codes

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I. INTRODUCTION AND DEFINITIONS

We generalize the notion of a low density parity check (LDPC) code by allowing its variable or check nodes to represent codes more general than repetition or single parity check codes. We connect a multitude of small and easily (soft-)decodable codes $\{C_i, i = 1, \dots, Q\}$ in a large network. Each component code C_i is an *atomic* code, and the large code formed by the network of Q atoms is a *molecular* code. An atomic code $C_i(n_i, k_i)$ with length n_i and dimension k_i has $b_i \leq n_i$ bonded edges emanating from its *network side* and $c_i \leq n_i$ charged edges on its *channel side*. An atom's charged and bonded edges correspond to subsets of its n_i code symbols. Atoms can be uncharged ($c_i = 0$), but unbonded atoms ($b_i = 0$) are uninteresting. Every bond joins two atoms and no pair of atoms is joined by more than one bond. Each bond imposes one additional constraint beyond the $n_i - k_i$ constraints imposed by the i th atom. A generic diagram of a molecular code is shown in Fig. 1.

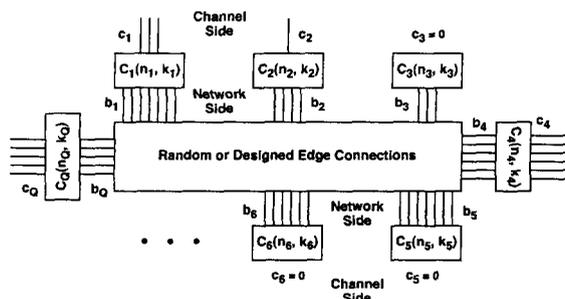


Figure 1: A molecular code with Q atoms.

II. A MOLECULAR CODE'S LENGTH AND RATE

The minimum dimension of the molecular code is $K = K^+ - B$, where $K^+ = \sum_{i=1}^Q k_i$ is the total dimension of its atoms and $B = \sum_{i=1}^Q b_i/2$ is the total number of its bonds. The molecular code's length is $N = \sum_{i=1}^Q c_i$, the total charge of its atoms.

The minimum rate of the molecular code is $R = K/N = (\bar{r} - \bar{\beta}/2) / \bar{\gamma}$, where $\bar{r} = (\sum_{i=1}^Q k_i) / (\sum_{i=1}^Q n_i)$ is a weighted average rate of all atoms, $\bar{\beta} = (\sum_{i=1}^Q b_i) / (\sum_{i=1}^Q n_i)$ is the fraction of atomic code symbols that are bonded, and $\bar{\gamma} = (\sum_{i=1}^Q c_i) / (\sum_{i=1}^Q n_i)$ is the fraction of atomic code symbols that are charged. As long as $\bar{\beta} < 2\bar{r}$, we can design any desired rate $0 < R < 1$ for the overall code by independently adjusting the fraction $\bar{\gamma}$ of code symbols connected to the channel.

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III. A DESIGN EXAMPLE

In Fig. 2 we connect via a bipartite graph q copies of a shortened Hamming code $\mathcal{H}(6,3)$ with $2q$ copies of a single parity check code $\text{SPC}(3,2)$ to produce two equivalent molecular codes of rate $1/6$. One code is obtained by fully charging ($c_i = n_i$) the Hamming atoms, and the other by fully charging the SPC atoms. In each case, all atoms are fully bonded ($b_i = n_i$). The Hamming atoms are bonded randomly to the SPC atoms, with no pair of atoms bonded by more than one edge. These two codes are equivalent because charge from the channel propagates to each of the B bonded edges, regardless of which side of the bipartite graph is charged. Bipartite molecular codes are like Tanner's original graph-theoretic code constructions [1], but generalized to allow vertices on both sides of the graph to represent arbitrary small codes, as in the expander code constructions of Barg and Zemor [2].

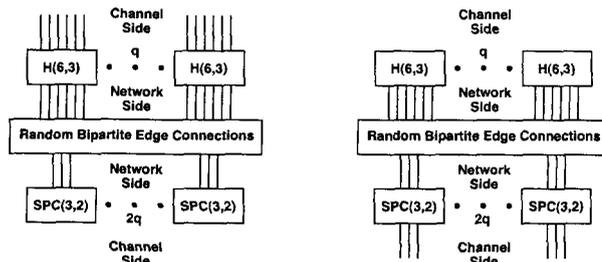


Figure 2: Examples of bipartite molecular codes.

IV. ITERATIVE DECODING

An iterative decoder for a molecular code sends extrinsic a posteriori probabilities (APPs) between bonded atoms in the same way as decoders for LDPC codes. Each atom computes its APPs by enforcing its own parity constraints jointly, e.g., by running the BCJR algorithm [3] on the atomic code's trellis. The iterative decoding threshold for the codes in Fig. 2 was found by Gaussian density evolution [4] to occur at a bit-signal-to-noise ratio E_b/N_0 of approximately 0.2 dB on an additive white Gaussian noise channel. This is much better than the threshold for a (5,6) regular LDPC code but still more than 1 dB higher than the capacity limit for rate-1/6 codes. Irregular molecular code constructions may reduce this gap.

REFERENCES

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