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基于贝叶斯模型的长码DS-CDMA信号扩频码与信息序列联合估计

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Joint Estimation of Spreading Codes and Information Sequences for Long Code DS-CDMA Signals Based on Bayesian Model

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摘要

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摘要

针对长码直接序列扩频码分多址(DS-CDMA)信号的盲解扩,在信号模型分析的基础上,提出了一种基于可逆跳跃的马尔可夫链蒙特卡罗(RJ-MCMC)扩频码和信息序列联合估计算法。该算法分别对建立的联合后验分布模型进行迭代抽样,并有效地在不同维数的子空间中跳转,从而构造一条马尔可夫链,使其平稳分布为待估参数的后验分布,最终拼接得到每个用户的完整扩频序列和信息序列估计。仿真结果表明:该方法在迭代二十几步时达到收敛;并且在功率相同和不同条件下,当信噪比(SNR)大于-9 dB时,估计序列与真实序列的相似度均超过0.95,信息序列的误码率低于0.01;同时算法对不同用户个数和不同调制样式具有较强的适应性,与Fast-ICA算法相比,估计性能平均提高了约3 dB。

关键词: 扩频通信 码分多址 贝叶斯模型 吉布斯采样 马尔可夫链蒙特卡罗 可逆跳跃

Abstract:

To deal with the blind despreading of long code direct-sequence code division multiple access (DS-CDMA) signals, this paper introduces an algorithm for joint spreading codes and information sequences estimation based on reversible jump Markov chain Monte Carlo (RJ-MCMC) by analyzing a signal model. The proposed algorithm analyzes and processes the signal models separately, and obtains the samples of distribution to be estimated through iterative sampling. It is able to construct a reversible Markov chain sampler that jumps between parameter subspaces of different dimensionality, so that the posterior distribution of parameters to be estimated is obtained. Finally, it estimates the entire spreading code and information sequence of each user by splicing. The simulation shows that the iteration converges after some twenty steps. Regardless of whether the power is equal or unequal, when the signal-to-noise ratio (SNR) is greater than -9 dB, the similarity degree between the estimated sequence and true sequence exceeds 0.95, with the bit error rate of information sequence less than 0.01. In addition, the algorithm has good adaptability for different number of users and different modulation styles. Compared with the fast-ICA algorithm, this algorithm improves the estimation performance by an average of about 3 dB.

Keywords: spread spectrum communication code division multiple access Bayesian model Gibbs sampler Markov chain Monte Carlo reversible jump

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