基于生物信息学的SNP候选位点搜寻方法 Discovery of Candidate SNP by Bioinformatic Methods

陈炜, 张戈，张思仲 CHEN Wei, ZHANG Ge, ZHANG Si-zhong

华西医科大学附属第一医院医学遗传研究室，成都 610041 Department of Medical Genetics,The First Affiliated Hospital,West China University of Medical Sciences,Chengdu 610041, China

摘要　　单核苷酸多态性(Single Nucleotide Polymorphism,SNP)是人类基因组中最常见的遗传多态，在遗传学研究的很多方面具有重要的作用。它的搜寻正受到广泛关注。近年来，国际上出现了一种基于生物信息学的发掘SNP新方法。本文对该方法的两种策略及其各自所存在的问题作一介绍。

Abstract：Single Nucleotide Polymorphism (SNP), the most common form of human genetic variation, represents a valuable resources for a variety of genetic research. There is considerable interest in the discovery of it. Recently, a new method based on bioinfomatics has been developed for the discovery of SNP. In this paper, the two strategy of this method and their respective problem are discussed.

关键词　　单核苷酸多态性(Single Nucleotide Polymorphism SNP)　生物信息学 Keywords　Single Nucleotide Polymorphism (SNP) bioinformatics

分类号

扩展功能

本文信息

- Supporting info
- PDF(0KB)
- [HTML全文](0KB)
- 参考文献

服务与反馈

- 把本文推荐给朋友
- 加入我的书架
- 加入引用管理器
- 复制索引
- Email Alert
- 文章反馈
- 浏览反馈信息

相关信息

- 本刊中 包含"单核苷酸多态性(Single Nucleotide Polymorphism"的相关文章

▶本文作者相关文章

- 陈炜
- 张戈
- 张思仲CHEN Wei
- ZHANG Ge
- ZHANG Si-zhong

Abstract

Key words

DOI:

通讯作者