

遗传学教学

人类群体遗传空间结构对应分析中的“蹄型效应”及其遗传学解释

薛付忠1, 王洁贞1, 郭亦寿2, 胡 平1

山东大学公共卫生学院流行病学与医学统计学研究所, 济南250012

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摘要 探讨了人类群体遗传结构对应分析中“蹄型效应”的产生机制及其遗传学解释。从分析基因频率矩阵的结构特点入手, 以实例验证和比较了对应分析中散点图的结构特征。发现当基因频率矩阵的结构不同时, 其对应分析中散点图的分布模式不同; 当基因频率矩阵中存在稀有基因时, 其对应分析的散点图则呈现明显的“蹄型效应”。“蹄型效应”经常会歪曲潜在遗传结构的真实形态, 其产生主要是因为对应分析中的c2距离不相似测度高估了稀有基因的作用。在人类群体遗传结构对应分析中, 当出现“蹄型效应”效应时, 需认真分析基因频率矩阵的结构, 寻找“蹄型效应”产生原因并给出合理的遗传学解释, 以免做出错误结论。

关键词 [人类群体遗传结构; 对应分析; 蹄型效应](#)

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The “Horse-Shoe Effect” of Correspondence Analysis for Human Population Genetic Structure and its Population Genetic Explanation

XUE Fu-Zhong1, WANG Jie-Zhen1, GUO Yi-Shou2, HU Ping1

Deptment of Epidemiology and Biostatistics, School of Public Health, Shandong University,

Abstract

At present study, the reasons of “horse-shoe effect” in correspondence analysis for analyzing human population genetic structure was explained. Based on the structure of gene frequency matrix, we displaye the different patterns of Scallergram of correspondent analysis from different types of loci (HLA-A locus, and STR- CSF1PO locus in Chinese Han populations). The results indicate that different types of loci showed different patterns of Scallergram of correspondent analysis. When some alleles have very low frequency in the gene frequency matrix, there would be “horse-shoe effect” in the Scallergram of correspondent analysis. The reason is that the c2 distance measurement in correspondent analysis usually overrates the effect of the genes with low frequencies. To carry out the correspondent analysis of human population genetic structure, when the Scallergram presents “horse-shoe effect”, one should examine the structure of gene frequency matrix, and confirm whether the “horse-shoe effect” shows the real pattern of population genetic structure. Only in this way, one can explain the “horse-shoe effect” correctly.

Key words [human population genetic structure; Correspondence analysis; “Horse-shoe effect”](#)

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