基于GA-LSSVM和近红外傅里叶变换的霉变板栗识别

Near-infrared spectral detection of moldy chestnut based on GA-LSSVM and FFT

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中文关键词: 遗传算法（GA） 识别 傅里叶变换 板栗 近红外光谱 最小二乘支持向量机（LSSVM）

英文关键词: genetic algorithms (GA) identification Fourier Transforms chestnut near infrared spectroscopy least squares support vector machine (LSSVM)

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中文摘要:

　　为克服板栗近红外光谱变量多、共线性强等缺点，该文对标准正态变量变换预处理后的板栗近红外光谱进行傅里叶变换，并用不同方法建模，提高识别精度。采用试探法提取近红外光谱傅里叶系数，建立了基于最小二乘支持向量机分类器的霉变板栗识别模型。当提取前35点傅里叶系数时，板栗的平均识别正确率为93.56%；构造GA-LSSVM算法，建立的霉变板栗识别模型所用傅里叶系数减少为13点，对测试集中合格板栗、表面霉变板栗和内部霉变板栗的平均识别正确率分别为95.89%、100%和98.25%，板栗的总体平均识别正确率提高到97.54%。为霉变板栗的识别提供了快速鉴别分析方法。

英文摘要:

　　To overcome the shortage of massive data and multi colinearity in near infrared spectroscopy analysis, Fourier transform was employed on chestnut NIR spectra which was preprocessed with standard normal variate (SNV), and different modeling methods were utilized to improve recognition accuracy. Fourier coefficients were extracted from NIR spectra through trial method, and then discrimination models of moldy chestnuts were established based on least squares support vector machine (LSSVM). The highest mean accurate recognition rate of 93.56% was obtained when the first 35 Fourier coefficients were selected, and a hybrid algorithm, GA-LSSVM was developed and used to optimize the number of Fourier coefficients. As a result, the number of Fourier coefficients used for building recognition models was successfully reduced to 13, while the mean accurate recognition rate was raised to 97.54% and the discriminating rates of qualified chestnut, surface moldy chestnut and internal moldy chestnut were 95.89%, 100% and 98.25% for prediction, respectively. It is suggested that near infrared spectroscopy coupled with Fourier transform and GA-LSSVM methods can be used for rapid detection of moldy chestnut.

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