

INTISARI

ESTIMASI KADAR ALBUMIN DALAM LARUTAN SUSU MENGUNAKAN PENGOLAHAN CITRA *DIPSTICK* BERBASIS ALGORITMA DETERMINISTIK KLASIK

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Penelitian ini mengembangkan sistem estimasi kadar albumin dalam urin menggunakan pengolahan citra digital berbasis algoritma deterministik klasik. Sistem ini ditujukan sebagai alternatif terhadap interpretasi visual pada pengujian strip *dipstick* konvensional yang bersifat subjektif dan terbatas pada skala semi-kuantitatif. Sistem memproses citra area reaktif melalui tahapan *cropping* ROI, konversi warna ke RGB, HSV, dan *Grayscale*, serta ekstraksi fitur numerik untuk menghasilkan estimasi kuantitatif kadar albumin.

Dataset penelitian dibentuk dari uji larutan manipulator protein berbasis susu bubuk soya untuk membuat dataset interpolatif. Lima sampel massa baru digunakan secara terpisah sebagai data uji. Model prediksi dibangun menggunakan metode interpolasi linear dan spline terhadap fitur warna *Hue* (H), *Blue* (B), dan *Grayscale*.

Hasil pengujian menunjukkan fitur *Hue* (H) dengan interpolasi Spline Akima memiliki performa terbaik dengan nilai $R^2 = 0,9794$ terhadap referensi semi-validasi dan $0,8382$ terhadap referensi interpolasi massa. Fitur *Blue* (B) dengan interpolasi Spline PCHIP menghasilkan $R^2 = 0,9503$ dan $0,7449$. Sementara *Grayscale* dengan interpolasi linear menunjukkan performa terburuk dengan R^2 negatif yaitu $-0,6635$ dan $-2,3106$. Meskipun belum tervalidasi secara klinis, sistem ini menunjukkan potensi sebagai alternatif yang terjangkau untuk mendeteksi albumin secara kuantitatif berbasis citra.

Kata kunci: albumin, pengolahan citra, *dipstick*, estimasi kuantitatif

ABSTRACT

ESTIMATION OF ALBUMIN CONCENTRATION IN MILK SOLUTIONS USING DIPSTICK IMAGE PROCESSING WITH CLASSICAL DETERMINISTIC ALGORITHMS

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This study develops a urine albumin level estimation system using digital image processing based on classical deterministic algorithms. The system serves as an alternative to conventional dipstick test visual interpretation, which is often subjective and limited to semi-quantitative scales. The system processes the reactive area of the dipstick image through ROI cropping, color space conversion to RGB, HSV, and Grayscale, followed by numerical feature extraction to produce quantitative albumin estimates.

The dataset was constructed from tests using protein-manipulated solutions based on powdered soy milk to create an interpolative dataset. Five additional samples with new mass values were separately used as test data. Predictive models were built using linear and spline interpolation methods applied to the extracted color features Hue (H), Blue (B), and Grayscale.

Experimental results show that the Hue (H) feature with Akima Spline interpolation achieved the best performance, with $R^2 = 0.9794$ against semi-validation references and 0.8382 against mass-based interpolation reference. The Blue (B) feature with PCHIP Spline interpolation yielded $R^2 = 0.9503$ and 0.7449 , respectively. Meanwhile, the Grayscale feature with linear interpolation showed the weakest performance with negative R^2 values of -0.6635 and -2.3106 . Despite the absence of clinical validation, this system demonstrates potential as an affordable image-based alternative for quantitative albumin detection.

Keywords: *albumin, image processing, dipstick, quantitative estimation*