INTISARI

EFEK SPOT SIZE TERHADAP NILAI BIOMARKER DENGAN MEMPERTIMBANGKAN KONDISI LINGKUNGAN MELALUI *BAYESIAN GENERALIZED ADDITIVE MODELS*

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Metode *Dried Blood Spot* (DBS) kian digunakan karena minim invasif dan mudah secara logistik, namun validitas biomarker sensitif terhadap faktor pra-analitik, termasuk ukuran spot. Penelitian ini menganalisis pengaruh suhu, kelembapan, waktu pengeringan, waktu pengiriman, dan ukuran spot terhadap tujuh biomarker (*cho_x4*, *crp_x4*, *trg_x4*, *cyc_x4*, *hdl_x4*, *thb_x4*, *a1c_x4*) menggunakan *Bayesian Generalized Additive Model* (Bayesian GAM) dengan family Gaussian atau log-normal sesuai karakter data, menggabungkan komponen parametrik dan *smoothing spline*, serta diestimasi melalui NUTS MCMC (3–4 rantai). Hasil penelitian menunjukkan bahwa Bayesian GAM mampu menghasilkan estimasi yang stabil dengan nilai $\hat{R} \approx 1.00$ serta *credible interval* yang relatif sempit, sehingga mengindikasikan konvergensi yang baik. Evaluasi model berdasarkan WAIC dan LOOIC memperlihatkan kecocokan yang memadai, khususnya pada biomarker *hdl_x4* dan *a1c_x4*. Selain itu, variabel lingkungan seperti suhu (*t_temp*) serta ukuran spot darah tertransformasi logaritmik (*log1p(t_sizeA)*) terbukti konsisten memberikan pengaruh signifikan terhadap sebagian besar biomarker. Temuan ini menegaskan bahwa pendekatan Bayesian GAM efektif dalam mengakomodasi variabilitas dan ketidakpastian data DBS, serta relevan untuk mendukung analisis biomarker dalam konteks penelitian epidemiologi berbasis risiko.

ABSTRACT

EFFECTS OF SPOT SIZE ON BIOMARKER LEVELS OF FIELD-COLLECTED DRIED BLOOD SPOTS USING *BAYESIAN GENERALIZED ADDITIVE MODELS*

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Dried Blood Spot (DBS) methods are increasingly used because they are minimally invasive and logistically simple; however, biomarker validity is sensitive to pre-analytic factors, including spot size. This study analyzes the effects of storage temperature, humidity, drying time, shipping time, and spot size on seven biomarkers (*cho_x4*, *crp_x4*, *trg_x4*, *cyc_x4*, *hdl_x4*, *thb_x4*, *a1c_x4*) using a *Bayesian Generalized Additive Model* (Bayesian GAM) with Gaussian or log-normal families, combining parametric components and *smoothing splines*, and estimated via NUTS MCMC (3–4 chains).The results demonstrate that Bayesian GAM yields stable estimates ($\hat{R} \approx 1.00$) with relatively narrow credible intervals, indicating good convergence. Model evaluation using WAIC and LOOIC revealed adequate fit, particularly for *hdl_x4* and *a1c_x4*. Environmental factors such as temperature (*t_temp*) and log transformed spot size (*log1p(t_sizeA)*) were consistently significant. These findings highlight the effectiveness of Bayesian GAM in accommodating variability and uncertainty in DBS data, making it highly relevant for biomarker modeling in risk-based epidemiological studies.