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Protein biomarkers for early detection of neonatal sepsis

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Sepsis is a serious infection of newborns affecting premature infants disproportionately. Early detection of the condition can lead to a reduction in mortality and morbidity in the neonatal intensive care unit (NICU). Towards this goal we enrolled 159 infants (50 cases and 109 controls) who met the inclusion criteria of ≤32 weeks of gestation, birth weight ≤1500 grams and post natal age ≥120 hours. All infants were enrolled from the NICU of the University of New Mexico Children's Hospital between July 2006 and January 2009. Apart from demographic, clinical and routine lab measurements, a focused proteomic assay of 90 potential protein biomarkers suspected to play a role in infection and inflammation was also performed using serum samples drawn at the time of blood draw for blood culture. We used a representative set of machine learning algorithms such as Naïve Bayes, C4.5, CART, ADT and Random Forest for sepsis prediction using a ten-fold cross validation based on just the proteomic profile. The best predictive models had an AUC of 0.85, accuracy of 0.80, sensitivity of 0.69 and specificity of 0.85. The results are encouraging but additional clinical validation of the models is necessary before clinical use is contemplated.

Biography

Subramani Mani, MBBS, Ph.D. is a physician and computer scientist interested in machine learning, data mining and learning mechanistic models from biomedical data. He is currently an Associate Professor in the Division of Translational Informatics of the Department of Medicine at the University of New Mexico School of Medicine.

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