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Experimental Model For Development Of Machine Learning To Detect Infection By A Bioweapon

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Pneumonic plague, caused by Yersinia pestis, is a rapidly lethal and aerosol-transmissible disease that has been responsible for three major pandemics with high mortality. Naturally occurring exposure to plague occurs in areas throughout the world where temperate climate supports a sylvatic cycle involving rodents and their fleas. The infection remains a challenge for medical treatment especially for the index case where hospitalization is common most likely occurring when an accurate diagnosis is delayed. Moreover, Y. pestis is readily amenable to natural and manmade genetic evolution, making the emergence of multi-drug resistant or chimeric weapons of mass destruction a serious concern, especially in battlefield situations. The long-term objective of this work is to develop machine learning algorithms that utilize biorhythms and simple blood tests to identify a patient that is infected with a genetically modified Y. pestis able to withstand antibiotic treatment and cause debilitating or lethal disease. In this work, we identify and validate biomarkers of progressing pneumonic plague following aerosol challenge of rats. We demonstrate that doxycycline treatment failure is detected by marked changes in the electrocardiogram that associate with incomplete bacterial clearance in the early treatment stage, leading to altered recruitment of inflammatory monocytes capable of contributing to systemic disease even when bacterial growth is controlled by the antibiotic. Together the data indicate that this model may be suitable for Al-based methods for detecting a Y. pestis bioweapon.