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Ellie Mainou* (ellie.mainou@emory.edu), 2310 Ava Place, Decatur, GA 30033, and **Robert Dorit, Gwen Spencer** and **Dylan Shepardson**. *Parsing a Crowd of Near Best Fits: Consensus Ranges for Drug-Resistant Tuberculosis Modeling*. Preliminary report.

According to WHO, one third of the world's population is infected with tuberculosis (TB), with drug resistance posing a major challenge to the management of TB. Strains resistant to the most common drugs for treatment (e.g. isoniazid, rifampin) are already widespread. To address the issue, we constructed a mathematical compartmental model described by differential equations depicting the transmission of TB in the US. The model encompasses four strains of different resistance to antibiotics, while taking into consideration immigration, which greatly contributes to the excessive transmission of latent TB. A set of 27 parameters was fitted to recent CDC data on TB morbidity and mortality, using a genetic algorithm to minimize an error function. producing reliable fits, by generating random parameter values within the ranges obtained from real-world data. Local minima were identified and multiple sensitivity analysis tests were performed to identify which parameters the model is sensitive to. (Received September 07, 2017)