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BILOGISTIC MODEL FOR DISEASE AND VIRULENCE DYNAMICS OF *M. TUBERCULOSIS* IN RUSSIA

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The virulence is a main property of pathogen, which defines its ability of adaptation to a host organism and higher probability to cause a disease. It has been shown that the virulence is not the individual pathogen's characteristics but exists and develops in interaction with the host only. It evolves in dependence on the sensibility or resistance of macro-organism to infection. Therefore, in the scale of epidemic outbreak, this microorganism's property could be an important factor, which regulates disease rate, its maximal strength and decay[1]. In particular, an extended SIR-model [2] of malaria developed recently considers the virulence as a phenomenological parameter included into the contact rate and the death rate induced by this disease.

In the present work, we explore "virulence-epidemiological state" by the example of tuberculosis in Russian Federation. It has been shown [3] that the epidemiological dynamics correlates linearly with the virulence of *Micobacterium tuberculosis* during the period 1967-2012. To construct an appropriate model, we have analyzed (using LogLet decomposition method) epidemiological WHO data (period 1980-2014) and obtained, as result of their integration, a curve approximated by the bi-logistic function. This fact allows to obtain a set of Verhulst-like models for parts of sub-population, where different constant virulences are introduced into each subsystem separately. Such a subdivision could be interconnected with the heterogenious structure of mycobacterial population that has a high ability of adaptation to the host and strong mutability.

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