1046-62-1901 **William W Hager** (`hager@math.ufl.edu`), PO Box 118105, Department of Mathematics, University of Florida, Gainesville, FL FL 32611, **Jiangtao Luo*** (`jiangtl@math.ufl.edu`), Po Box 118105, Department of Mathematics, University of Florida, Gainesville, FL FL 32611, and **Rongling Wu** (`rwu@ufl.edu`), PO Box 110339, Institute of Food and Agricultural Sciences, University of Florida, Gainesville, FL FL 32611. *A Computational Model for Functional Mapping of Genes that Regulate HIV Drug Therapy and Virus Load.*

Genes have been recognized to control
the development of HIV, but have been difficult to detect
because the growth dynamic of it is sensitive to environmental changes.

We present a statistical model for mapping
and characterizing specific genes or quantitative trait loci (QTL)
that affect treatment of HIV. This model integrates
a system of differential equations into the framework for
functional mapping, allowing for the hypothesis tests of the
interplay between genetic actions and HIV drug therapy. We study the properties of the statistical model and a
simulation approach based on treatment and virus load has been designed to test statistical properties of the model.

The model will have great implications
for probing the molecular genetic mechanism of HIV drug therapy through the detection of the corresponding QTL
throughout the genome. (Received September 16, 2008)