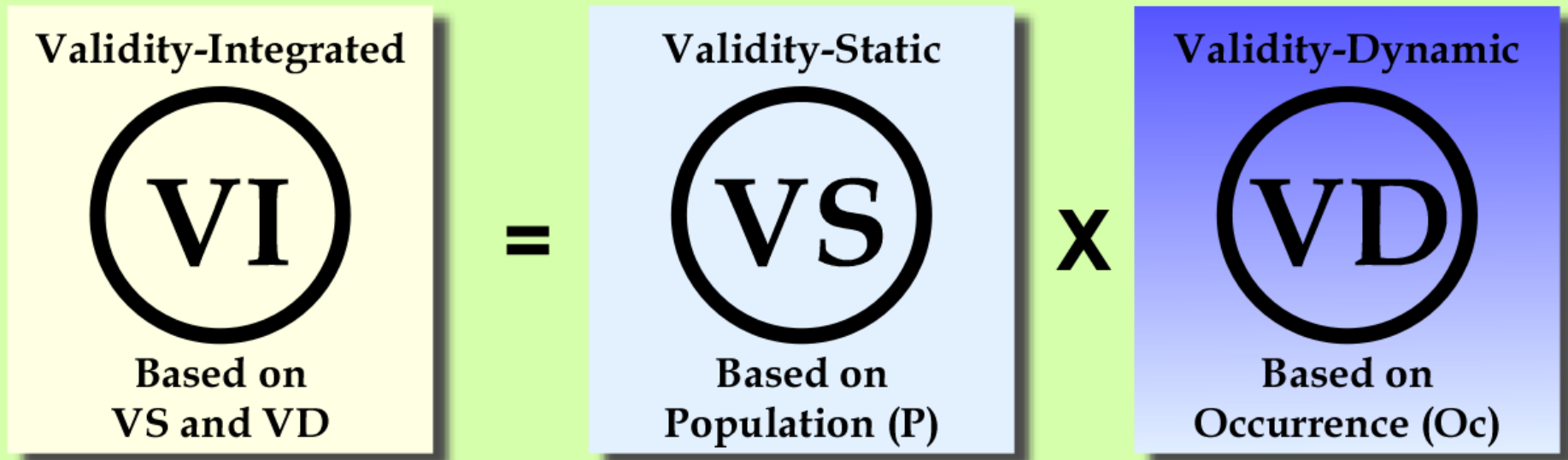


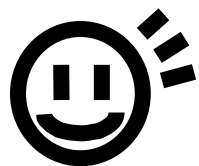
VI: Validity-integrated



$$VI(x)[\%] = \frac{1}{100} \sum_{i=1}^n (VS(x)_i \times VD(x)_i)$$

where n is number of windowed sequences including constituent sequence of motif x.

GenoPoemics™ System based on Genome Poemics (遺伝詩工学) idea.

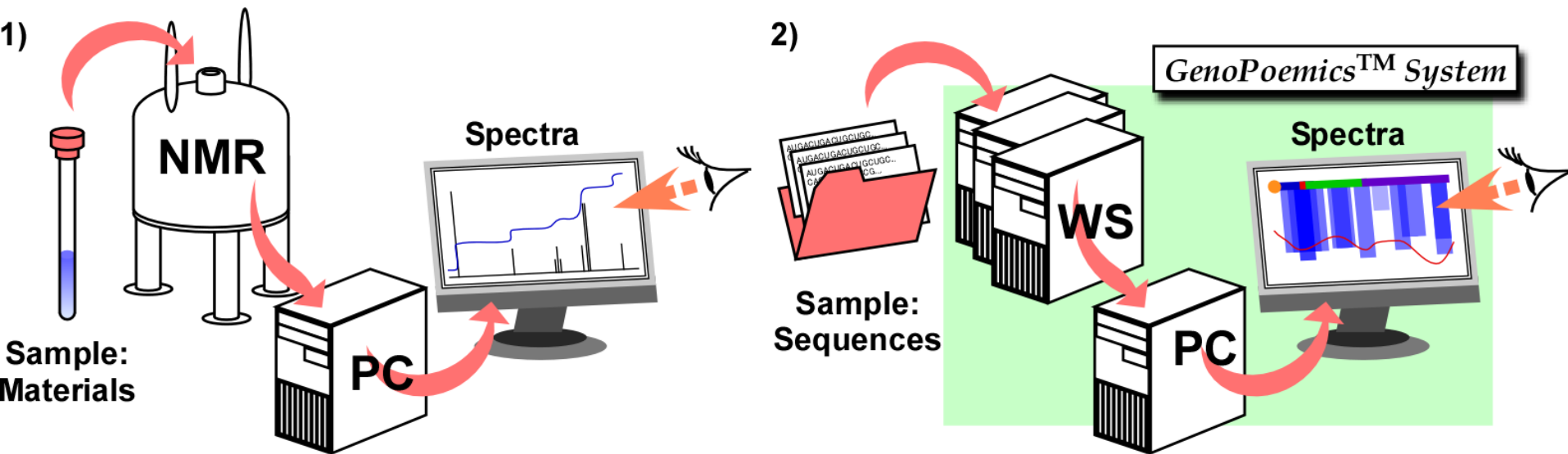


All prediction results were accumulated prior to visualization.

All were implemented in the *GenoPoemics™* system.

The *GenoPoemics*TM system: Overview

The *GenoPoemics*TM system is the *in silico* spectrometer to visualize structures of mRNAs to help our validation of the structures.



The GP "spectrometer" utilizes regular secondary prediction software (such as mfold, UNAFold, vsfold, etc) as probe to obtain spectra on certain long RNAs.

