

## Conime: Automated Analysis and Generation of RLGS Electrophoresis Gels

Dr. Rephael Wenger, OSU Dept. Computer Science and Engineering

Restriction Landmark Genomic Scanning (RLGS) is a two-dimensional gel electrophoresis method for detecting DNA molecular changes that occur near restriction enzyme sites. Genomic DNA is split into subsequences using enzymes which are then spread out on a two dimensional gel. Autoradiography or phosphor imaging is applied to the dried gel producing an “RLGS profile” of approximately 2500 spots. DNA subsequences correspond to spots on this gel while changes in DNA correspond to added, missing or amplified spots. Such spot changes can be used to identify methylation changes caused by cancer.

Commercial software for analysis of 2D protein gels is not suitable for RLGS analysis. In RLGS, spots are often lighter and smaller than protein spots, making identification of individual spots more difficult. It is often the lightest spots, their existence or lack thereof, which is of most interest in detecting DNA methylation.

Conime is an open source software package developed at The Ohio State University for analyzing RLGS gels. The software automates spot detection and identification, image registration and spot matching and comparison. It provides a graphical user interface for viewing the RLGS gels, editing spots and annotating the profile. Related software generates “virtual” RLGS gels from genome databases.

In this talk, we will discuss RLGS gel analysis and describe Conime and its algorithms. We will also discuss how virtual RLGS gels are generated from genome databases.

Joint work with Dr. Christoph Plass, OSU Dept. of Molecular Virology, Immunology and Medical Genetics and Human Cancer Genetics Program.