Epigenetics is a rapidly evolving scientific discipline (e.g. circa 2005) that studies changes in the expression of genes without changing of the genes themselves.

The discipline of epigenetics is the interaction between physics, chemistry and biology, not biophysics or biochemistry as they have evolved because of "flaws" in genomics that have been incorporated into those two disciplines.

Gene theories were disrupted in 2012 when researchers at Weill Cornell Medicine in NYC discovered the fact that genomic modeling is skewed because a 5th nucleobase was overlooked in the original work of Watson and Crick.

Despite the fact that industry journals concerning the discovery stated that "once again(it) forces us to rewrite our textbooks" an explicit and replicable model for gene expression has not been elucidated. Simply, the use of the DNA alphabet of A - C - T and G requires a complex algorithm that needs 3.4 billion base pairs to assay activities, an expensive process that fails to yield adequate granularity to identify specific variances that are the causes of chronic diseases.

Confusion reigns!

"New definitions of a gene are needed."

Professor Thomas Gingeras, Ph.D., Cold Spring Harbor Laboratory (CSHL), leader of the huge collaborative effort called ENCODE (Encyclopedia of DNA Elements), a research team comprised of 441 scientists from 32 institutes in 5 countries that spanned a 5 year period.

http://www.eurekalert.org/pub_releases/2012-09/cshl-img090412.php

Starting in 2005, based on a discovery that cellular level epigenetic activities were based on elements alone or in conjunction with amino acids (as opposed to current theories that they were formed exclusively from amino acids), interactions and imbalances dictated by the principles of physical science were used to "model" epigenetic activities.

By 2010, the original findings of the Center for Modeling Optimal Outcomes were transferred to MCFIP Inc. and a series of additional epigenetic discoveries were developed.

Since the modeling process was theoretical based on in silico processes, it was necessary for MCFIP to wait for their hypotheses to be confirmed by peer-reviewed research.

MCFIP assumes the role of a moderator who interfaces the three disciplines and translates the process into terms that are business-friendly for individuals who work in biomedical application. None of the facets of epigenetics are too foreign for anyone with a basic understanding of biology. However, ample time must be allocated to "bridge" communications.

Using the principles grounded in particle physics, MCFIP developed a novel application of epigenetics using homeostasis and elements as constituents of signaling molecules. These changes identified the following verifiable factors:

- Epigenetic biomarkers exist in 3s and they identify on off and modulating status; e.g. alternating current for homeostasis in epigenetic activities
- Epigenetic biomarkers are comprised of elements and amino acids; the amino acids regulate on – off activity
- Data must be collected to enable MCFIP to use its modeling tools to convert biological markers (e.g. those collected and retained in patient records) to be converted into epigenetic markers that have been identified and catalogued since 2007.
 Without an explicit model to identify interactions, data
- Without an explicit model to identify interactions, data collected can only show an isolated biomarker that are determinative) and not reflective of the interactions and imbalances that are causal factors for chronic diseases; i.e. theranostic (predictive) testing

Examples of the discoveries of MCFIP include but are not limited to the following:

- ✓ An explicit explanation for how small molecule drugs can be developed as a result of catabolic activity (cleaving) of gasotransmitters that are constituents of key cytokines
- Verifiable models for cellular defenses need to maintain cellular health such as apoptosis, ferroptosis, autophagy and mitophagy.
- ✓ Step-by-step explanations for all aspects of endocytosis that enables interaction between extracellular matter and the cytoplasm in cells.

Proof of Concept

Two examples of outcomes when the epigenetic modeling of MCFIP was applied include:

- ✓ HPV16 and HPV21 have been identified as viruses responsible for head and neck cancers when they can be verified as epigenetic markers that regulate the length of telomeres.
- Research has validated one of the primary causes of Crohn's disease (550,000 patients in the US) as being the interactions and imbalances between two bacteria (*E. coli* and *Serratia marcescens*) and a fungal organism (Candida tropicali). This research validated the MCFIP hypothesis for horizontal transfer between bacteria and fungi that is the primary cause of antibiotic resistant bacteria.

The two examples of outcomes from the modeling of the epigenome are provided for discussion purposes; i.e. to establish a dialogue with interested parties to discuss chronic diseases of interest and how MCFIP's modeling can be applied for commercialization.