

What is claimed is:

1. A method for production of a risk assessment data map comprising the following steps:
 - (a) selecting from a mass data collection a set of data elements having an association with a condition of interest;
 - (b) constructing an integrated multidimensional network from the initial selected set of data elements by collecting data, for each element, relating to interactions with any other element;
 - (c) sorting the information from the integrated multidimensional network using mathematical functions to eliminate elements of lesser relevance to the condition of interest, by minimization of bias; and
 - (d) applying quantitative metrics to the retained elements of the multidimensional network to create a data map that gives relative weight to the retained elements and element interactions, identifying the criticality of each element and interaction with respect to the condition of interest.
2. A method for assessing the risk of realizing a condition of interest from an individual set of elements comprising:
 - (a) comparing said individual set of elements to a risk assessment data map according to Claim 1, and
 - (b) assessing the degree of matching of individual elements with corresponding elements of the risk assessment data map that is associated with the condition of interest.
3. A method for producing a risk assessment map for a physiological condition comprising the steps:
 - (a) selecting a set of biomolecular constructs associated with a physiological condition to be diagnosed or treated;
 - (b) constructing an integrated multidimensional network detailing biophysical and biochemical properties and interactions of the selected biomolecular constructs;
 - (c) tuning the amount of information to be retained in the multidimensional network using mathematical functions to ensure minimization of bias to yield an unbiased multidimensional network; and

- (d) computing the criticality of each biomolecular construct in the resulting unbiased multidimensional network by application of graph metrics, to yield a risk assessment map detailing the biomolecular constructs and interactions between biomolecular constructs that are critical to development of the physiological condition.
4. A method for assessing the susceptibility of an individual or group of individuals to developing a physiological condition of interest, the method comprising:
- (a) preparing a risk assessment map by the method according to Claim 3;
 - (b) establishing a profile for an individual, from a biological sample obtained from the individual, by identifying the set of biomolecular constructs corresponding to the set selected in the preparation of said risk assessment map;
 - (c) computing the risk of the individual to develop the physiological condition of interest by mapping the profile of step (b) to said risk assessment map and assessing the differences between the profile and the biomolecular constructs and interactions between biomolecular constructs that are critical to development of the physiological condition of interest, as detailed in said risk assessment map.
5. The method of Claim 3, wherein said biomolecular constructs are selected from genes, genetic polymorphisms, transcribing elements of genomic material, proteins, genetic mutations, protein isoforms, and combinations thereof.
6. The method of Claim 5, wherein said biomolecular constructs are genetic polymorphisms.
7. The method of Claim 6, wherein said biomolecular constructs are single nucleotide polymorphisms (SNPs).
8. The method of Claim 3, wherein said physiological condition is a disease or syndrome.
9. The method of Claim 8, wherein said selecting step (a) is carried out by compiling a database of biomolecular construct elements associated with said physiological condition by interrogating one or more mass data collections.
10. The method of Claim 9, wherein said mass data collections include one or more omics data repositories.

11. The method of Claim 10, wherein said tuning step (c) is carried out by maximizing entropy of the data of the multidimensional network.
12. The method of Claim 11, wherein said computing step (d) is carried out by applying to the unbiased multidimensional network resulting from step (c) a series of graph metrics including degree of connectivity, degree of clustering, assortativity, and network diameter.
13. A diagnostic method for determining susceptibility of an individual to develop arteriosclerosis comprising monitoring two or more proteins selected from the group consisting of:

ADCY9	EIF3H	AIM1	LRIG1	FADS1
ERCC4	FGA	NCAM1	ATP6V1C2	WDR1
FGB	ABCA1	WVOX	GCKR	FBLIM1
LPL	APOB	LRAT	EDC4	TFAP2B
AK1	GJA1	BACE1	TAGLN	GALNT2
YKT6	GPN1	PROCR	CETP	GRID1

to detect dysregulation of the proteins in said individual.

14. The use of an agent effective to at least partially correct dysregulation in an individual of a protein selected from the group consisting of:

ADCY9	EIF3H	AIM1	LRIG1	FADS1
ERCC4	FGA	NCAM1	ATP6V1C2	WDR1
FGB	ABCA1	WVOX	GCKR	FBLIM1
LPL	APOB	LRAT	EDC4	TFAP2B
AK1	GJA1	BACE1	TAGLN	GALNT2
YKT6	GPN1	PROCR	CETP	GRID1

to decrease the susceptibility of said individual to developing arteriosclerosis.