



Figure 1. Landscape analysis of gene/protein interaction networks. Coordinates (X- and Y-axis) represent normalized values of the input network topology. Color gradient (Z-axis) represents the functional state mapped onto the graph for the data input and normalized by the highest value of the output matrix. The landscape is generated by ViaComplex V1.0 with the following options: plot as "3D-Graph", build on "edge&node", resolution "level-50", contrast "level-50", smoothness "level-50" and zoom "level-0".