Dm Toolbox V0.3

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to meet the increasing demand of metabolic network modelling, the original raven (reconstruction, analysis and visualization of metabolic networks) toolbox was developed to facilitate gem reconstruction, curation, and simulation [9]. in addition to facilitating the analysis and visualization of existing gems, raven particularly aimed to assist semi-automated draft model reconstruction, utilizing existing template gems and the kegg database [10]. since publication, raven has been used in gems reconstruction for a wide variety of organisms, ranging from bacteria [11], archaea [12] to human gut microbiome [13], eukaryotic microalgae [14], parasites [15 17], and fungi [18], as well as various human tissues [19, 20] and generic mammalian models with complex metabolism [21, 22]. as such, the raven toolbox has functioned as one of the two major matlab-based packages for constraint-based metabolic modelling, together with the cobra toolbox [23 25]. the raven 2.0 toolbox includes a few unique features to assist constraint-based modeling. first, a new reconstruction checker is included to ensure that a model is as consistent as possible. the reconstruction checker was developed using the modularity and consistency metrics [17, 30]. the modularity metric computes the similarity of gene assignments to the expected reaction list. the consistency metric checks whether there are at least two metabolic pathways that support the same pathways, which may indicate the presence of dead-end metabolites. both metrics are used to detect unreasonably high or low gene-reaction assignments and to identify inconsistencies that require manual editing. second, a new reconstruction task is included to identify the metabolic pathways that belong to a given cell or tissue type. raven 2.0 can utilize several data sources to identify the metabolic pathways (e.g., tigr, metacyc, and tgc). in this study, we integrated a tissue/cell type-specific model generation task into raven 2.0, which can generate a tissue/cell type-specific model for s. coelicolor. this task includes the generation of a scaffold model by the cofactormapper [19], followed by the prediction of the reactions and genes for each tissue/cell type, as well as the construction of the respective gem.

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the dm toolbox kit ((dm toolkit: physical edm or digital edm) is a practical take on the dark matter framework as a means of building an equitable and equitable future. the kit is designed for educators in schools that would like to engage students on these themes with a heavy consideration to pbl. when used together, the kit provides an innovative instructional method that can be used as a model for other schools, districts, classrooms or academies to step away from the use of top-down approaches that inevitably reinforce the systems that perpetuate inequities and place students in a position of disadvantage. dmtoolbox is a highly expandable set of tools allowing the development of custom function modules using either vb (visual basic for applications) or matlab. it is now possible to use the scripting framework of matlab to access the common functions of cobra toolbox and import external tools developed by other users. we have also integrated a wealth of tools for custom functions. these are added to our standard set of functions to provide the necessary functionality for a wide range of standard analyses. thus far, both elm and cobra toolbox are implemented in a client/server manner to establish a network between the human (computer operator) and the respective server. to integrate the human with the server, a new tool, elmer, has been developed. for easier integration, the cobra toolbox is now available in a new version. also, a new cobra-fseof module was developed to perform flux variability analysis (fva) on genome-scale metabolic models. another improvement is that all these modules are compatible with the new cobra toolbox v3 and elm v2.5. for v3, we developed a new data import tool, which imports the standard ore types. in addition, we developed a new data export tool to export these types to standard ore files. finally, we are now using a network-based platform. this allows the entire toolbox to be accessed and run via a web server. users can use either a desktop/laptop or web browser-based environment to access and analyze the models. for both the client and server, a common data exchange is set up. we have also developed the framework to incorporate new tools at any time. this enables tool support and service to be effectively updated. 5ec8ef588b

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