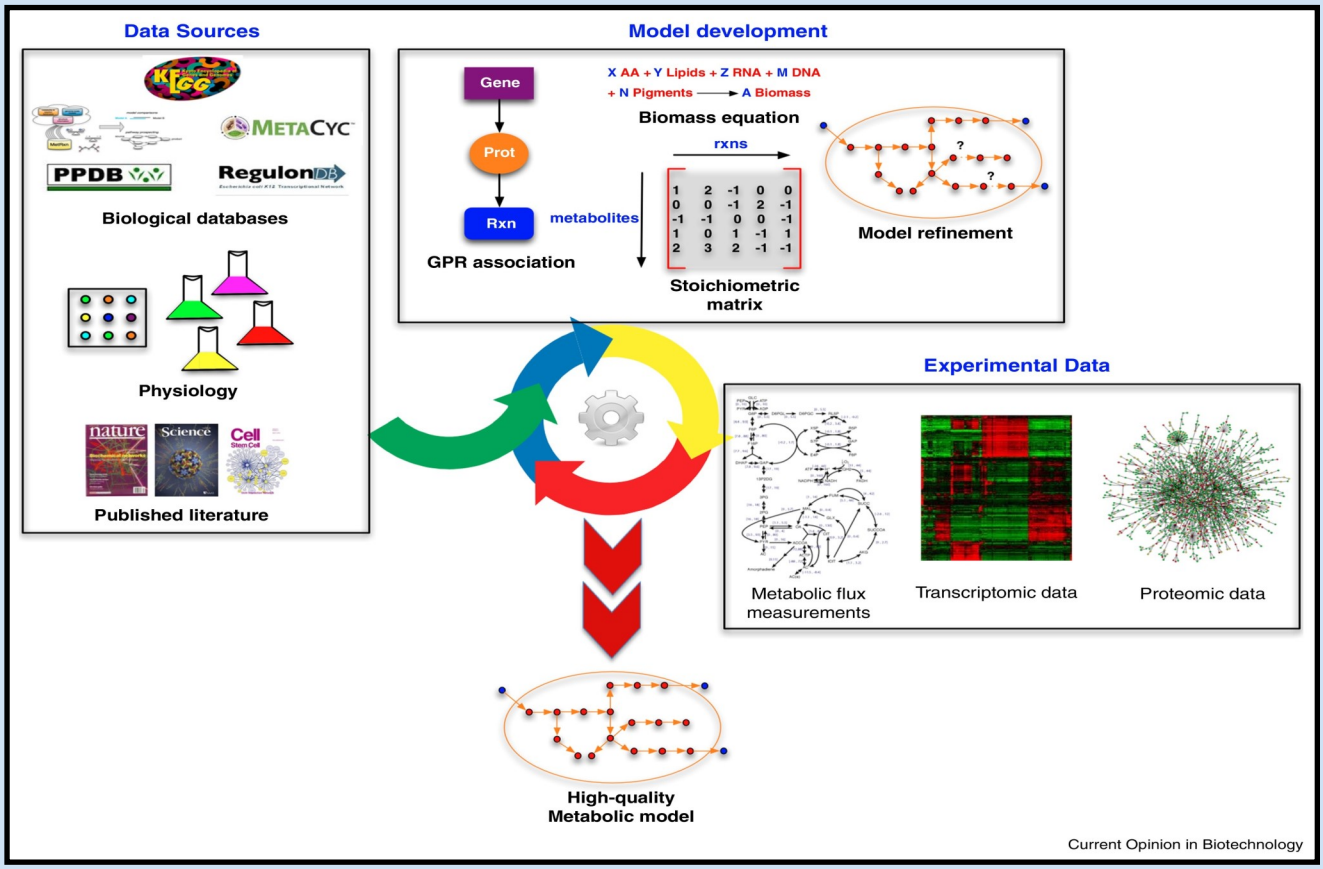
The Metabolic Crystal Ball:

Genome level models of metabolic processes:

[1]

Background:

Metabolic models have been used to characterize biological systems and develop strategies to reengineer them for better production of their biological byproducts [2]. They have also been applied to things like metabolic disease drugs, target identification, and the study of microbial pathogenicity and parasitism [2]. Rapid development and validation of these models has been achievable through improvements of sequence and annotation technology [3].



[2]

Approaches to metabolic model construction:

1. Sequence and annotation of genome. Can be done using NGS or using PDB.
2. Functions are assigned to all of the Open Reading Frames. All functions with "metabolic fingerprints" are also assigned with their chemical transformations.
3. Use transcriptomic, proteomic and fluxomic data to improve the model's accuracy. Can be used as regulatory constraints

Challenges and Future Work:

There are significant knowledge gaps in the modeling methods that could further use next generation sequencing.

- One example is the effect of regulation. By utilizing tools like RNA-Seq and transcriptomic studies, we can understand the directionality of regulation in metabolic models
- Another challenge is the labeling protocols that indicate metabolites in a high throughput manner. [2]

[1] http://thespringcenterfornaturalmedicine.com/wp-content/uploads/2016/01/mightychondrion_by_velica.jpg
[2] R. Saha, A. Chowdhury, C.D. Maranas, Recent advances in the reconstruction of metabolic models and integration of omics data, Current Opinion in Biotechnology 29 (2014) 39-45.
[3] T.Y. Kim, S.B. Sohn, Y.B. Kim, W.J. Kim, S.Y. Lee, Recent advances in reconstruction and applications of genome-scale metabolic models, Current Opinion in Biotechnology 23 (2012) 617-623.