



# Revealing Methanotrophic Syntrophy through Community Models

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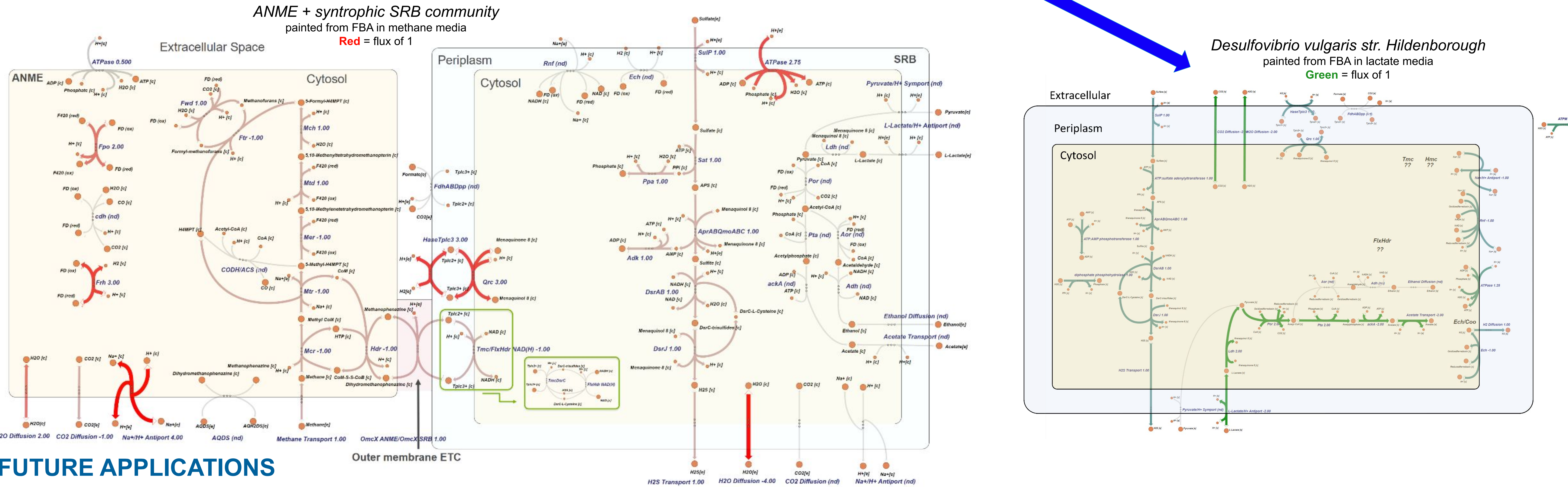
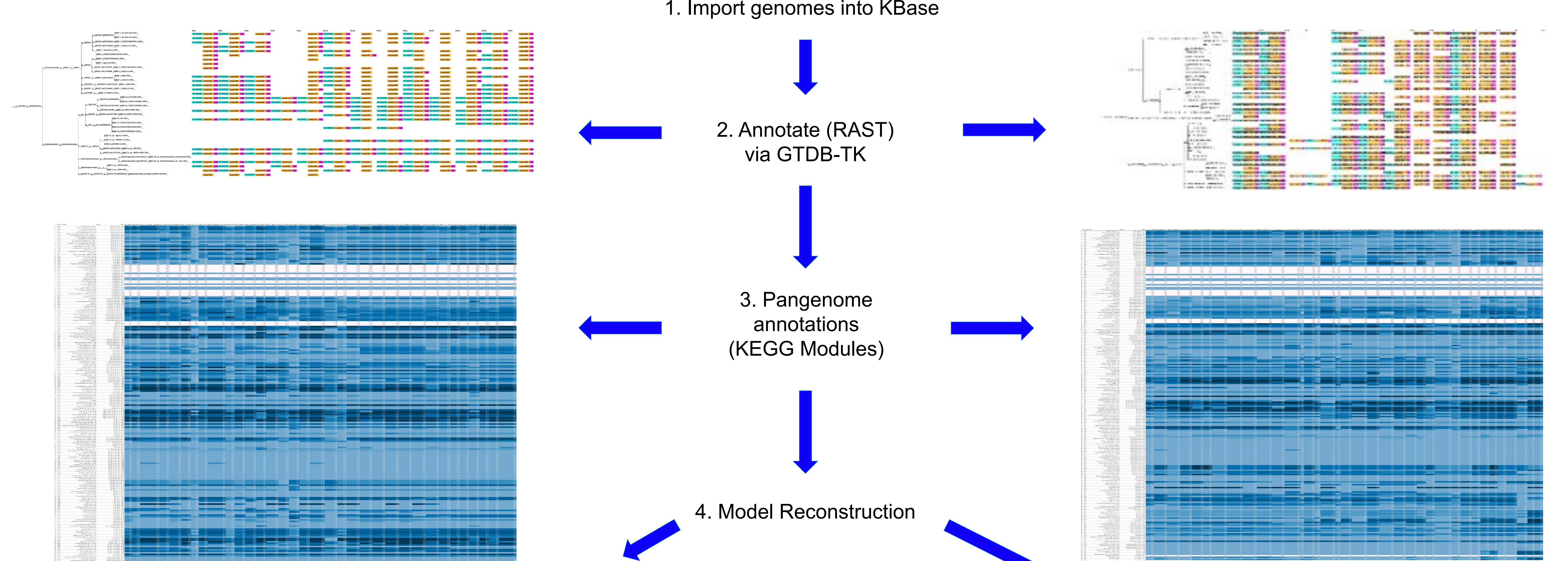
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## INTRODUCTION

Microbial communities of methanotrophic archaea (ANME) and sulfate-reducing bacteria (SRB) annually prevent the release of gigatons of methane into the environment, and are therefore critical agents in climate regulation and geochemical cycling. The “reverse methanogenesis” pathway of methane oxidation in ANME, which transfers electrons via sulfate groups with SRB and anaerobically oxidizes methane, is the proposed syntrophy of these communities; however, ecological details remain experimentally opaque. Metabolic modeling is an alternative research tool that can elucidate community interactions, yet models of archaeal and SRB metabolism remain insufficient for full simulations. We therefore expanded the ModelSEED reconstruction pipeline and model templates to capture new metabolic pathways and reaction intermediates. We annotated >40 genomes, assembled pangenomes of each clade to compensate inconsistencies, and developed new biochemical templates to capture more metabolism.

### Anaerobic Methanotrophic Archaea (ANME)

### Sulfate-reducing bacteria (SRB)



## FUTURE APPLICATIONS

Once we complete the annotation and clustering processes that are described in this Poster, we will constructed state-of-the-art ANME and SRB metabolic models that enable community-level metabolic simulations. We anticipate gleaning a) syntrophic interactions under native conditions; b) support or refutation for the “reverse methanogenesis” hypothesis; and c) possibly pivotal cross-feeding or member characteristics that explain the experimental peculiarity of precise pairings: only certain SRB with each ANME. These insights will broaden basic understanding of microbial ecology, methanotrophic and sulfate-reducing metabolisms, and will have applied value to either a) rationally engineer these communities as a biological tool to mitigate climate change or b) assess causation of anthropogenic influences on these marine biogeochemical cycles. The later can guide policy to best conserve the critical ecological services of this community and more generally become better stewards of marine environments. We may additionally explore the dynamics of this community, and refine FBA approaches that integrate expression data, to better resolve the interactions in these mysterious communities.

We finally plan to ingrain the new ModelSEED annotations and templates into KBase for open-source use by investigators of archaea or sulfate-reducing bacteria. This would complete the comprehensive automated pipeline of simulating ANME communities beginning only from experimental genomes: genome annotation, model reconstruction into metabolic models, and model simulation via existing tools in KBase.