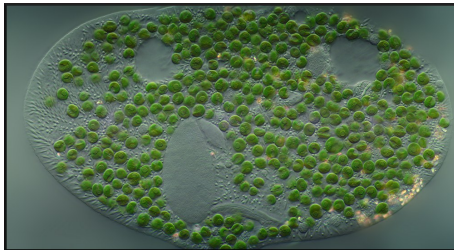


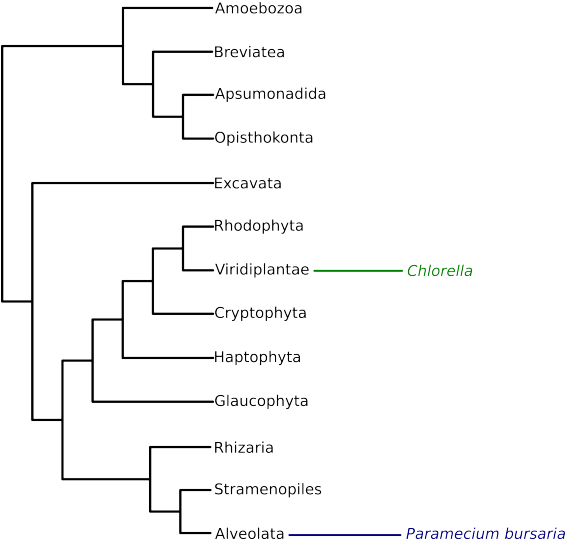
Key proteins implicated in the maintenance of  
photosynthetic endosymbiosis between  
*Paramecium bursaria* and *Chlorella*

Finlay Maguire  
University College London & Natural History Museum



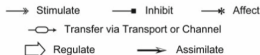
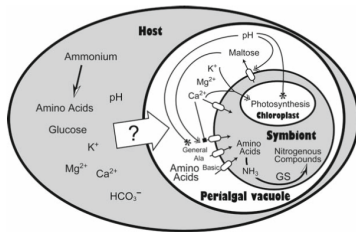
- ▶ Background
  - ▶ Phylogenetics & Molecular biology
  - ▶ Utility as a model organism for evolution of endosymbiosis
- ▶ Transcriptomics
  - ▶ Day/Night transcriptomes
  - ▶ Single cell transcriptomes
  - ▶ Assembly
  - ▶ Saturation analysis
  - ▶ Phylogenomic-SVM binning of transcripts
  - ▶ Differential expression analysis
- ▶ Metabolic reconstruction
  - ▶ Mapping
  - ▶ Comparative analysis
  - ▶ Predictions
- ▶ Further data to collect
  - ▶ Carbohydrate metabolism
  - ▶ Amino acid metabolism
  - ▶ Total metabolites
- ▶ Testing of predictions
  - ▶ RNAi
  - ▶ qtPCR

# Paramecium - Chlorella Phylogenetics



# A model for endosymbiosis

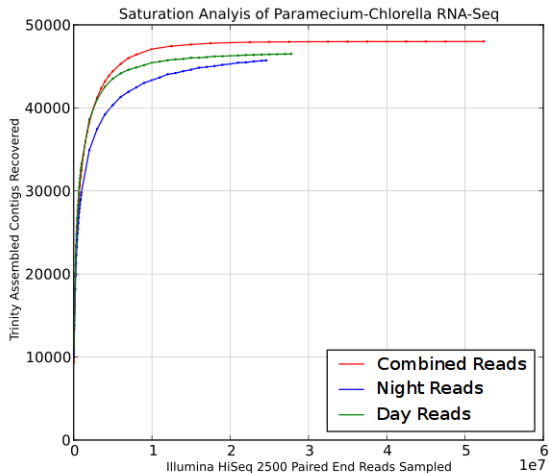
- ▶ Facultative endosymbiosis
- ▶ Evolution of secondary photosynthetic endosymbioses
- ▶ Established model organism
- ▶ RNAi available



# Day/Night Transcriptomics

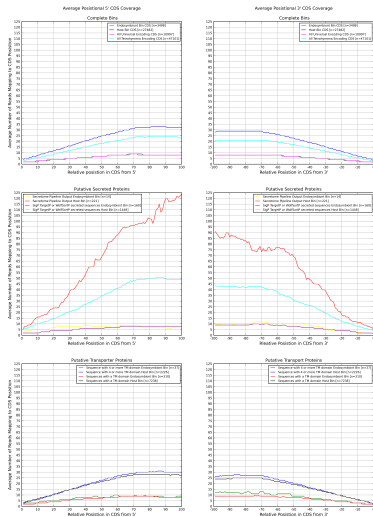
- ▶ Day/Night Transcriptomics
  - ▶ Midday and Midnight
  - ▶ Removing bacterial foodstock
  - ▶ RNA Extraction
  - ▶ Sequencing
- ▶ Single cell transcriptomics
  - ▶ Paraquat treatment
  - ▶ Confocal microscopy
  - ▶ Single cell picking
  - ▶
- ▶ Assembly De-Novo (Oasis vs Trinity)
- ▶ Referenced Assemblies

# Saturation analysis



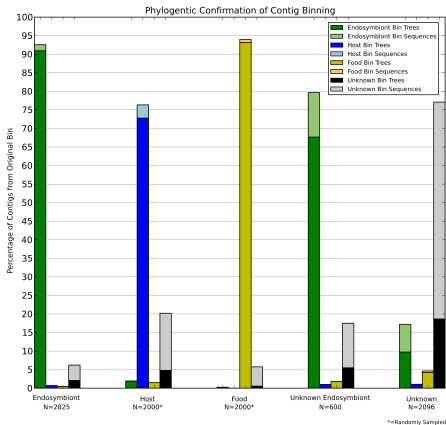
# Terminal End Coverage

Average Terminal Coverage for subsets of Paramecium-Chlorella RNA-Seq Data



# Phylogenomic binning

- ▶ Initial binning - BLAST hit and predicted CDS
- ▶ ML Phylogenomic pipeline

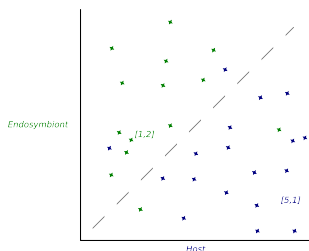


Initial Bins after Reassignment after Phylogenetic Confirmation

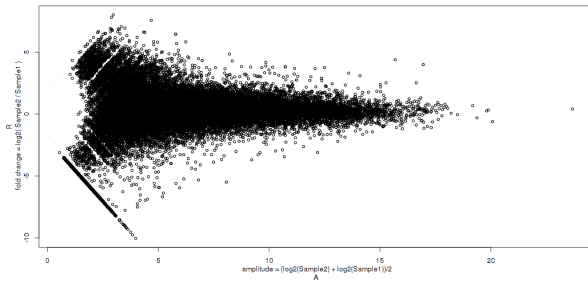


# Machine learning automation

- ▶ 10,000 phylogeny manual labelling
- ▶ Taxonomic lookup via NCBI API
- ▶ Convert each phylogeny into a vector e.g.  
$$V_i = \left[ \frac{1}{Endosymbiont_i}, \frac{1}{Host_i}, \frac{1}{Food_i}, \frac{1}{Unknown_i} \right]$$
- ▶ Train Multi-class Support Vector Machine on manually curated subset
- ▶ Cross-validation of SVM
- ▶ Optional unsupervised machine learning (e.g. clustering)

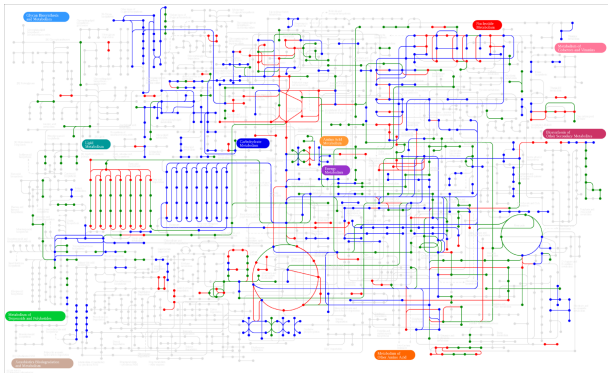


# Differential Expression Analysis



# Metabolic Reconstruction

- ▶ Annotation of partitioned datasets:
  - ▶ Trinotate
  - ▶ Blast2GO
  - ▶ KAAS
- ▶ Differential expression cut-offs:
  - ▶ day/night
  - ▶ With/without endosymbiont
- ▶ Pathway reconstruction:
  - ▶ Automated connection of units
  - ▶ Confidence based on prediction scoring
  - ▶ Manual handling of disjoints and inconsistency



- ▶ Candidate endosymbiont proteins:
  - ▶ 2 Amino Acid Permeases
  - ▶ Plasma Membrane Hydrogen ATPase
  - ▶ Ammonium Transporter
  - ▶ Plasma Membrane Iron Permease
  - ▶ Potassium Transporter
  - ▶ Sulfate Transporter

# Work in progress

- ▶ Metabolomics data
  - ▶ Carbohydrate metabolism
  - ▶ Amino acid metabolism
  - ▶ Total metabolites
- ▶ RNAi
  - ▶ RNAi vector synthesised
  - ▶ *E. coli food-stock transformation*
  - ▶ Bug22 verification
  - ▶ Microinjection