

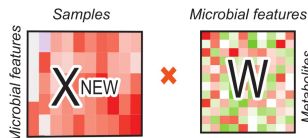
## MelonnPan - Predict



**Input:**  
Reads from  
microbiome  
sequencing

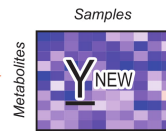


**Step 1:**  
Taxonomic or  
functional  
profiling (e.g.  
HUMANn2)



### Step 2:

Identify predictive microbial features  
as determined by a pre-trained  
MelonnPan model and multiply the  
abundances by their trained weights  $W$



### Output:

Table of relative  
abundances of  
metabolites  
of interest



**Downstream  
statistical analysis**

