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|  | Zozaya et al. | GRIMER | microbIEM | DECONTAM |
| **Goal** | * Decontaminate low-biomass microbiome pipelines | * Create interactive report/dashboard from DECONTAM output * Make accessible for non-coding researchers | * ID contaminants based on relative abundance in negative controls * Provide GUI for non-coding researchers | * Provide R package with statistical classification to ID contaminants based on:  1. Contaminants at higher frequencies (sample) 2. Contaminants often found more in negative controls (control) |
| **Method** | Sample-based approach, control-based approach, blacklist-based approach | Control-based approach, sample-based approach (both from decontam) | Control-based approach | Control-based approach, sample-based approach |
| **What is the difference?** | * Not wrapped in R package * Used limma * Not streamlined | * Uses prior method, just puts into dashboard | * Focuses on one method | * Leverages two methods, not uses blacklist approach * Lacks dashboard approach? |
| **What can we pull from this?** | Overall pipeline layout/order | Dashboard/HTML output makes more accessible and sharable for dissemination of information? | Mock communities to test effectiveness  Youden’s index | Prevalence method (step 2)  ~ Should we consider the frequency method? |

Methods to compare to:

* MicrobIEM (Hülpüsch et al., 2023)
  + R Shiny
* GRIMER (Piro et al., 2023)
  + HTML
  + Leverages Decontam?
* Decontam (Davis et al., 2018)
  + R
  + Primarily for high-biomass
  + Both prevalence and frequency filters
* Frequency filter
  + Remove all below abundance threshold
* Presence filter
  + Removes all sequences appearing in negative control
* SourceTracker (Knights et al., 2011)
  + R
  + Bayesian