Methods section:

* Overview on metaWRAP architecture (Figure 1)
* Description of each module (Figure S1)
* Detailed description of the Bin\_refinement module (Figure S2)
* Detailed description of the Reasemble\_bins module (Figure S3)

Results section:

* Bin\_refinement module gives the best bins on synthetic metagenomic data sets compared to individual binners and other binning refinement algorithms (Figures 2, S4)
* Bin\_refinement module also produces the best bins on real data sets from a range of microbiome types (Figures 3, 5)
* Bin\_refinement module dynamically adapts its output to prioritize completion and contamination thresholds that the user wants (Figures 5, S5, S6)
* Reasemble\_bins module consistently and significantly improves bins (except in soil) (Figures 4, 5)
* Combining the Bin\_refinement and Reassemble\_bins modules, metaWRAP as a whole produces the best binning results out of all current competitors (Figure 5)
* The Kraken module estimates taxonomy distributions of communities (Figure S7)
* The Quant\_bins estimates bin abundances in different samples (Figure S8)
* Classify\_bins is a conservative first-pass way to estimate bin taxonomy (Figures S9, S10)
* Blobology is a useful way to visualize binning success (Figures 6, S11).