

Metagenome Assembly

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graph TD; A[Metagenome Assembly] --> B[Metagenome-assembled genomes (MAGs)]; B --> C[CheckM2  
MAG quality assessment  
QS > 50%]; C --> D[skANI  
Species-level novelty  
ANI < 95%]; D --> E[Novel MAGs]; E --> F[Sourmash gather  
Community composition  
estimation]; F --> G[Community Abundance Matrix]; G --> H[Diversity analysis];
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The flowchart illustrates a seven-step process for metagenome analysis. It begins with 'Metagenome Assembly' in a dashed box, followed by 'Metagenome-assembled genomes (MAGs)'. The next three steps are green boxes: 'CheckM2' (MAG quality assessment, QS > 50%), 'skANI' (Species-level novelty, ANI < 95%), and 'Sourmash gather' (Community composition estimation). These are followed by two gray boxes: 'Novel MAGs' and 'Community Abundance Matrix'. The final step is a green box labeled 'Diversity analysis'. Arrows indicate the sequential flow from top to bottom.

Metagenome-assembled
genomes (MAGs)

CheckM2

MAG quality assessment
QS > 50%

skANI

Species-level novelty
ANI < 95%

Novel MAGs

Sourmash gather

Community composition
estimation

Community Abundance
Matrix

Diversity analysis