# ASV Analysis Workflow



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1 Specimen Collection & Processing
(Sampling, Sorting, Imaging, ID, DNA Extraction)
        │ DNA Extract
        ▼
2 Molecular Data Generation
(COI PCR Amplification, Illumina Sequencing)
        │ Raw Paired-End Reads
        ▼
3 Bioinformatics Pipeline
Raw Reads → Filtered Reads & ASV FASTA
Tools: cutadapt, pear, vsearch, filtertranslate
```

Input: Original Metadata

```
        │ ASV FASTA                        │ Metadata Table
        ▼                                  ▼
Sequence Analysis Script          4 Phylogenetic Framework Construction
(Analysis of Features & Quality)  (Mitogenome Assembly, Tree Building)
Tools: Python (pandas, BioPython) Tools: MAFFT, RAxML
```

Analysis Table
(incl. Quality Scores, Motifs etc.)

Phylogenetic Reference Tree

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5 ASV Authentication & Classification
(MRCT, Phylo Placement, Rules, ML)
Tools: Python (pandas, scikit-learn)
        │ Final Classification Table
        ▼
6 Statistical Analysis
(Generate Manuscript Stats & Summaries)
Tools: Python (pandas, scipy)
        │ Results
        ▼
Final Outputs:
Authenticated Barcodes &Results (Stats, Summaries)
```

## Methodology Legend

- Specimen & Molecular
- Bioinformatics
- Phylo Framework
- Sequence Analysis
- Classification
- Statistics
- Final Output