<table>
<thead>
<tr>
<th></th>
<th>BROCC</th>
<th>MARTA</th>
<th>MEGAN</th>
</tr>
</thead>
<tbody>
<tr>
<td>Votes on multiple high identity % identities</td>
<td>Votes within highest bit score</td>
<td>Selects Lowest Common Ancestor above bit score threshold</td>
<td></td>
</tr>
<tr>
<td>Uses percent identity</td>
<td>Uses bitscore</td>
<td>Uses bit score</td>
<td></td>
</tr>
<tr>
<td>Filters for percent identity, coverage, and classification level</td>
<td>Filters for coverage and percent identity</td>
<td>Filters for bitscore</td>
<td></td>
</tr>
<tr>
<td>Adjustable consensus thresholds at each taxonomic rank</td>
<td>Adjustable consensus thresholds at each taxonomic rank</td>
<td>Requires full consensus at assigned rank</td>
<td></td>
</tr>
<tr>
<td>Adjustable coverage filter</td>
<td>80% coverage filter</td>
<td>No filter</td>
<td></td>
</tr>
<tr>
<td>Excludes adjustable set of generic db classifications</td>
<td>Excludes all &quot;uncultured&quot; or &quot;unidentified&quot; db classifications</td>
<td>Includes generic db hits in decision</td>
<td></td>
</tr>
<tr>
<td>Begins voting at bottom of taxonomy</td>
<td>Begins voting at bottom of taxonomy</td>
<td>n/a</td>
<td></td>
</tr>
<tr>
<td>Can use any blast implementation</td>
<td>Uses megablast</td>
<td>Can use any blast implementation</td>
<td></td>
</tr>
<tr>
<td>Queries NCBI online for taxonomy</td>
<td>Queries SQL database for taxonomy</td>
<td>Uses NCBI taxonomy in program</td>
<td></td>
</tr>
<tr>
<td>Implemented in Python</td>
<td>Implemented in Java</td>
<td>Implemented in Java</td>
<td></td>
</tr>
<tr>
<td>Can integrate into Qiime</td>
<td>Requires intervention for use with Qiime</td>
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<td></td>
</tr>
</tbody>
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*Comparison of BROCC, MARTA, and MEGAN.*

BROCC
- Votes on multiple high identity % identities
- Uses percent identity
- Filters for percent identity, coverage, and classification level
- Adjustable consensus thresholds at each taxonomic rank
- Adjustable coverage filter
- Excludes adjustable set of generic db classifications
- Begins voting at bottom of taxonomy
- Can use any blast implementation
- Queries NCBI online for taxonomy
- Implemented in Python
- Can integrate into Qiime

MARTA
- Votes within highest bit score
- Uses bitscore
- Filters for coverage and percent identity
- Adjustable consensus thresholds at each taxonomic rank
- 80% coverage filter
- Excludes all "uncultured" or "unidentified" db classifications
- Begins voting at bottom of taxonomy
- Uses megablast
- Queries SQL database for taxonomy
- Implemented in Java
- Requires intervention for use with Qiime

MEGAN
- Selects Lowest Common Ancestor above bit score threshold
- Uses bit score
- Filters for bitscore
- Requires full consensus at assigned rank
- No filter
- Includes generic db hits in decision
- n/a
- Can use any blast implementation
- Uses NCBI taxonomy in program
- Implemented in Java
- Can integrate into Qiime