

# **BLAST Logic**

# BLAST Logic

- BLAST Logic is a language for comparative genomics
- Two types of statements:
  - **Quantifiers** define which regions of a BLAST result will be displayed
  - **Logic operators** combine quantifiers together to form more complex regions
- Quantifiers are linked by logic operators  
ex: { Quant } Logic { Quant } Logic { Quant }
- A BLAST Logic job has a global reference file, and each quantifier has an associated query file

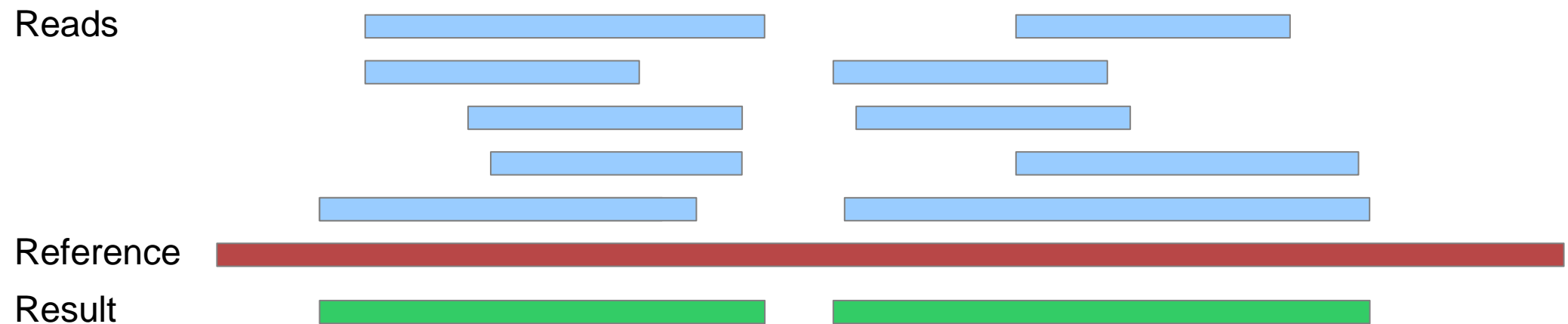
# Quantifiers

- Takes filtering and BLAST parameters to control a BLAST operation
- Four sections:
  1. Quantifier operation – *ANY, ALL, NOT IN, SOME*
  2. BLAST parameters
  3. File features
  4. Filtering values

```
{ ANY; file:sequence.gb; blasttype:blastn;  
  filter-complexity:false; e-value:1e-10;  
  genetic-code:11; ref-feature:CDS;  
  query-feature:CDS; hsp-length:100; pid:80; }
```

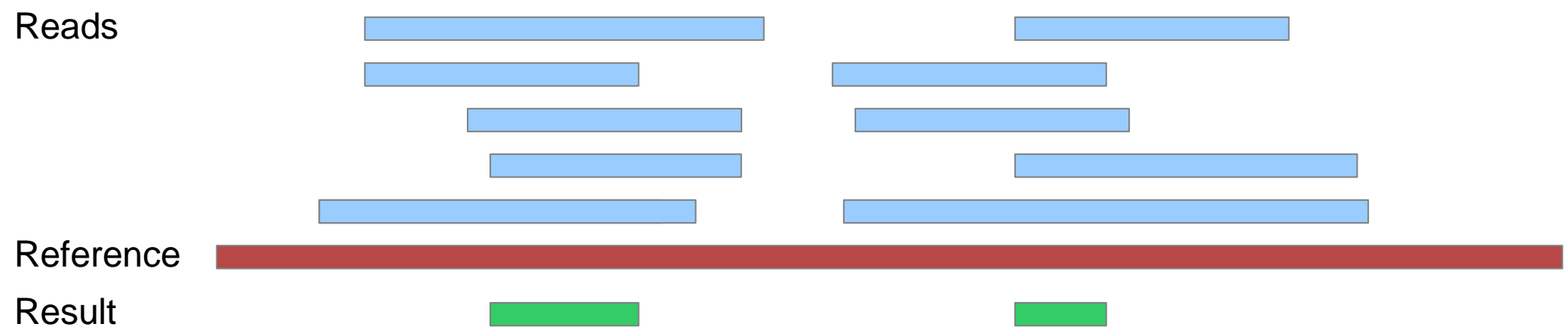
# ANY

- Displays BLAST hits to any sequence in the query



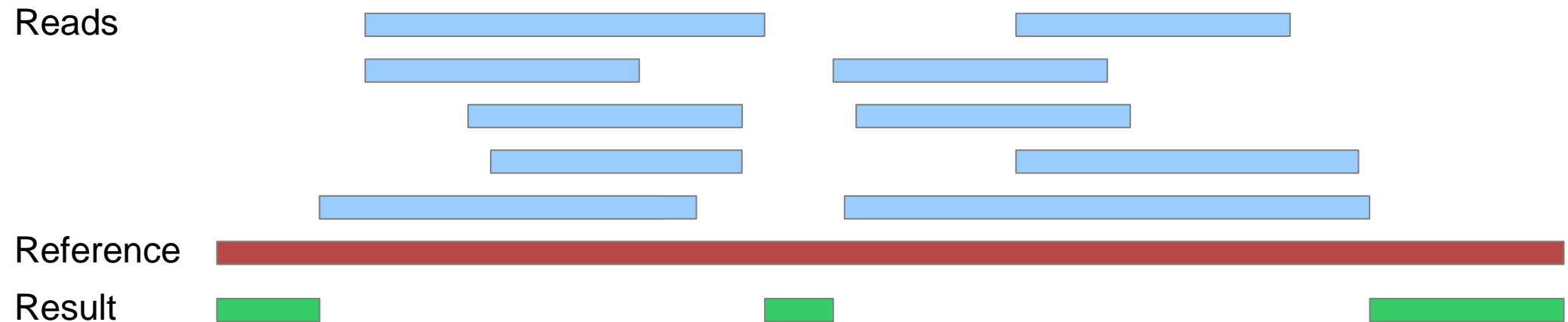
# ALL

- Displays regions with BLAST hits to all sequences in a query



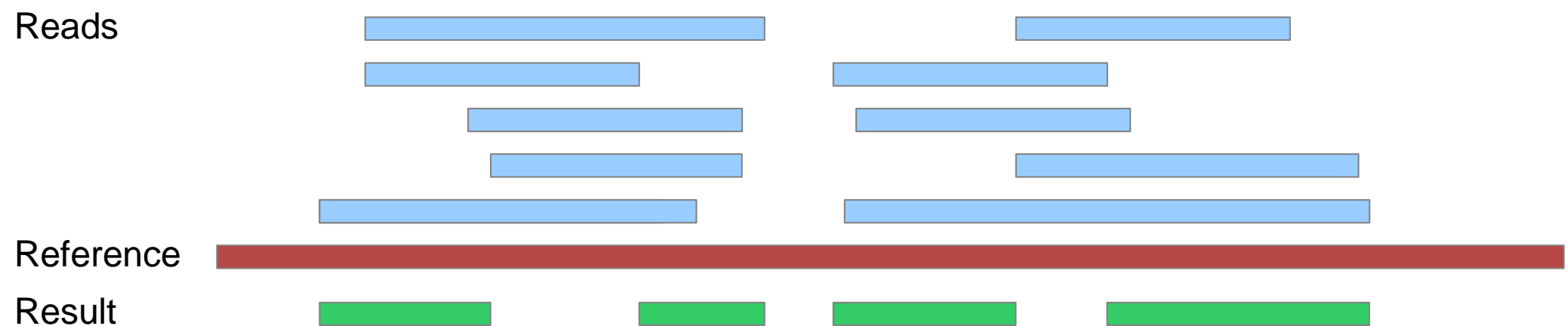
# NOT IN

- Displays regions that do not have BLAST hits to the query file

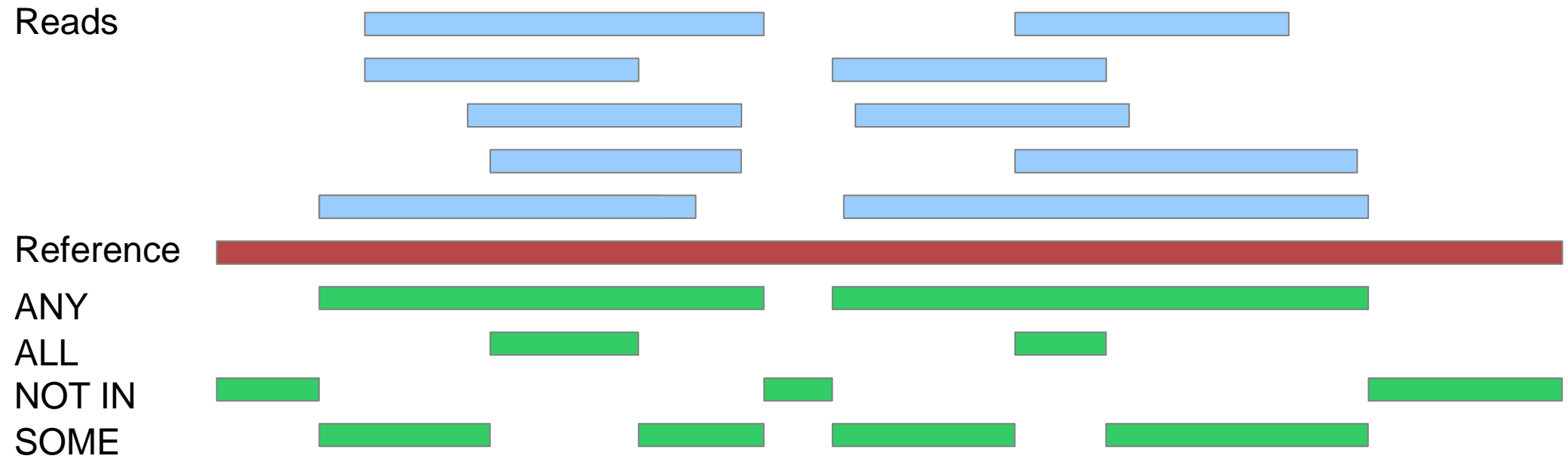


# SOME

- Displays regions where there are hits to some but not all reads in the query



# Comparison





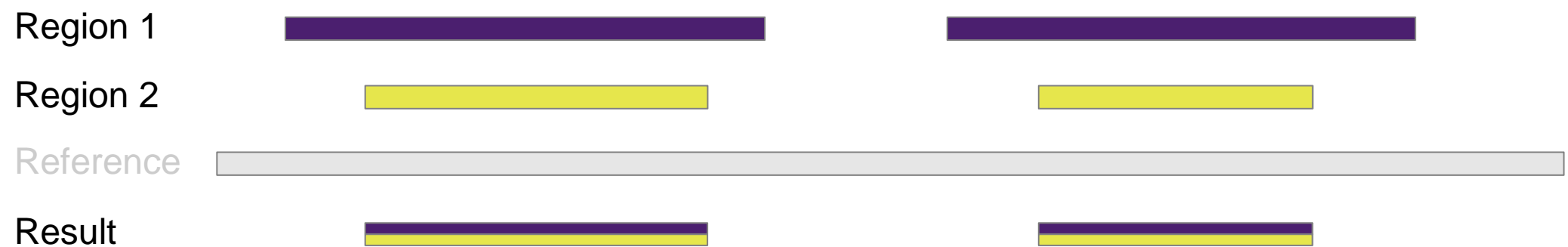
# Logic Operators

- Used to combine and connect quantifier statements
- Performs a math-like operation between two regions and outputs a single combined region
- Three types: *AND*, *OR*, *SUBTRACT*

{ ANY; ... } AND { ALL; ... }

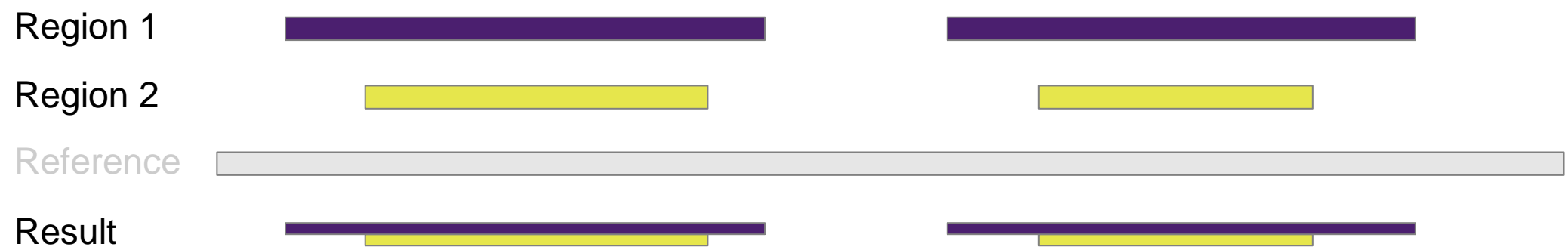
# AND

- Hits must exist in both regions to be displayed
- Similar to ALL quantifier



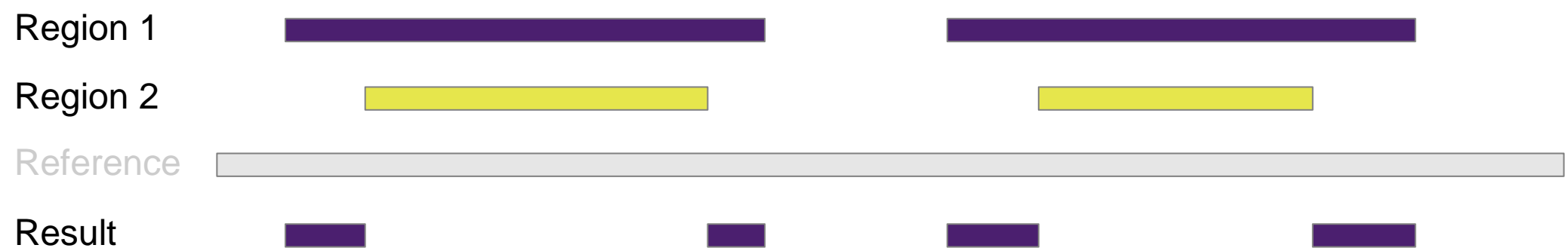
# OR

- Combines all hits from region 1 with region 2
- Similar to ANY quantifier



# SUBTRACT

- Displays hits in region 1 that don't exist in region 2



# Comparison



# Complex Statements

- Multiple logic statements can be combined
- Statements can be grouped using brackets “[ ]” to form an order of operations

{ ANY; ... } AND { ALL; ... } AND { ALL; ... }

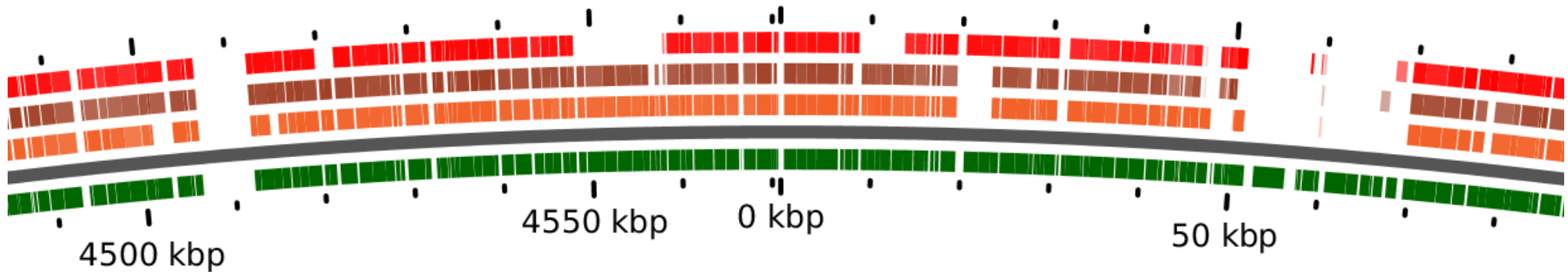
[ { ANY; ... } AND { ALL; ... } ] SUBTRACT { NOT IN; ... }

# BLAST Logic in GView Server

- Used in the analysis engine of GView Server
- Each analysis type is a different BLAST Logic operation:
  - BLAST Atlas – { ANY }
  - Core genome – { ALL }
  - Accessory genome – { SOME }
  - Unique genome – { NOT IN }
  - Signature genes { ANY } AND { NOT IN }

# BLAST Atlas

- Each track is an individual { ANY } operation





# Logic Construction

**BLAST Sequence**

**Analysis type**  
BLAST Logic analysis type: **Custom BLAST Logic** Perform customized logical and set operations on BLAST results

**Select a sequence file**  
Sequence(s) to BLAST against reference (example): **Choose File** NC003197.gb

**Select a sequence file**  
Sequence(s) to BLAST against reference (example): **Choose File** NC006905.gb

**Select a sequence file**  
Sequence(s) to BLAST against reference (example): **Choose File** NC012125.gb

Drag and drop to re-arrange logic operations

BLAST ANY NC003197.gb    Logic AND    BLAST ANY NC006905.gb    Logic SUBTRACT    BLAST ANY NC012125.gb

Add BLAST    Add Logic    Add Open Bracket    Add Close Bracket    Valid: ✓

```
{ ANY; file:NC003197.gb; blasttype:blastn; ref-feature:sequence; query-feature:sequence; e-value:1e-10; genetic-code:11; hsp-length:100; pid:80; } AND { ANY; file:NC006905.gb; blasttype:blastn; ref-feature:sequence; query-feature:sequence; e-value:1e-10; genetic-code:11; hsp-length:100; pid:80; }
```

# Custom Logic

[ { ANY; file1 } AND { ANY; file2 } ] SUBTRACT { ANY; file 3 }

