

## Requirements

- project multiple scaffolds
- project any annotated feature with scaffolds in any order
- annotate / modify features across scaffolds
- project around exons (transcripts less so)
- use any set of HTMLFeature track to project (OGS is most important though)

## Important Architectural Pieces

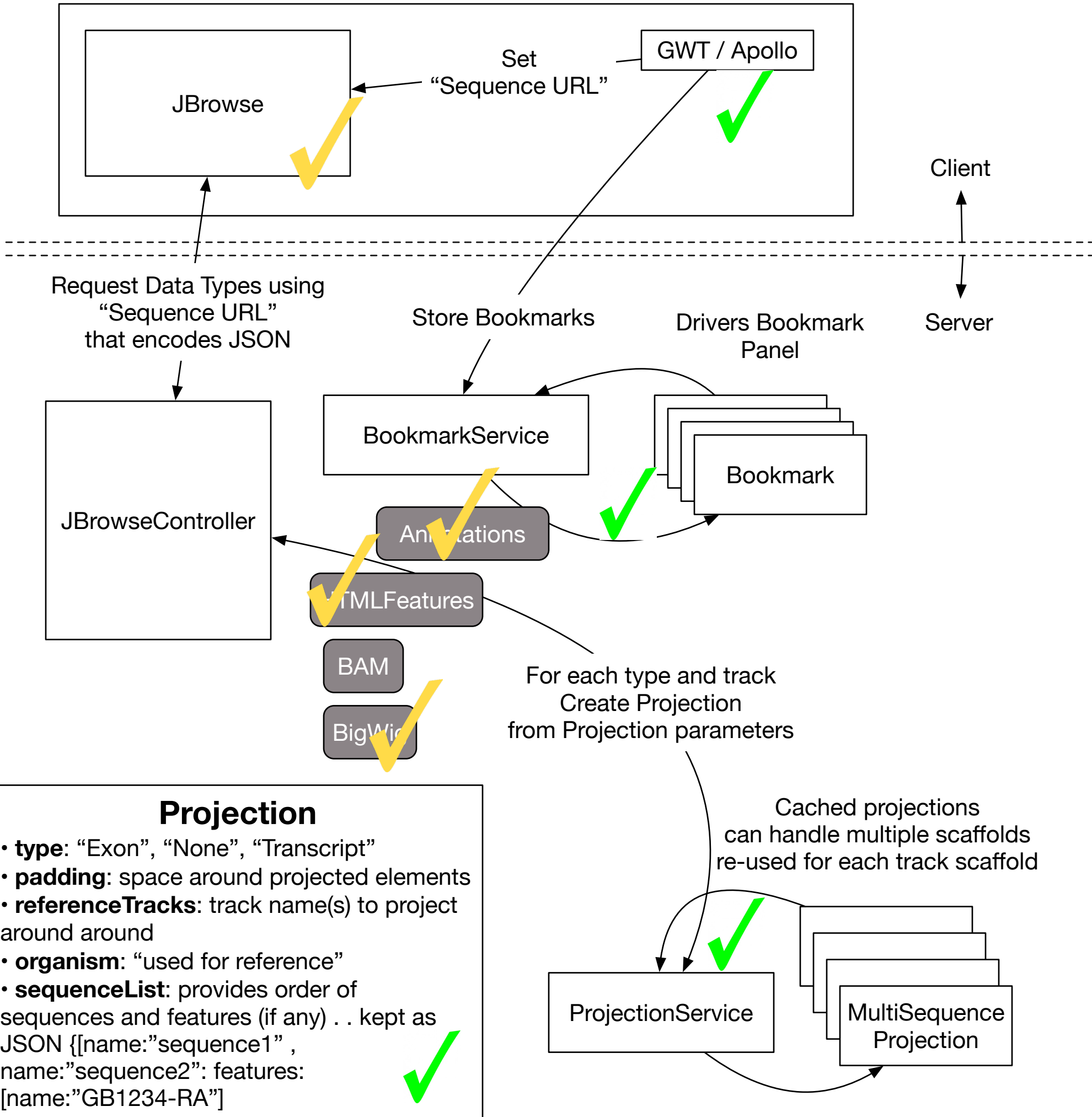
- create projection setting
- calculate alterations
- alter returned JSON
- revert projected JSON on input

## Future Requirements?

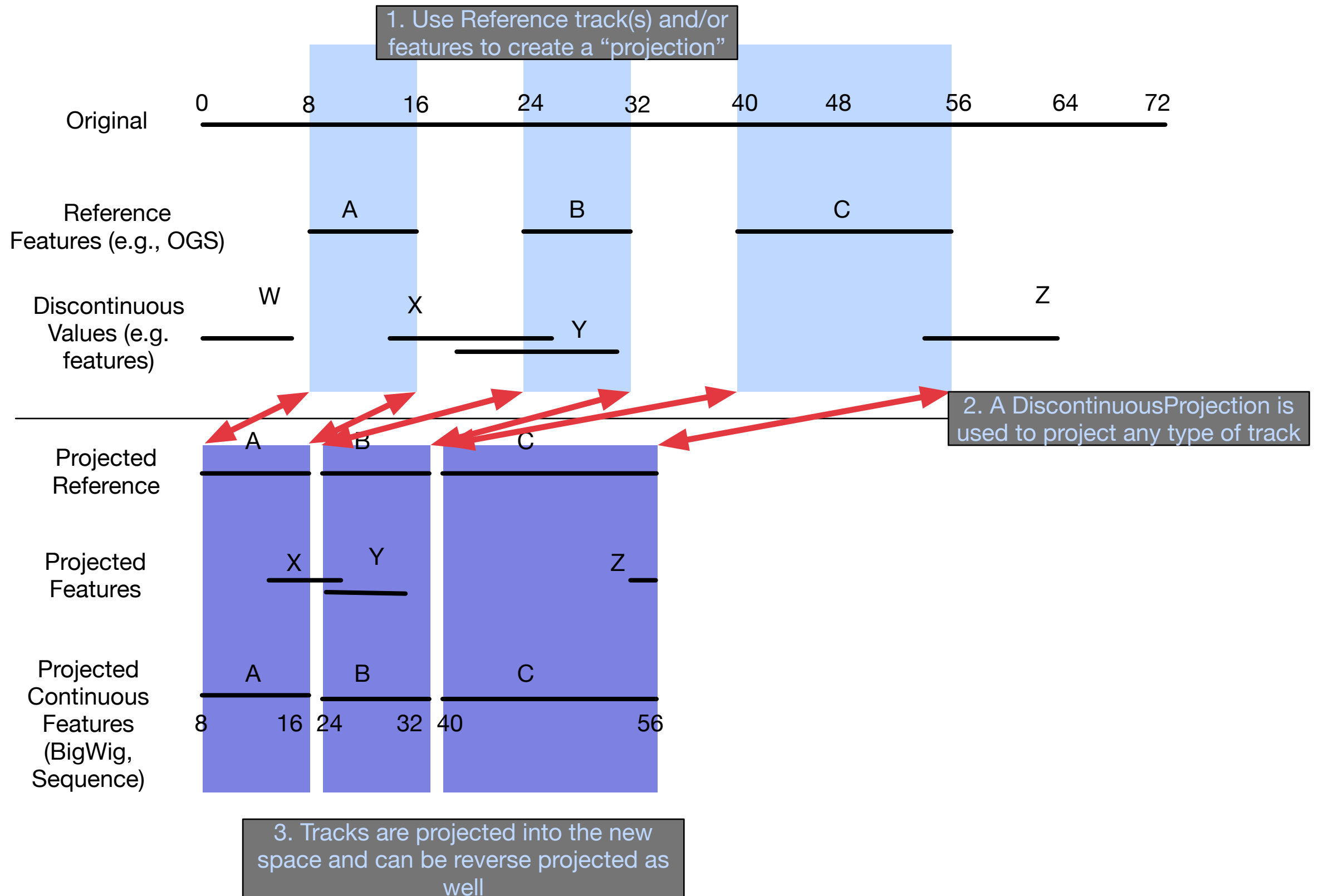
- multi organism alignment
- project across BAM and VCF
- additional variation

## Projection

- **type**: “Exon”, “None”, “Transcript”
- **padding**: space around projected elements
- **referenceTracks**: track name(s) to project around around
- **organism**: “used for reference”
- **sequenceList**: provides order of sequences and features (if any) . . kept as JSON {[name:”sequence1” , name:”sequence2”: features: [name:”GB1234-RA”]



# Discontinuous Projection



# MultisequenceProjection - holds multiple Discontinuous Projections

1. Use Reference track(s) and/or features to create a "projection"

Scaffold I

Scaffold II

