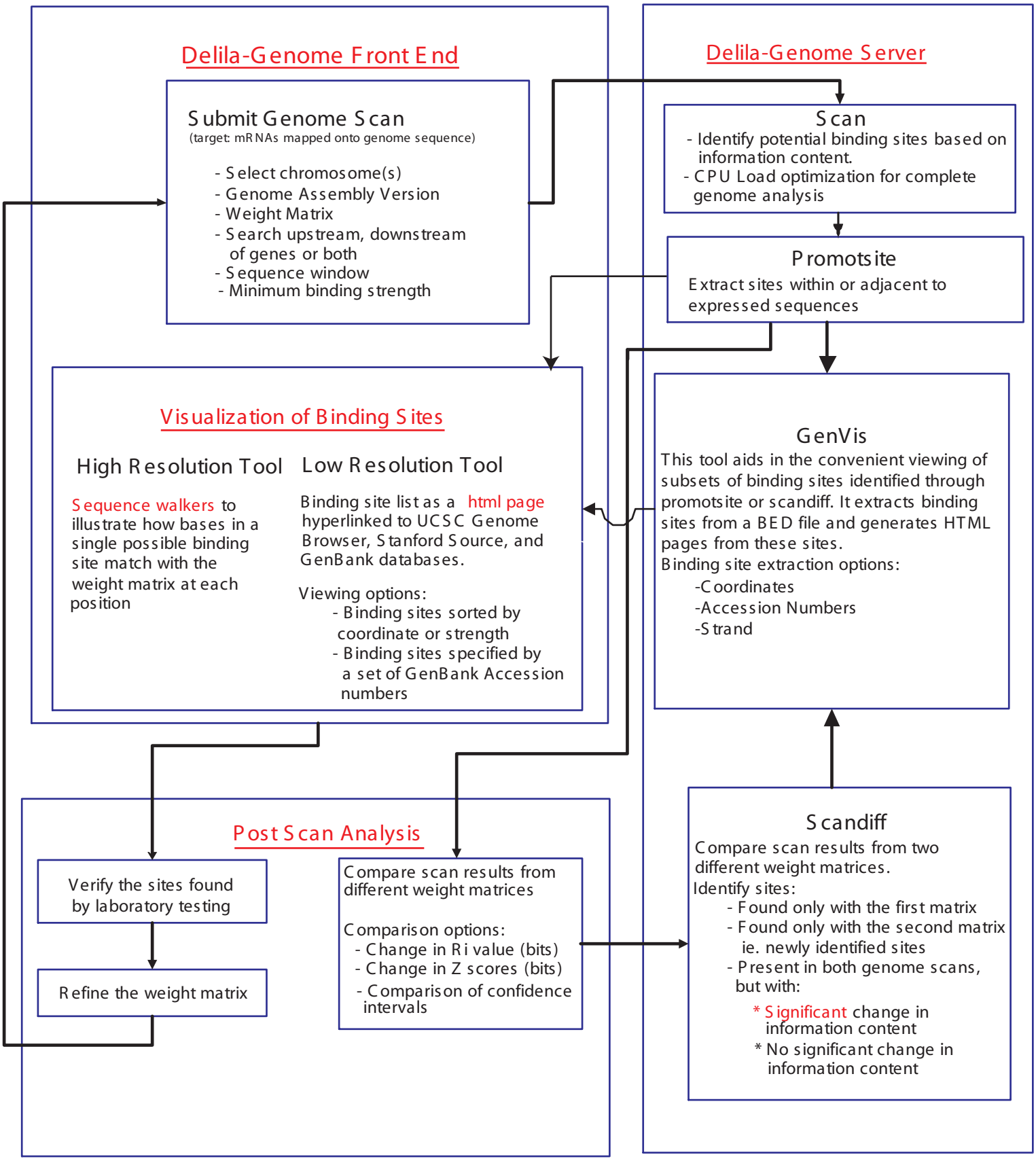
Delila-Genome Front End
Submit Genome Scan
(target: mRNAs mapped onto genome sequence)
- Select chromosome(s)
- Genome Assembly Version
- Weight Matrix
- Search upstream, downstream of genes or both
- Sequence window
- Minimum binding strength
Delila-Genome Server
Scan
- Identify potential binding sites based on information content.
- CPU Load optimization for complete genome analysis
Promotsite
Extract sites within or adjacent to expressed sequences
Visualization of Binding Sites
High Resolution Tool
Sequence walkers to illustrate how bases in a single possible binding site match with the weight matrix at each position
Low Resolution Tool
Binding site list as a html page hyperlinked to UCSC Genome Browser, Stanford Source, and GenBank databases.
Viewing options:
- Binding sites sorted by coordinate or strength
- Binding sites specified by a set of GenBank Accession numbers
GenVis
This tool aids in the convenient viewing of subsets of binding sites identified through promotsite or scandiff. It extracts binding sites from a BED file and generates HTML pages from these sites.
Binding site extraction options:
-Coordinates
-Accession Numbers
-Strand
Post Scan Analysis
Verify the sites found by laboratory testing
Refine the weight matrix
Compare scan results from different weight matrices
Comparison options:
- Change in Ri value (bits)
- Change in Z scores (bits)
- Comparison of confidence intervals
Scandiff
Compare scan results from two different weight matrices.
Identify sites:
- Found only with the first matrix
- Found only with the second matrix ie. newly identified sites
- Present in both genome scans, but with:
* Significant change in information content
* No significant change in information content