In Silico Southern Blotting

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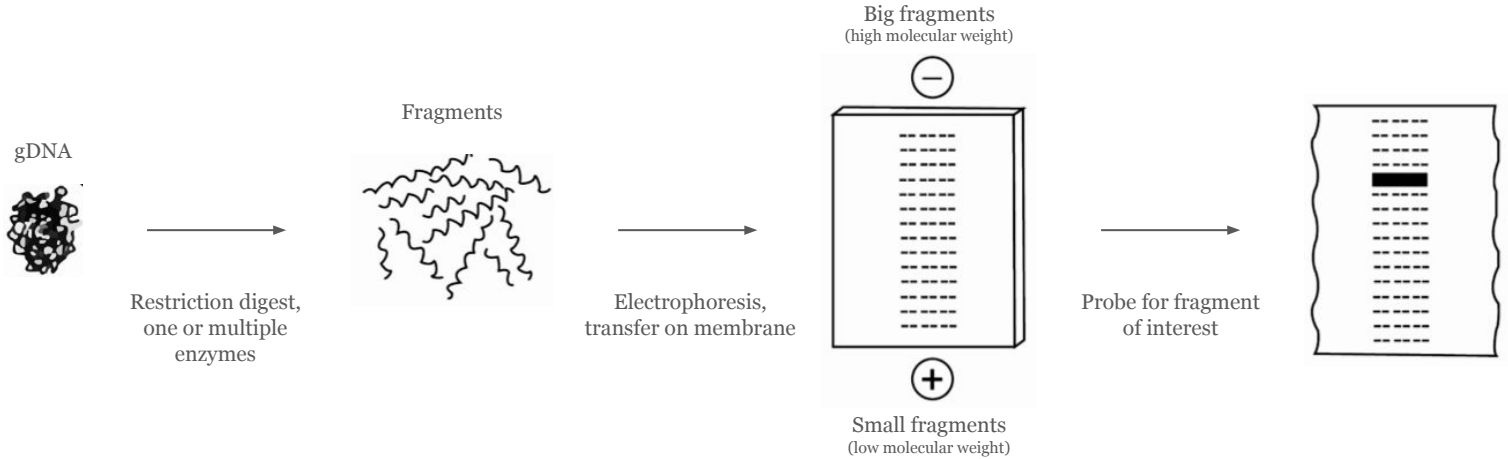
Programming for Biology 2025 , CSHL

Southern Blotting



Experimentally complex and error-prone due to poor probe specificity, incorrect hybridization temperatures and suboptimal gel electrophoresis conditions

✨ In Silico Southern Blotting Tool to streamline experimental design and reduce errors ✨

Inputs:

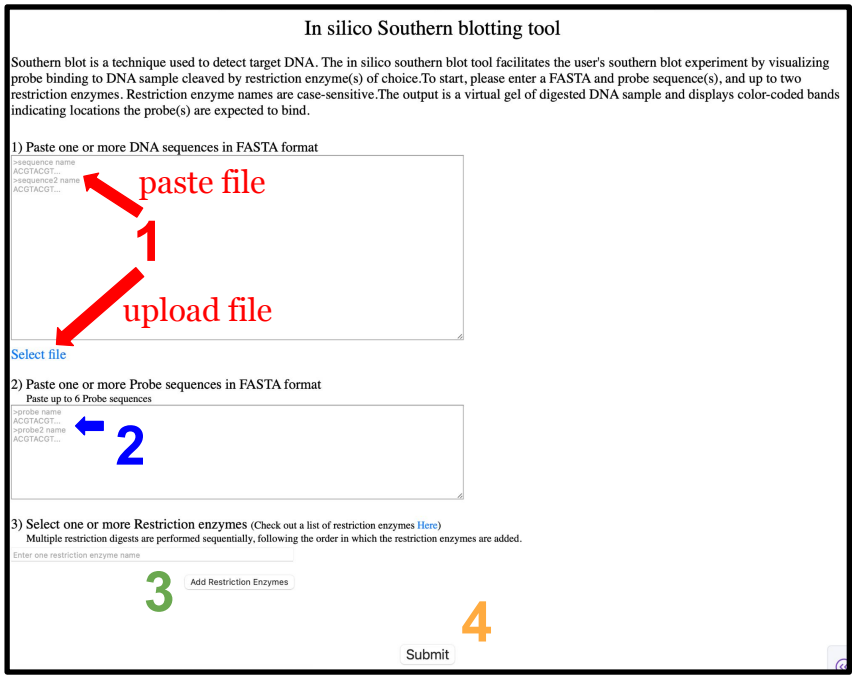
1). Seq FASTA file
2). Probe FASTA seq
3). Enzyme names
4). “Submit”

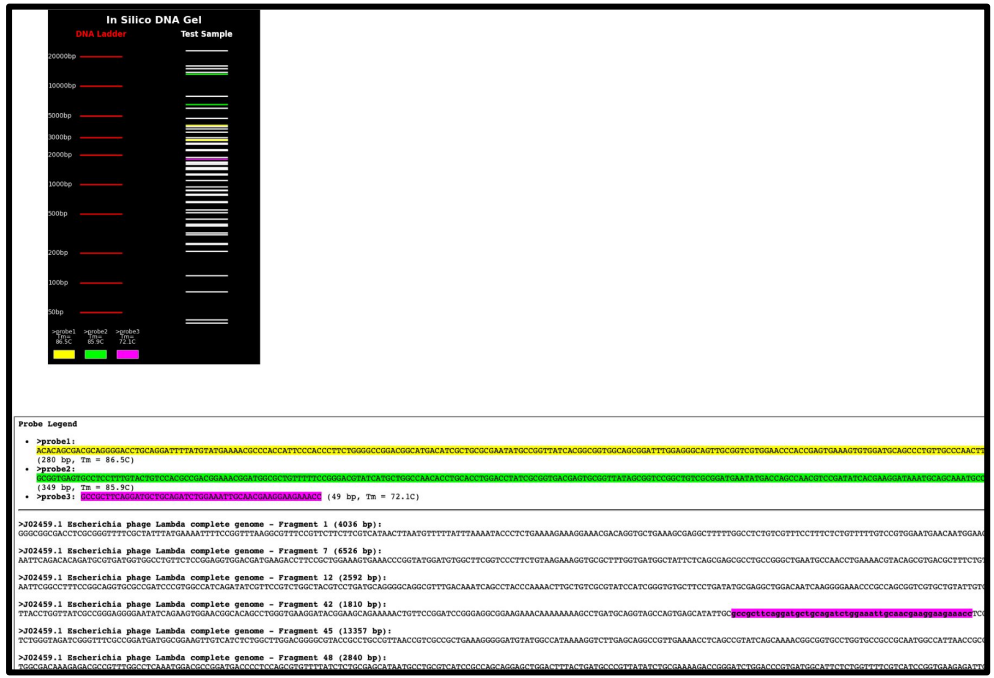
Functions:

1). FASTA parsing (seq & probes)
2). Retrieve restriction enzyme motifs
3). Restriction digest reactions
4). Probe hybridization & Tm calculation
5). Gel image generation
6). HTML generation

Output:

1). Gel Image
(adaptive DNA ladder, Sample Lane with colorized probe, and Tm)
2). HTML Depiction
(colorized probe legend, sequence matching, and Tm)





Future Directions

- Alter the code to tolerate some mismatches in the probe sequence(s).
- If >1 probe binds to a fragment, we would like to enable a feature when hovering over such a band will display the binding probes.
- Add a function, in which a message will appear following successful .fa file upload.
- Suggest optimal electrophoresis condition based on band length the probe(s) are expected to bind
- Optimize a downloadable .txt file of fragment sizes, Tm, probe length, and matches
- Reconfigure Dash script to make more user friendly...

Thank you