## **DNA Sequence – Data Quality Assessment**

- 1. Go to "https://digitalworldbiology.com/FinchTV"
- 2. Download and install the FinchTV DNA analysis software.
- 3. Run the software

FinchTV				
File Edit View Finch Help				
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	Go to Base No. Find Sequence			
Scale	Drag chromatogram file here to get started			
Reset	Scales Horizontal Scale			

4. Drag and drop your sequence file (.abi) onto the software interface



- 5. In a new tab, visit the NCBI page for Standard Nucleotide BLAST: <u>https://blast.ncbi.nlm.nih.gov/Blast.cgi?PAGE\_TYPE=BlastSearch</u> (Hint: this should be the first Google hit for "blastn"
- 6. Copy your sequence from the DNA analysis software (Copy regions with reasonable clean sequencing; you can use the Phred scores as a guide for this.)
- 7. Paste onto the NCBI interphase as seen below:
  - Select "nr/nt" (non-redundant/nucleotide)
  - Select "Somewhat similar sequence"
  - Click BLAST (Basic Local Alignment Search Tool)

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Enter Query	Sequence BLASTN programs search nucleotide databases using a nucleotide query, more	Reset page Bookman	
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Or, upload file	Choose File Ino file selected 😥		
Job Title	Enter a descriptive title for your BLAST search 📦		
C Align two or r	nore sequences 🛞		
Choose Sea	irch Set		
Database	Human genomic + transcript Olouse genomic + transcript Others (ar etc.): Nucleating collection (n/n)		
Organism Optional	Enter organism name or ist-completions will be suggested  Enter organism common name, binamital, or tax id. Only 20 top taxa will be shown ap		
Exclude Optional	Models (XM/XP) Uncultured'environmental sample sequences		
Limit to Optional	Sequences from type material		
Entrez Query Optional	Tuuling Create custom database Enter an Entrez query to limit search 😥		
Program Sel	lection		
Optimize for	Highly similar sequences (megablast)		

- 8. Confirm if the search result corresponds with your marker e.g. 23S, Scar 3, Scar 4 and Scar 5.
- 9. Complete the form assigned to you by your TA.