Personal Genomic Toolchain

Dakota Blair

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- Potentially increase mobility of diagnostic tools

Project Goals

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- Increase confidence

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- Memory is now a limiting factor.

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- Sequences consist of billions of base pairs.
- Typical raw reads are ~60 Gb.
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- Individual bases are difficult to distinguish.

Called word:

Confidence:

Partial word:

Called word: A

Confidence: 90

Partial word:

Called word:

Confidence:

Partial word:

A	C				
90	70				

Called word:	A	C	G	
Confidence:	90	70	20	
Partial word:				

Called word:

A	C	G	T
90	70	20	80

Partial word:

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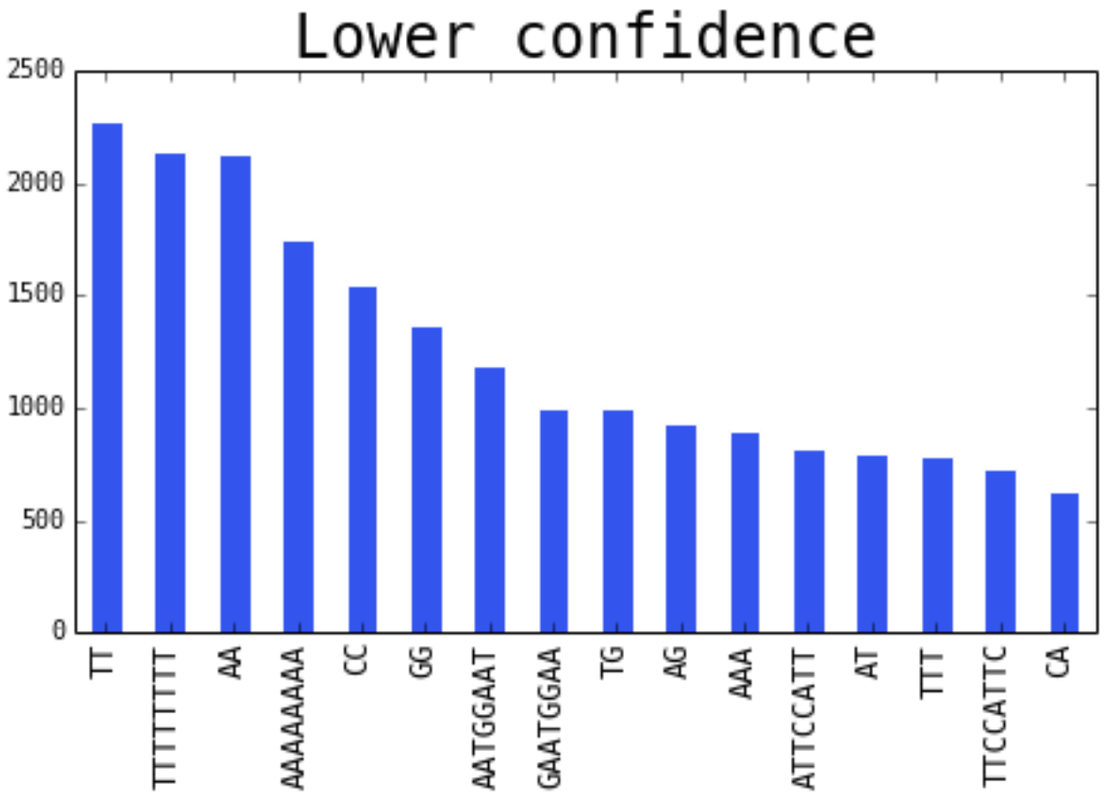

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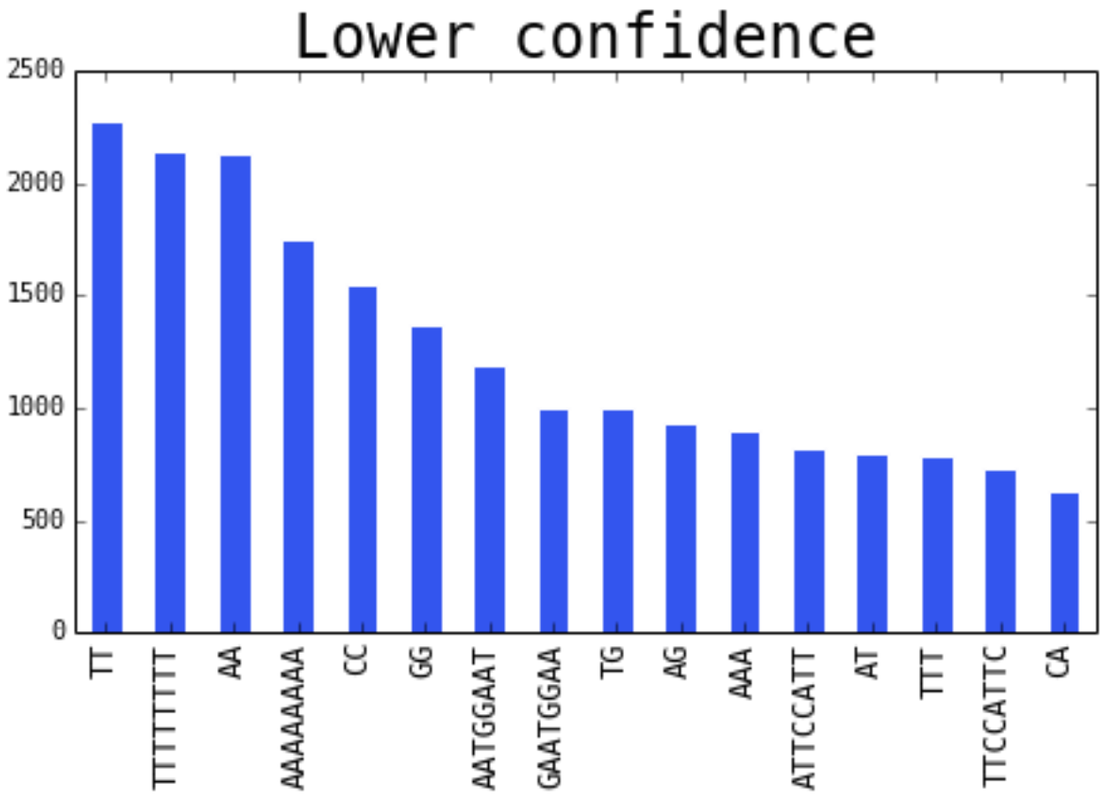

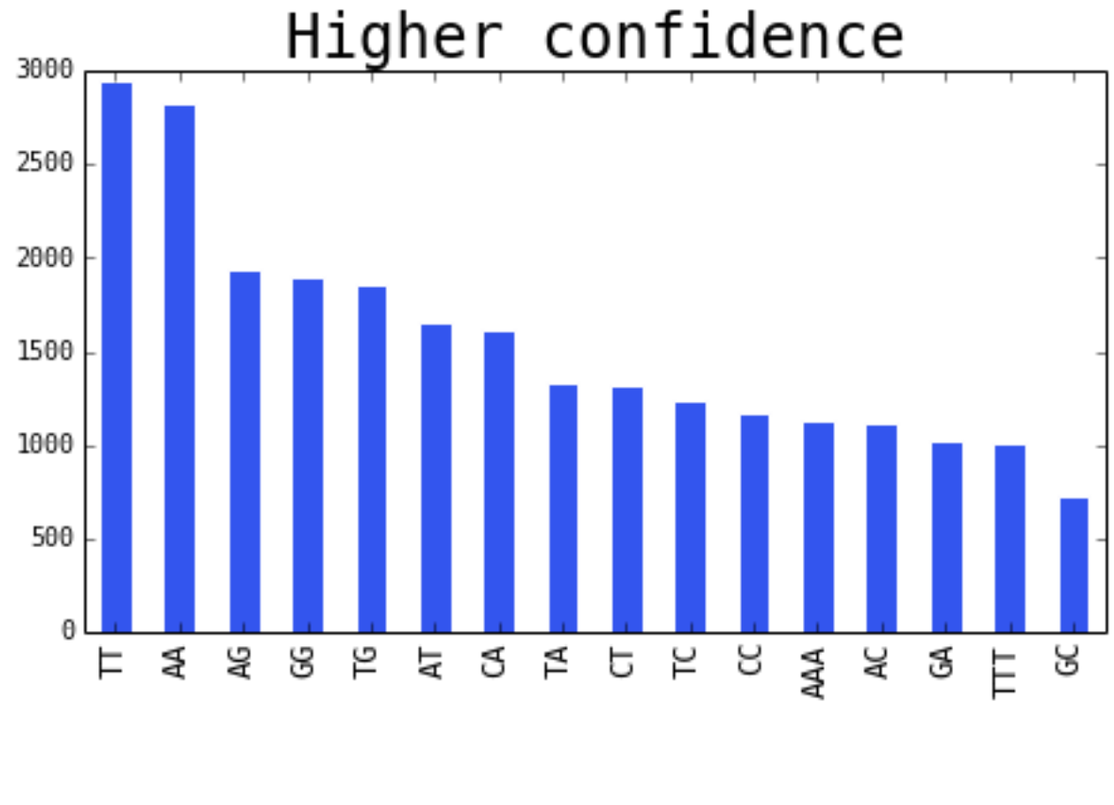

Next steps

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- Implement genome alignment

Other Applications

- Improve ngram intent analysis

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- Enhance recommendation engines

Thank you!