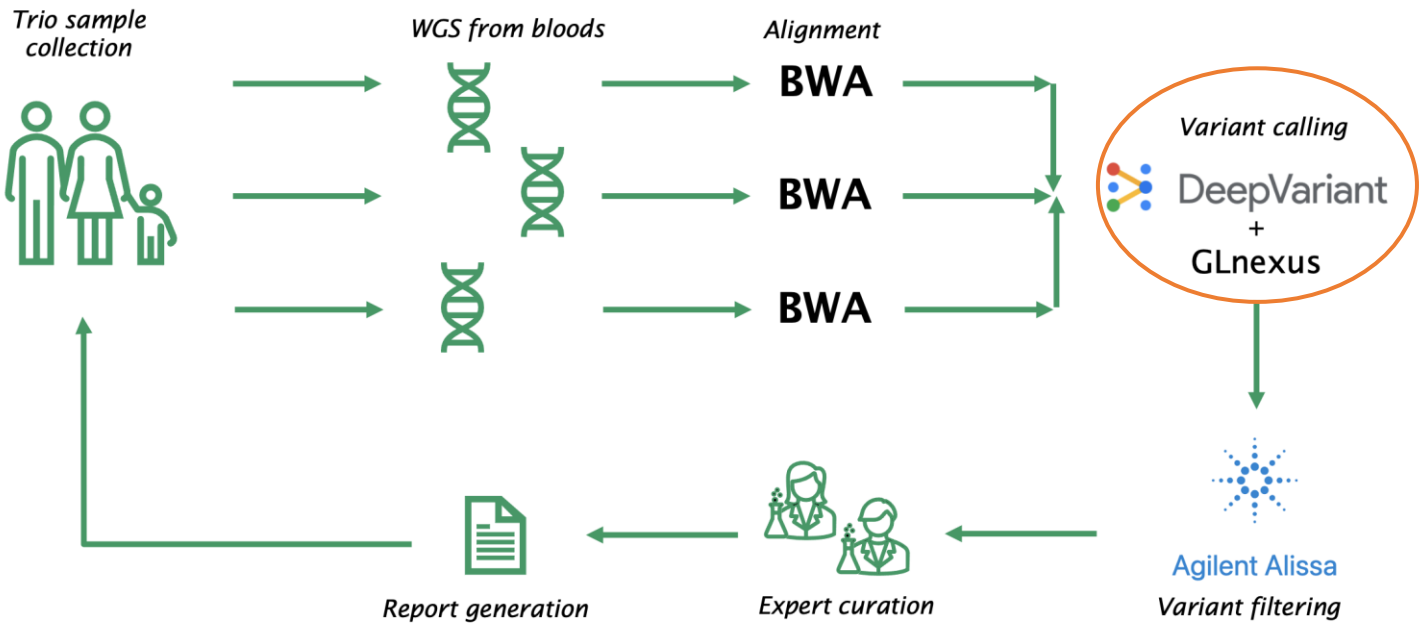
Hey Siri, how can I use Deep Learning for Variant Calling in my Familial Whole Genome Sequencing Studies?

Macabe Daley, Mark Pinese.

Children's Cancer Institute,
Lowy Cancer Research Centre, UNSW Sydney

- familial based trio-analyses,
- whole genome sequencing, and
- deep learning for variant calling.



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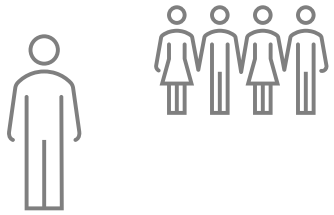
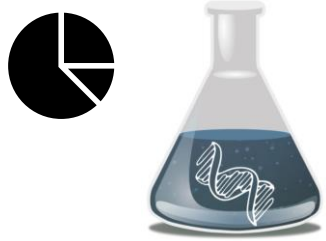
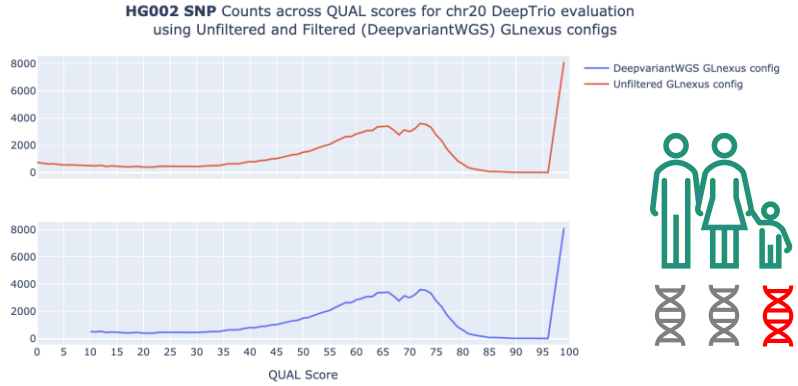
1 Consider the limitations of **validating** your model





2 Ensure your study **goals** are aligned with the model

The quick brown fox
jumps over the
lazy brown dog.



3 Stay aware of the bigger picture and biological **context**

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