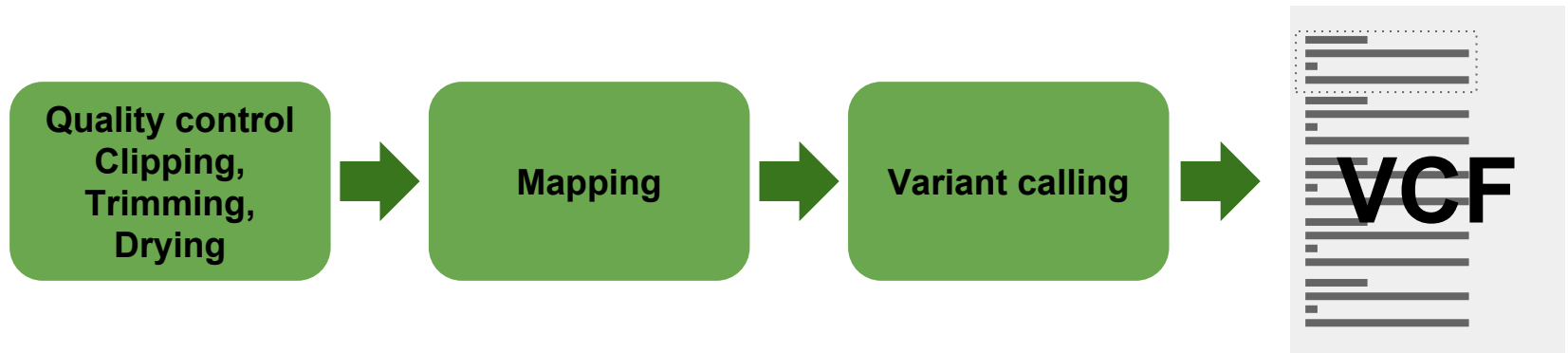


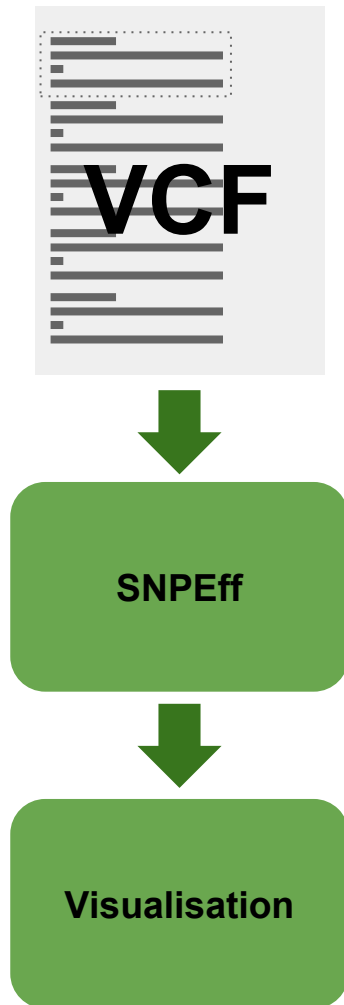
Call me, maybe - Integrating SNP visualisation from CandiSNP into Galaxy

**Christian Schudoma, Martin Page, Dan MacLean
Bioinformatics Team, The Sainsbury Laboratory**

I got a VCF... and now?



Variant annotation and visualisation with SNPEff and CandiSNP



CandiSNP: identifying candidate SNPs in genomes

CandiSNP classifies, annotates and visualises SNPs on genomes. Provide it with a list of SNP positions and allele frequencies and CandiSNP will return the type of each SNP and an interactive visualisation that you can explore to identify potential causative mutations.

If you use CandiSNP please cite: Etherington, Monaghan et al "Mapping mutations in plant genomes with the user-friendly web application CandiSNP." *Plant Methods* 2014, 10:306. doi:10.1186/s13007-014-0041-7.



version 0.3.0 - "la chenille charmant"

Control Panel

Choose spot colours

- Non-synonymous coding CT/GA
- Non-synonymous coding
- Annotated region
- Non-annotated region

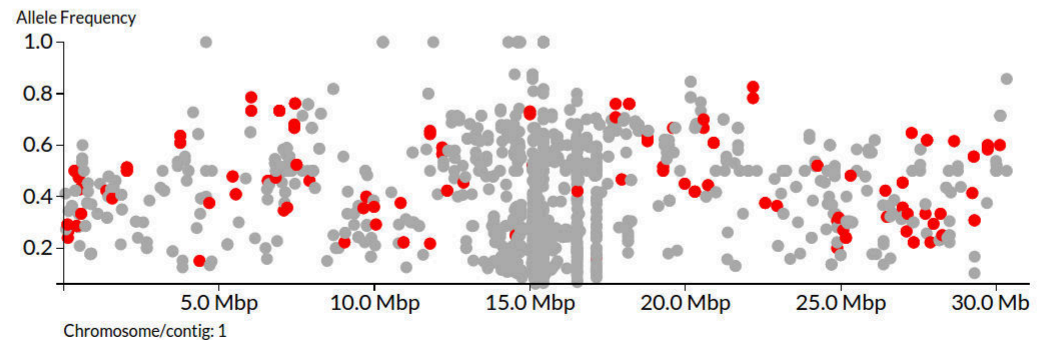
Set allele frequency range

Hide Centromere Region SNPs

Download SVG

Download PNG

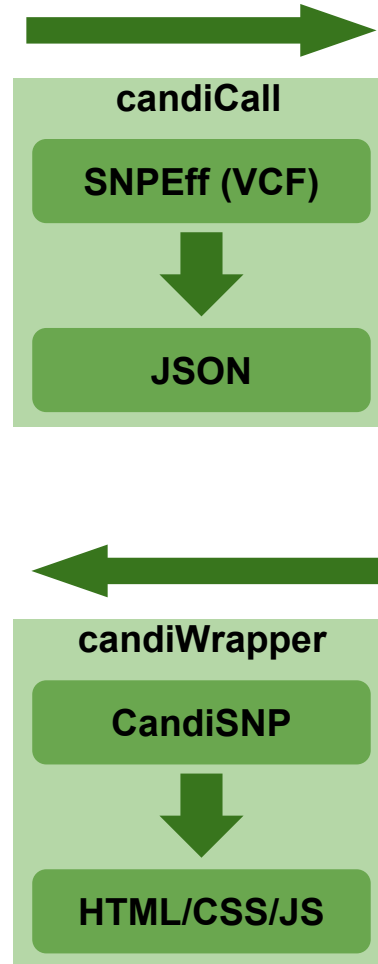
Download Annotated SNPs



How to get Candi to go out with Galaxy?



`sanitize_all_html = False`



<http://candisnp.tsl.ac.uk>

Look for **candiSNP** in the testtoolshed

Did it work out?

CandiSNP:
identifying candidate SNPs in genomes

CandiSNP classifies, annotates and visualises SNPs on genomes. Provide it with a list of SNP positions and allele frequencies and CandiSNP will return the type of each SNP and an interactive visualisation that you can explore to identify potential causative mutations.

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version 0.3.0 - "la chenille charmant"

Control Panel

Choose spot colours

- Non-synonymous coding CT/GA
- Non-synonymous coding
- Annotated region
- Non-annotated region

Set allele frequency range

0.75 - 1

Hide Centromere Region SNPs

Download SVG

Download PNG

Download Annotated SNPs

Allele Frequency

1.0
0.8
0.6
0.4
0.2

Position: 4374672
Allele Frequency: 0.15
Locus: Exon_1_4374412_4375053
Change: D/N
Reference base: C
Alternate base: T

5.0 Mbp 10.0 Mbp 15.0 Mbp 20.0 Mbp 25.0 Mbp 30.0 Mb

Chromosome/contig: 1

History

- candicall
- 160: candisnp
- 159: candisnp
- 158: candisnp
- 157: candisnp
- 156: candisnp
- 155: candisnp
- 154: candisnp
- 153: SnpEff on data 82
- 152: SnpEff on data 82
- 151: candisnp
- 150: SnpEff on data 145 - stats
- 149: SnpEff on data 145
- 148: candisnp
- 147: candisnp
- 146: candisnp
- 145: error.vcf
- 144: candisnp
- 143: candisnp
- 142: candisnp
- 141: Select on data 83
- 140: candisnp

And so they'll live happily ever after..

Planned: full integration using BioJS
visualisation in Galaxy

Acknowledgements

TSL Bioinformatics Team

Martin Page (candiWrapper & dealing with IT)

Dan MacLean (CandiSNP)

TGAC

Graham Etherington (CandiSNP)

Galaxy Team

Dannon Baker (sanitize_all_html)

NBI Computing

Mohamed Imran (opening port 8080)