Promotes collaborative research and training to improve understanding and conservation of Australia’s biodiversity through cross-institutional:

- Synthesis Groups
- Ignition Grants
- Conferences
- Skills-based training workshops
- Seminars
- International visitors
- Engagement with policy-maker & managers
Overview:
Tuesday: Data
• Data filtering: theory & bioinformatics
• CBA welcome mixer
Wednesday: Population genomics
• Population structure & adaptation
• Dinner
Thursday: Phylogenomics
• Species trees
• Species delimitation
SNPs come in many flavours

RE reduction
ddRAD, GbS, DArT

From targeted or whole genome sequencing

Target capture
UCEs
Exons
RADseq

RNASeq

Whole Genome Resequencing

AHE
Custom
....and have an increasing breath of applications across taxa
Insights into Platypus Population Structure and History from Whole-Genome Sequencing

2018 Mol. Biol. Evol
Historical “skinomics” – change over 100 yrs in retracting Alpine chipmunks (Bi et al. in review)
Exon capture to (DArT) SNPs

RaxML
583 loci
Some considerations

**Reliability:**
- Technical replicates
- SNP calling and genotype quality; paralog filters
- Context dependent – phylo vs popgen

**Reproducibility** of bioinformatics
- Pipeline versions, filters etc.

**Reuseability**
- Short-read archive; genome (v?) coordinates

**Connectibility**
- Linking to specimens via public databases

Platypus SNP calls across duplicate samples: Martin et al. 2018