**Article Title:** Phylogeography and species delimitation of *Cherax destructor* (Decapoda: Parastacidae) using Genome-wide SNPs.

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**Journal** Marine and Freshwater Research, MF18347, Accepted 09 December 2018

**List of Files**

DCra15\_Chdes\_SNP\_2row.csv SNP dataset (DArTSeq) provided by Diversity Arrays Technology in 2-Row format (refer to <https://www.diversityarrays.com/> for further information on data formats)

DCra15\_Chdes\_SilicoDArT.csv Presence/Absence data (SilicoDArT) provided by Diversity Arrays Technology (refer to <https://www.diversityarrays.com/> for further information on data formats)

cherax\_data\_input.R R script to read DCra15\_Chdes\_SNP\_2row.csv into genlight objects (CRAN package adegenet) to facilitate analysis. Creates two genlight objects, one for the full dataset and one for the ingroup taxon only (see below).

cherax\_ind\_metadata.csv Metadata to assign to individuals when the two genlight objects are constructed. Used by script gl.read.dart() in Cherax\_data\_input.R.

cherax\_prelim\_ind\_recode.csv Recode table to tidy up individual labels, duplicates and other issues that arose during the sequencing.

cherax\_prelim\_pop\_recode.csv Recode table to tidy up population labels, and other issues that arose during the sequencing.

cherax\_full\_gl.Rdata The full dataset saved in compact binary form as a genlight object. Can be read with gl <- readRDS(cherax\_full\_gl.Rdata)

cherax\_recode\_ingroup\_only.csv Recode table to select ingroup taxa only.

cherax\_ingroup\_only.Rdata The ingroup dataset saved in compact binary form as a genlight object. Can be read with gl <- readRDS(cherax\_ingroup\_only.Rdata)

cherax\_full\_filter.R Script to filter the full dataset on callrate, repeatability and secondaries, and to combine sampling sites within a single drainage and with very low sample sizes.

cherax\_ingroup\_filter.R Script to filter the ingroup dataset on callrate, repeatability and secondaries.

**Pipeline**

The files cherax\_data\_input.R , cherax\_ind\_metadata.csv, cherax\_prelim\_ind\_recode.csv, cherax\_prelim\_pop\_recode.csv, cherax\_recode\_ingroup\_only.csv are provided only to illustrate how the saved datasets cherax\_full\_gl.Rdata and cherax\_ingroup\_only.Rdata are created. To replicate the analysis, access the data using

gl <- readRDS("cherax\_full\_gl.Rdata")

gl <- readRDS("cherax\_ingroup\_only.Rdata")

The filters are then applied using

cherax\_full\_filter.R

cherax\_ingroup\_filter.R

and the analysis can proceed as outlined in the manuscript. We have not provided a script for this because R package dartR is not backward compatible.