

SUPPLEMENTARY SECTION 1: Additional information on the five *Acacia* species studied.

Table S1: Ecological and functional information available for the five *Acacia* species studied.

Species	<i>Acacia linifolia</i> (Vent.) Willd.	<i>Acacia longifolia</i> (Andrews) Willd.	<i>Acacia suaveolens</i> (Sm.) Willd.	<i>Acacia terminalis</i> (Salisb.) J.F.Macbr.	<i>Acacia ulicifolia</i> (Salisb.) Court	References
Common name	flax wattle	Sydney golden wattle	sweet wattle	sunshine wattle	prickly moses	Plantnet *
Subspecies [§]	None	2	None	4	None	Plantnet
Habit	Tall slender shrub 2–6 m	Small prostrate to large spreading shrub or small tree 1–8 m	Sparingly branched shrub 1–3 m	Variable shrub occasionally small tree 1–4 m	Small straggly shrub 1–2 m (rarely taller than 1.5m)	Plantnet, Worldwidewattle #
Longevity	10–15 years	25–60 years	5–10 years	5–20 years	5 years	[65]
Flowering time	December to April	July to October	April to September	February to October; varies but overlaps among subspecies	April to October	Plantnet, Worldwidewattle
Pollination	Unknown	Mixed insect and wind	Unknown	Insects and birds	Unknown	[66]
Mating system	Unknown	Mostly outcrossing but self-compatible	Outcrossing but self-compatible (van der Merwe <i>unpub.</i>)	Self-incompatible	Self-compatible	[24,67]
Pollination	Unknown	Mixed insect and wind	Unknown	Insects and birds	Unknown	[66]
Seed dispersal and agent	Aril/not known likely ant	Aril/bird and ant-dispersed	Aril/ants	Aril/ants	Undeveloped aril/not known	Plantnet, Worldwidewattle; [68,69]
Frost tolerant	Frost hardy	Frost hardy	Frost Hardy	Frost hardy	Frost hardy	[65]
Fire response	Sensitive	Sensitive	Sensitive	Variable response	Variable response	[65,70]
Seedbank/Resprouting	Soil stored seedbank	Soil stored seedbank	Soil stored seedbank	Soil stored seedbank and basal sprouts	Soil stored seedbank and root suckers	[65]
Invasiveness	Unknown	Aggressive weed within and outside Australia	Not known as a weed but successful cultivation outside native range	Not known as a weed	Mentioned as a possible weed in Victoria	[71,72]

[§] Recognised by National Herbarium of NSW; * Plantnet—<http://plantnet.rbgsyd.nsw.gov.au/>; # Worldwidewattle—<http://worldwidewattle.com/>.

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Table S2. Sampling location for all populations included for the five *Acacia* species studied.

<i>Acacia linifolia</i>		<i>Acacia longifolia</i>		<i>Acacia suaveolens</i>		<i>Acacia terminalis</i>		<i>Acacia ulicifolia</i>	
Latitude	Longitude	Latitude	Longitude	Latitude	Longitude	Latitude	Longitude	Latitude	Longitude
-32.9807	150.6866	-28.3249	153.5704	-28.6062	153.5711	-29.23207	151.70185	-28.6102	153.3923
-33.1447	151.0967	-28.6529	153.621	-29.0287	153.4405	-29.52986	152.28288	-28.7654	153.5827
-33.3196	151.2741	-29.228	151.5823	-29.1769	153.3906	-29.62024	153.29308	-28.9535	152.0377
-33.3719	151.3202	-30.0365	153.1972	-29.5342	152.2769	-30.03020	153.01253	-29.1778	153.3913
-33.392	150.8654	-30.6121	153.0097	-30.0299	153.0123	-32.30141	150.04385	-29.5321	152.2507
-33.4078	150.9445	-30.8856	153.0756	-31.0258	153.0252	-32.41896	152.48424	-29.5715	153.3177
-33.476	150.7771	-31.7234	152.7875	-31.6302	152.8265	-32.57179	151.95456	-30.4187	152.2528
-33.4851	151.187	-32.2532	152.5341	-33.1544	151.0933	-32.72437	152.16470	-30.5709	151.7258
-33.5082	151.0268	-32.5903	151.7682	-33.1844	151.6145	-32.80019	150.90161	-30.9735	151.9028
-33.5246	150.5647	-32.7209	152.1626	-33.2417	150.6471	-32.86724	150.24797	-31.0262	153.0251
-33.594	150.6259	-33.42	150.2129	-33.4914	150.4979	-32.88226	151.44929	-31.0674	151.4155
-33.6611	150.614	-33.4276	151.4489	-33.5521	151.2935	-33.18896	151.61233	-31.1463	152.3584
-33.6669	151.074	-33.5552	150.4121	-33.7854	150.6114	-33.32179	150.12100	-31.345	152.8665
-33.6722	150.5478	-33.6729	151.1354	-33.7947	150.4041	-33.55276	151.29035	-31.9523	148.9229
-33.6752	151.1364	-33.8224	151.2998	-33.9805	151.0077	-33.66126	150.61345	-32.5687	151.3961
-33.7059	150.5573	-34.0085	151.2228	-34.1626	150.489	-33.68225	151.15103	-32.7528	152.1324
-33.7199	150.4708	-34.0148	150.8813	-34.1844	150.9798	-33.76927	151.27654	-32.8365	151.3943
-33.7568	150.6302	-34.6285	150.1903	-34.3524	150.63	-33.79508	150.40556	-33.5506	151.302
-33.7924	151.1455	-34.7811	150.7943	-34.6884	150.3785	-33.80510	151.29619	-33.5802	151.3253
-34.068	150.4401	-35.1169	150.2988	-34.9733	150.7711	-33.81191	151.30102	-33.6297	150.4021
-34.0748	151.0005	-35.2024	150.559	-35.109	150.6614	-33.97137	151.23600	-33.7947	150.4041
-34.1134	151.0665	-35.4939	150.3915	-35.4733	150.3746	-34.01078	151.22422	-34.1372	150.9962
-34.129	150.9538	-35.9312	150.1582	-36.4406	150.0528	-34.14682	150.99347	-34.5205	150.2131
-34.1601	150.83	-36.3852	150.0724	-36.7624	149.9295	-34.17733	150.83775	-35.1897	150.5366
-34.1629	150.4888	-36.5829	150.0309	-36.8342	149.9289	-34.32561	150.47542	-35.2893	150.0812
-34.1837	150.9802	-36.9479	149.9348	-36.9874	149.9175	-34.35269	150.63111	-35.9594	150.0045
-34.3253	150.4746	-37.151	149.5052	-37.0063	149.7892	-34.50720	150.24011	-37.2303	150.0044
-34.3286	150.746	-37.366	149.7459	-37.236	149.8458	-34.62644	149.88422		
-34.3523	150.6302			-37.2546	150.0384	-34.67381	150.71384		
						-34.67088	150.38209		
						-35.06385	150.67142		
						-35.04074	150.13536		
						-35.11398	150.66115		
						-35.40697	149.62257		
						-36.11048	149.57199		
						-36.13979	150.11910		
						-36.44082	150.05284		
						-36.72972	149.96222		
						-36.94569	149.70751		
						-36.98760	149.91752		
						-37.10389	149.34172		
						-37.25496	150.03878		
						-37.34913	149.62999		
						-37.43224	149.95668		

SUPPLEMENTARY SECTION 2: Kinship analysis for *Acacia ulicifolia*.

Genetic similarity between individuals located at the same site and corresponding cultivated material was estimated using the unweighted pair group method with arithmetic mean (UPGMA) hierarchical clustering method as implemented in the R package phangorn v2.4.0 [73]. Kinship (relatedness) measurements were used in assessing the degree of clonality across *A. ulicifolia* individuals. Pairwise kinship coefficients were estimated from the genotype data using an Identity-by-descent analysis in R package SNPrerate v1.17.1 [49]. Distance matrices of pairwise kinship were generated for each *A. ulicifolia* site based on observation from preliminary results from principal component and network analysis. The matrices were combined to generate a supermatrix that was drawn using the heatmap function from the R package Phytools v0.6-60 [74].

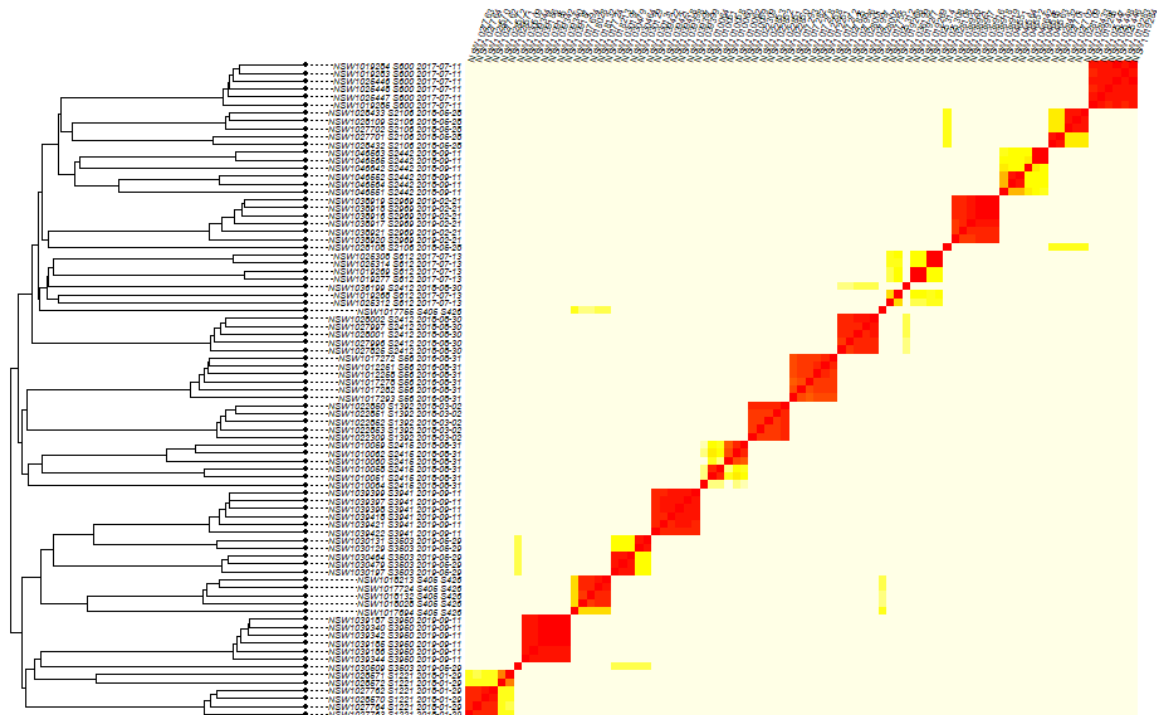


Figure S1. Composite UPGMA tree/Kinship heatmap of 14 out of 27 *Acacia ulicifolia* sites with clones detected. The heatmap above consists of pairwise kinship coefficients displayed as colours: RED colouration corresponding to the highest pairwise kinship coefficients (0.4 or greater = clone), ORANGE-YELLOW colouration corresponding to medium pairwise kinship coefficients (less than 0.4 but greater than 0.25 = sibling) and EGGSHELL WHITE colouration corresponding to the lowest pairwise kinship coefficients (0). The descending red diagonal on the graph is the result of an individual matched with itself.

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SUPPLEMENTARY SECTION 3: Comparison of hull generating methods for assessing coverage of subsets of samples in genetic PCA-space.

We investigated the performance and usefulness of alternatives to convex hulls when assessing the degree to which geographically defined subsets of samples included or “covered” observed genetic

variation. The methods investigated included: alpha hulls, concave hulls, and a form of concave or non-convex hull implemented in the R-package INLA.

These notes describe each of the options investigated and their ability to consistently measure coverage of subsets of samples relative to the coverage of the full set of samples. Summary results and conclusions are presented in this supplement.

Convex hull

A convex hull is the simplest convex polygon (no internal angle > 180 degrees) enclosing a set of points in the plane. Convex hulls have the following properties:

1. The convex hull of a set of points always encloses every point of the set (inclusiveness or extensivity property)
2. The convex hull of any subset of points selected from the original set is guaranteed to be nested within the convex hull of the full set (nestedness or non-decreasing property)
3. There is one and only one convex hull for a given set of points (uniqueness or idempotent property)

Convex hulls require no control parameters to be chosen making them highly objective tools. An example of a nested set of convex hulls made using all points and then two subsets is shown in figure S2.

One concern when applying convex hulls to measure coverage of samples is that they inherently enclose regions in which there are no samples. That is, they include regions for which there is no empirical evidence for it being occupied or available to the population from which samples were drawn. For example, samples collected along gradients often display an arch or horse-shoe distribution when analysed using ordination or dimension-reduction methods such as principle components analysis (PCA; [75]). A convex hull around such a set of points in PCA-space infers inclusion or “coverage” of unobserved conditions.

Many non-convex hull alternatives have been proposed to address this problem. These include alpha hulls and alpha shapes [76], χ -shapes [77], and various methods referred to loosely as concave or non-convex hulls [78-80]. Three non-convex alternatives which are readily computed using resources with the R statistical environment [81] were examined to see if they provided information or insights not possible using convex hulls applied to genetic PCA plots. They include: alpha hulls from the R-package `alphahull` [82], concave hulls produced by the R-package `concaveman` (<https://CRAN.R-project.org/package=concaveman>), and non-convex hulls from the R package INLA (<http://www.r-inla.org/>).

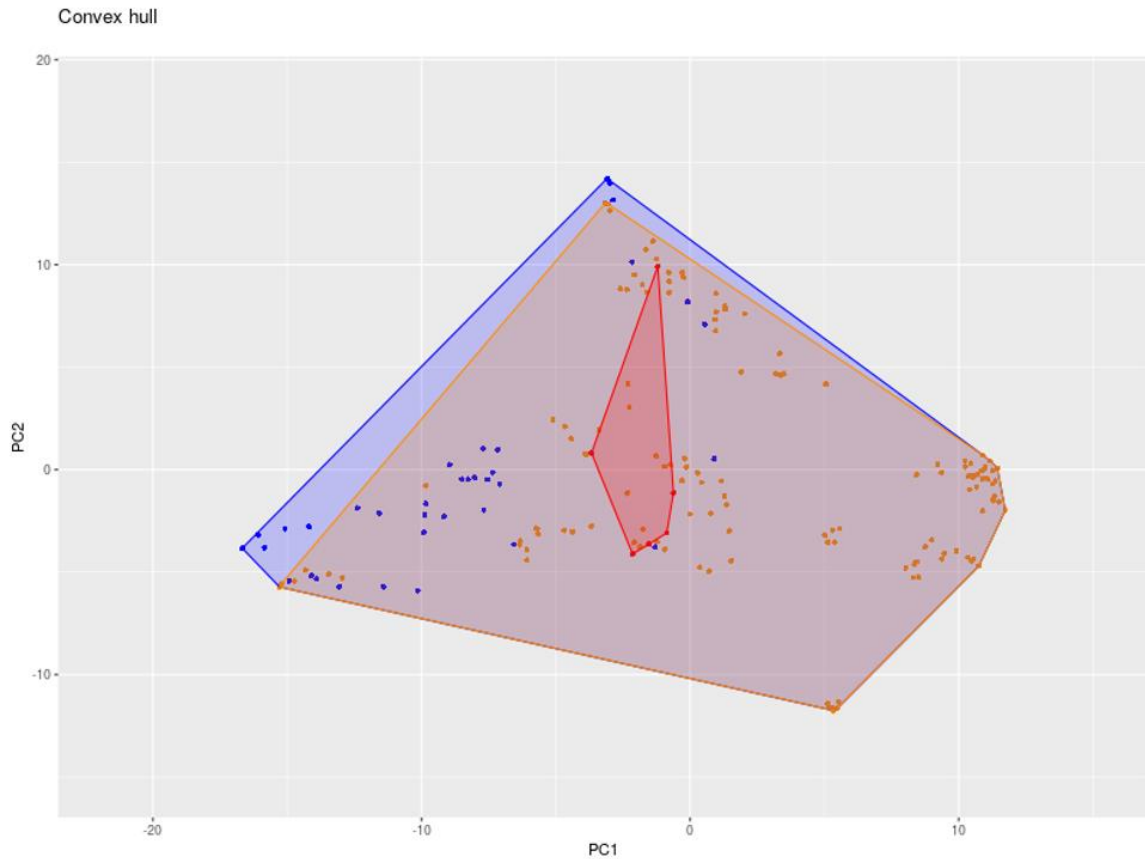


Figure S2. Convex hull for full sample set(blue), and two subsets, one large subset (orange) and a smaller subset (red).

Alpha hull

Alpha hulls, and the linked alpha shapes, are constructed by filtering links between points computed from a Delaunay triangulation of the points under the control of a parameter, alpha. The parameter alpha is a free parameter meaning that there is no formal, standardised method for selecting a value. Some suggestions have been developed for computing a value.

The only property in common with convex hulls is the inclusiveness or extensivity property. For example, the alpha hull shown in figure S3 shows that all points are included in computed alpha hulls for given set of points and for subsets of those points. However, depending on the value of alpha, single or isolated points may be generated, and the filtering of inter-point distances from the Delaunay triangulation may introduce constructed vertices. That is, vertices which do not correspond to sample points.

In addition, although not found in this example, internal void spaces may be generated within enclosing outer hulls [76].

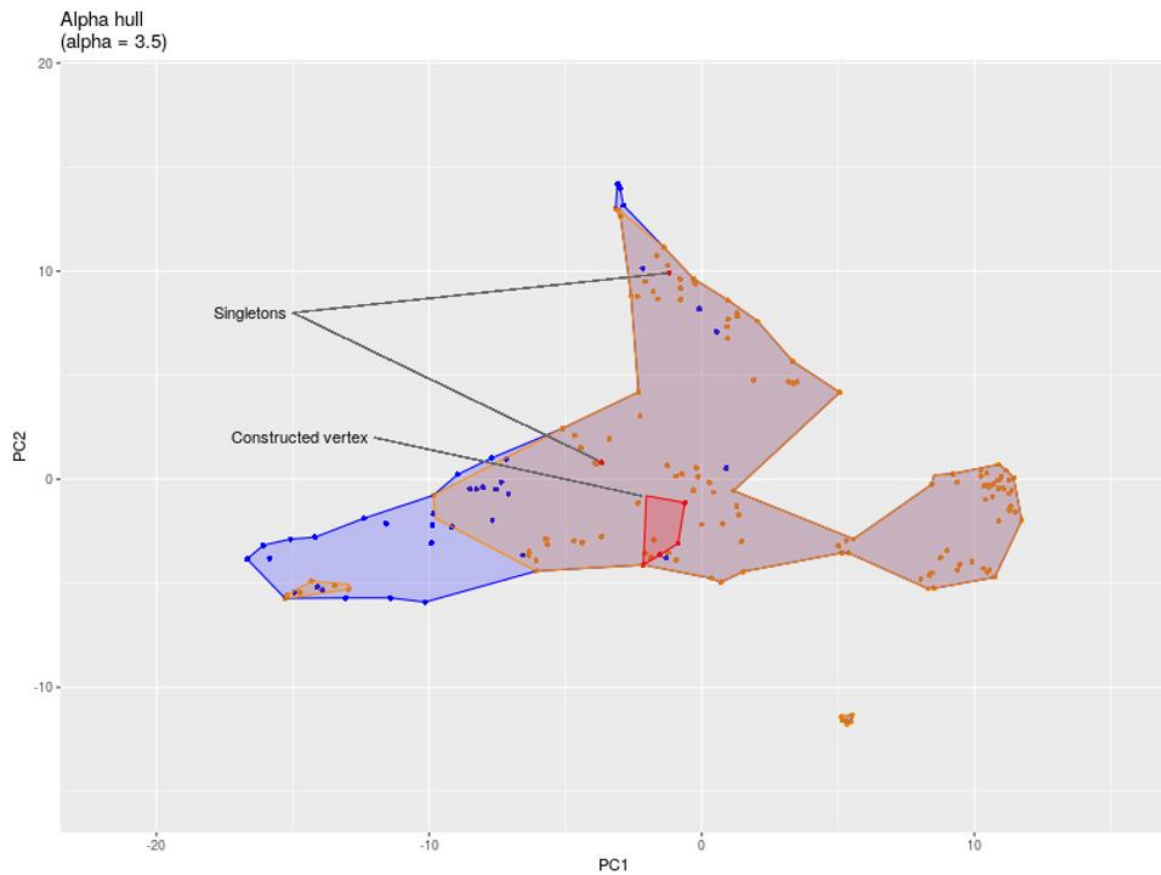


Figure S3. Alpha hull for a full sample set (blue) and two subsets (orange and red). This plot illustrates a number of artefacts which alpha hulls may exhibit.

Concave hull

The form of concave hull computed by the function *concaveman* in the R-package *concaveman*, requires values to be chosen for two free parameters, concavity and length threshold (<https://CRAN.R-project.org/package=concaveman>). The algorithm used is a port of code developed in javascript for plotting non-convex hulls in a web-based mapping platform. Like the alpha hull, this form of concave hull only guarantees compliance with the first property of convex hulls. That is, a concave hull of a set of points will enclose all of the points in the set. It does not generate isolated points like alpha hulls but shares with that method the ability to include areas in hulls for subsets of points which are not enclosed by the hull computed for the full set of points. This is illustrated in figure S4.

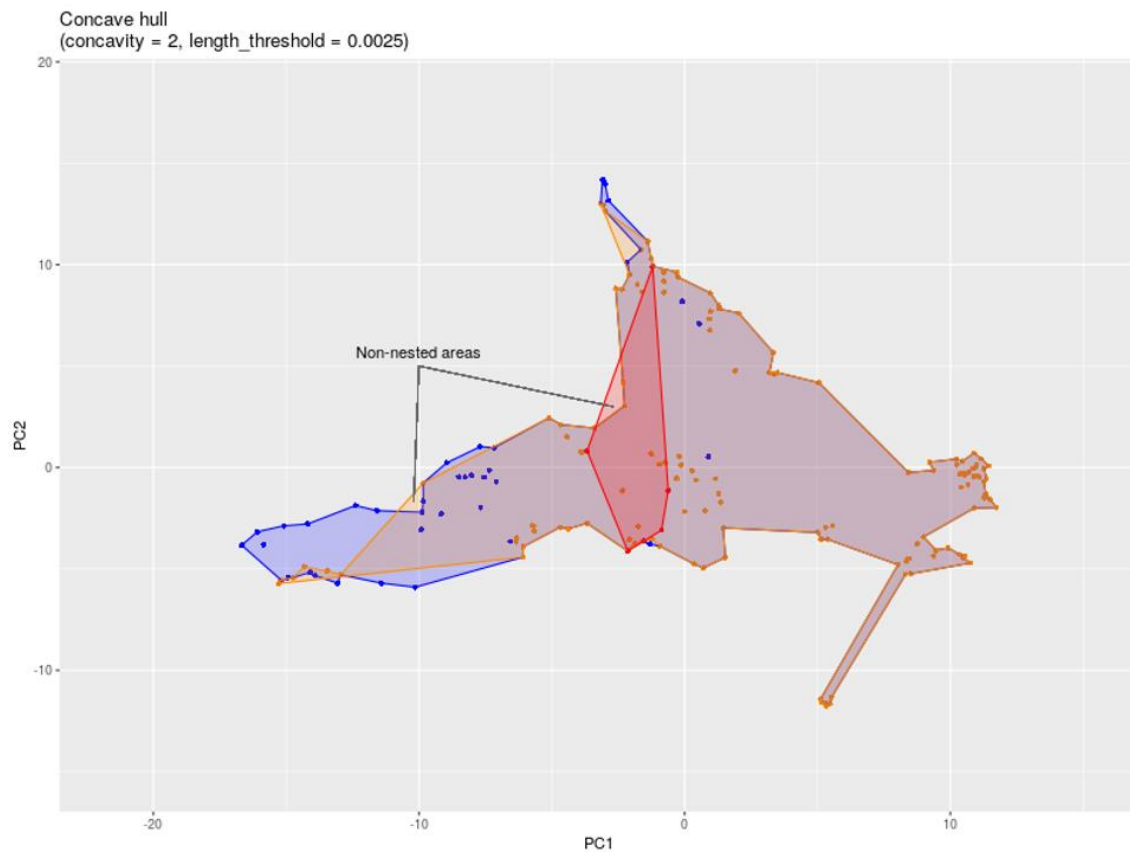


Figure S4. Concave hull for full sample set (blue) and two subsets of samples (orange and red). Concave hulls of subsets frequently display non-nestedness as shown in this example.

INLA non-convex hull

The non-convex hull computed using the function *inla.nonconvex.hull.basic* in the R-package INLA (<http://www.r-inla.org/>) performs a buffering operation by taking the union of a set of circular buffers placed at each sample point. The perimeter of the union forms the non-convex hull for the set of points. Two parameters control this process: convexity and resolution.

Again, the method complies with the inclusiveness property of convex hulls, and with the nestedness property. Like alpha hulls, isolated points may occur as shown in the example of figure S5. This example also shows internal voids for the chosen values of convexity and resolution. Although there are no strict algorithms for choosing values for the controlling parameters, the function warns when particular values cause computational errors and so constrains the range of possible values to some degree.

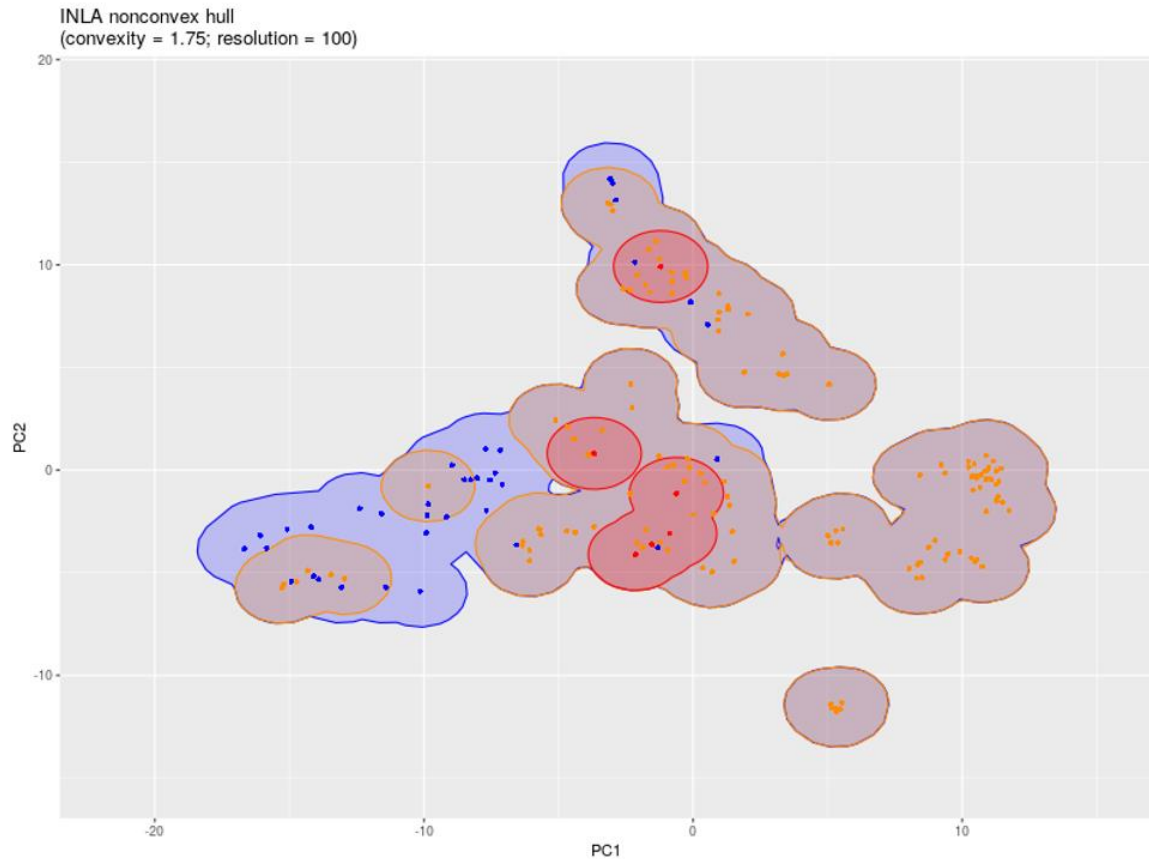


Figure S5. Non-concave hull from the R-package INLA for a full sample set (blue) and two subsets (orange and red). This method may generate voids like alpha hulls, but does display true nestedness like standard convex hulls.

Summary of results

We found that all methods provided similar rank orderings but varied in their computational efficiency and interpretability. All methods provided areas for subsets as expected: all samples (largest area), provenance region computed from a GDM model (middle area value), and a generic 20 km radius provenance region (smallest area) (Table S3). Note, that for *Acacia suaveolens*, the GDM-derived provenance was approximately 20 km in radius and therefore the latter two areas were very close, and for *Acacia linifolia*, a species with a very restricted distribution, the GDM provenance spanned the entire distribution of the species so that the full convex hull and GDM convex hulls are the same.

Computational efficiency was assessed in two ways: lines of code required to implement each method, and computing times (Table S4). Convex hulls are clear leaders in both categories. All non-convex hull methods require multiple runs to select values for the free parameters controlling their behaviour and will therefore require much longer run times.

The application of standard convex hulls can also be scaled easily to automatically process many taxa, or to be applied in studies requiring evaluation of many subsets of samples.

Table S3. Areas of four alternative hull methods calculated in PCA-space applied to the five *Acacia* test species.

Method	<i>Acacia linifolia</i>			<i>Acacia longifolia</i>			<i>Acacia suaveolens</i>			<i>Acacia terminalis</i>			<i>Acacia ulicifolia</i>		
	All	GDM	20 km	All	GDM	20 km	All	GDM	20 km	All	GDM	20 km	All	GDM	20 km
Convex hull	171.25	171.25	14.00	409.42	369.15	23.45	666.69	1.53	1.53	236.61	148.41	3.12	735.40	267.00	0.86
Alpha hull	117.13	117.13	9.71	182.28	168.39	23.45	366.30	1.02	1.02	69.51	50.66	2.16	68.68	39.19	0.70
Concave hull	138.06	138.06	12.07	177.61	146.75	3.49	33.62	1.53	1.53	71.01	48.45	2.99	100.92	30.45	0.82
INLA Non-convex hull	203.18	203.18	51.71	319.34	263.59	40.95	226.83	20.35	20.35	201.65	147.90	25.08	233.80	97.47	20.76

Table S4: Computational complexity (as the lines of code required to compute and plot figure) and execution times for each hull method.

Method	Complexity (Lines of code)	Efficiency (execution time, sec)				
		<i>Acacia linifolia</i> (n = 162)	<i>Acacia longifolia</i> (n = 175)	<i>Acacia suaveolens</i> (n = 256)	<i>Acacia terminalis</i> (n = 165)	<i>Acacia ulicifolia</i> (n = 195)
Convex hull	21	0.243	0.158	0.146	0.149	0.152
Alpha hull *	110	0.322	0.343	0.392	0.313	0.311
Concave hull *	27	0.245	0.251	0.221	0.224	0.210
INLA non-convex hull *	197	1.537	2.536	2.161	1.665	1.818

* For these methods, execution time is for a single run at a fixed set of values for the ancillary parameters. Therefore, total execution time for these methods is an indeterminate multiple of the reported value since a number of runs will be required to select appropriate values for free parameters. In contrast, the standard convex hull time is fixed as it requires a single execution.

Conclusions

All the tested hull methods ranked the coverage of genetic variation of sample subsets as expected. The methods varied widely in computational complexity and execution times. The interpretation of results for some methods (e.g. alpha hulls and concave hulls) may also be problematic: alpha hulls may introduce isolated points (contributing zero area to the coverage estimate), and both methods may include areas in subset hulls which are not part of the hull computed for the full sample set.

Convex hulls may suffer from an over-estimation of coverage, but their ease of computation, freedom from arbitrary parameter selection and problematic artefacts (isolated points, non-included areas) indicate that they should be used as the most efficient and reliable method for estimating coverage of genetic variation.

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SUPPLEMENTARY SECTION 4: Current and future Environmental Niche Models for the five *Acacia* species studied.

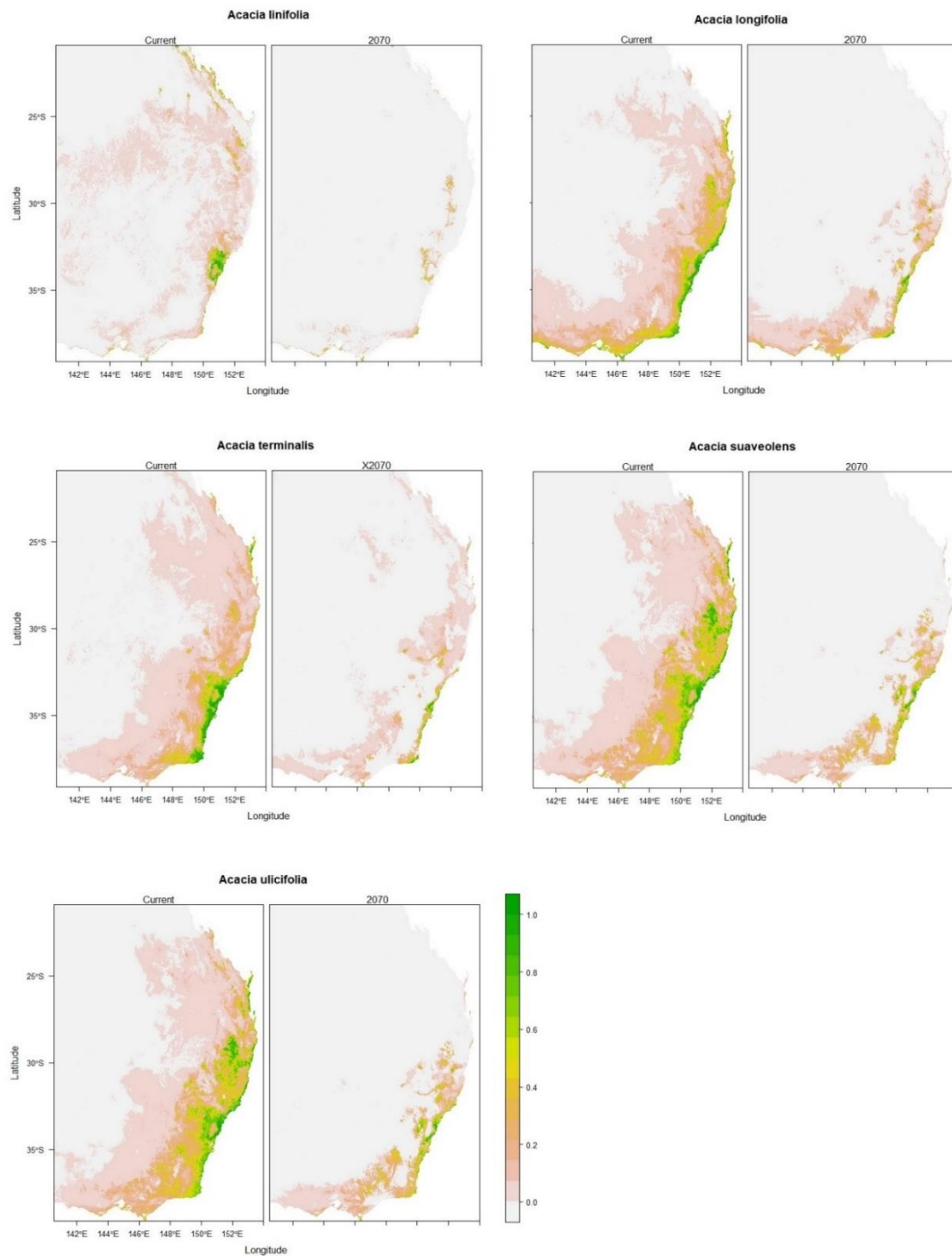


Figure S6. Environmental niche suitability of *Acacia* species in mainland eastern Australia modelled in MaxEnt. Models are based on the current distribution (left image) of the study species and projected onto eight environmental forecasts for 2070 (four Generalised Circulation Models and two emissions scenarios; right image). Output is the mean logistic habitat suitability of the top five performing models minus 2x the standard error.

SUPPLEMENTARY SECTION 5: Population structure (K=2 to K=5) for the five *Acacia* species studied.

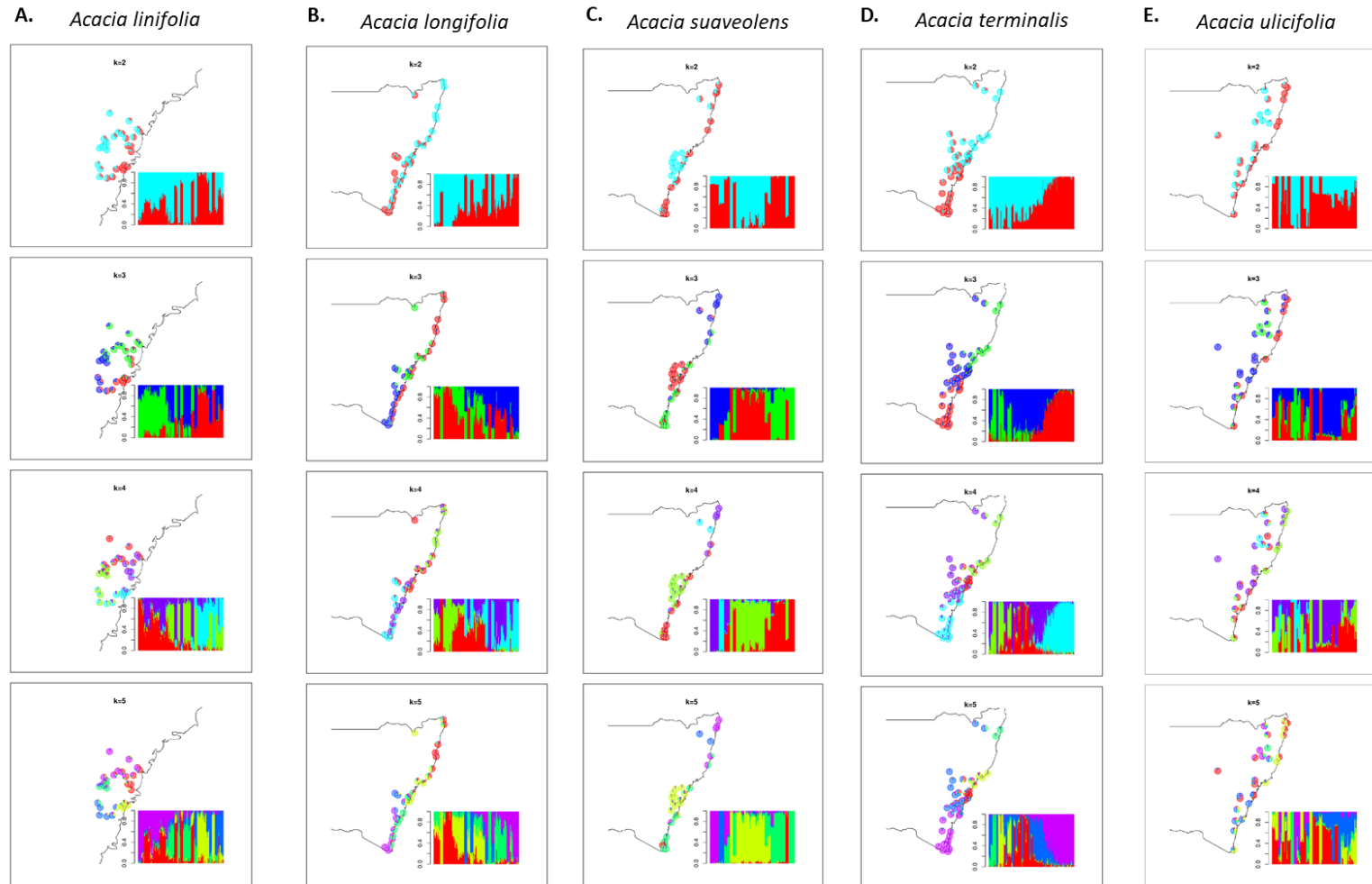


Figure S7. Geographic patterning of snmf results for the five *Acacia* species. For each species, each map indicates geographic population structure (K = 2 to K = 5 from top to bottom), and each barplot on the bottom right of the map depict the ancestry proportions summed over all individuals for each population.