SUPPLEMENTARY MATERIALS

for

Socioecology of the Australian Tree Skink (*Egernia striolata*)

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Please note: there is repetition in the Supplementary Materials with the manuscript to ensure clarity.

1 Supplementary Methods and Results

All analyses, unless stated otherwise, were completed in R version 3.4.4 (R Core Team, 2018).

1.1 The Natural History of Tree Skinks

The Tree Skink, *Egernia striolata,* is a medium-sized skink (180 to 220 mm in total adult body length; Cogger, 2014). Their dorsal coloration (grey to brown with white mottling; Figure 1) affords them superb camouflage on rocks or trees. Their ventral coloration varies among individuals from light grey, cream, or a pale pinky-orange within our study population (J. Riley, unpublished data). Tree Skinks do not exhibit sexual dimorphism in their coloration or morphology, with the exception of slight sex-specific differences in head shape and size. In our study population at Albury, New South Wales (Figure S1), females (n = 116) had an average SVL of 100 mm (standard deviation = 8 mm, range = 82 to 117 mm) and an average total length of 183 mm (standard deviation = 20 mm, range = 125 to 232 mm). Males had an average SVL of 102 mm (standard deviation = 5 mm, range = 88 to 111 mm) and an average total length of 195 mm (standard deviation = 14 mm, range = 161 to 234 mm).

Female Tree Skinks are viviparous and have Type 1 placentas (Weekes, 1935; Chapple, 2003). Females give birth to offspring from January to March each year, and litter size ranges from 1 to 6 offspring (Chapple, 2003). Tree Skinks may take several days to complete parturition of a litter, also termed prolonged parturition (Chapple, 2003) or asynchronous birth (While et al., 2007). Female Tree Skinks have been reported to take between 1 to 7 days to complete parturition of one litter (Chapple, 2003). The Tree Skink lifespan is unknown, but it is estimated to be between 10 to 20 years based on data from similar species (i.e., White's Skink, *Liopholis whitii*: G. While, pers. comm.). Juveniles reach sexual maturity in the wild at 2 to 3 years of age (Chapple, 2003), and, within captivity, at 1.5 years of age (Riley et al., 2017).

Tree Skinks are one of the most widely distributed Egernia-group species, and can be found in dry sclerophyll forest, woodlands, and rock outcrops throughout south-eastern Australia. Tree Skinks live in cracks, hollow limbs, and beneath the bark of standing trees or fallen timber, and they also inhabit crevices in rock outcrops (Cogger, 2014). Tree Skinks aggregate in these crevices and hollows, and the size and structure of these social groups is thought to vary among and within populations. Tree Skinks are hypothesized to be a species' complex or group (M. Gardner, pers. comm.), so phylogenetic differences may account for the inter-population variability observed but sociality may also affect their fine-scale genetic structuring (Pearson et al., 2020).

Within arboreal populations, like the forested habitats of the Pilliga region in northern New South Wales, the social structure has been described as non-gregarious with only 13% (33/250) of skinks observed in groups, which had a maximum size of three individuals (Bustard, 1970). Yet, a later study in the same region found Tree Skinks aggregating in 63% of observations (12 groups of up to 4 individuals in 29 trees; Duckett et al., 2012). Similarly, in the mallee woodlands of South

Australia, Derez (2004) observed adults and neonates sharing crevices and group basking. In mainly saxicolous populations, like rock outcrops at Para Wirra Recreation Park in South Australia, Tree Skinks were observed in groups, of up to six, 78% of the time (57/78 observations; Bonnett, 1999). Similarly, in rock outcrops throughout the southern South-Western Slopes bioregion of New South Wales, Tree Skinks were found in groups, of up to 4, during 47% (191/403) of observations, (Michael et al., 2010). From this mix of published and unpublished reports, it is clear there is variability the size, structure, and occurrence of Tree Skink groups among populations. Yet, the majority of studies (4/5), as well as anecdotes (Swanson, 1976; Ehmann, 1992), have described Tree Skinks as social and gregarious, and it is unknown whether the variability reported in these studies may also be due to substantial differences in methodology.

Tree Skink behavior is very cryptic. They are sit-and-wait foragers that, in the wild, spend on average 98% of their time stationary (Riley, 2017). Generally, Tree Skinks spent their days waiting beside or within crevices to capture passing invertebrates. That being said, occurrences of active foraging have been observed; in the spring Tree Skinks would eat flowers and insects while moving on the ground (J Riley, pers. obs.) and similar behavior has been observed in other populations (Bonnett, 1999). They are omnivorous, and no ontogenetic changes in diet have been found in this species (Bustard, 1970). Prey groups for this skink include Coleoptera, Dictyoptera, Orthoptera, Hymenoptera, and Hemiptera (Bustard, 1970), and over a third of their diet consists of plant material (39.7%; Chapple, 2003).

1.2 Population Size and Structure

Using the mark-recapture data, we estimated the size of our Tree Skink population using the R packages '*EasyMARK*' to manipulate and organize our data and '*Rcapture*' to run our population size estimation (Baillargeon and Rivest, 2007; Waller and Svesson, 2016).

From December 2014 to April 2016, we surveyed areas immediately surrounding our main site. The total surveyed area, outside of our main site, was 32.2 ha in size. In total we captured $n = 114$ individuals (70 females, 38 males, and 5 juveniles), and only 1.8% ($n = 2$) of which were previously marked during surveys on our main site and then migrated offsite. Overall, this reflects a closed population structure, because there is negligible emigration, immigration, and high site fidelity. Thus, we used the function '*closedp*' from the R package '*Rcapture*' to fit a variety of log-linear models for closed population size estimation. We assessed model fit using Akaike information criterion (AIC) values to select the most appropriate size estimate (Baillargeon and Rivest, 2007), which in our case was a capture-recapture model with heterogeneity and behavioral response (i.e., the Mbh capture-recapture model; Norris and Pollock, 1995).

Population size was estimated to be 240 ± 42.2 (standard error, *SE*) skinks. Across three years of field surveys on our main study site in Albury, we captured and observed 203 unique individuals. These observations were split across an initial trip in December 2013, and then capturing 169 individuals in the 2014/15 season, and 134 individuals in the 2015/16 season (56% of which were recaptures; Table S1). Over all surveys we found that the population consisted of 17% juveniles and 83% adults, and these proportions remained relatively consistent across seasons (Table S1). The sex ratio was female-skewed, and this skew was similar across field seasons (Table S1).

1.3 Additional Analyses Quantifying Skink Sociality

1.3.1 Social Associations Across Years

Using the same methods as described in the main manuscript, we calculated separate overall and preferred social networks for both study years (2014/15: $n_{ind} = 139$, $n_{obs} = 1308$, the number of observations varied between 1 to 28 per individual; 2015/16: $n_{ind} = 127$, $n_{obs} = 2285$, the number of

observations varied between 1 to 57 per individual). To test if social associations were related between field seasons, we used a multiple quadratic assignment procedures (MRQAP) following (Dekker et al., 2007) with 10,000 permutations (using the function '*mrqap.dsp'* from the '*asnipe'* R package; Farine, 2013) and using a double-permutation approach (Farine and Carter, 2020). We used separate MQRAPs to test correlations between overall and preferred association strength (HWI) matrices between field seasons. These matrices contained data from 98 skinks whose grouping behavior was observed in both study seasons. Our fieldwork protocol and effort was similar across field seasons, but our sample size of individuals and observations that were collected did slightly differ. Regardless, the comparison between seasons gives an indication of Tree Skink social association stability and indicate whether data can be pooled.

The results from our analyses indicate that the strength of Tree Skink social associations are correlated between seasons. Specifically, overall association strength matrices were significantly, positively related across years (MQRAP estimate controlled using double-permutations [r] = 0.657, $p < 0.001$, $R^2_{adj} = 0.367$), and the same trend was found between preferred association strength matrices (MQRAP estimate controlled using double-permutations [r] = 0.656, $p < 0.001$, $R^2_{adj} = 0.367$).

1.3.2 Analysis of Social Network Metrics

We used three separate linear models (using the function *'lm'* from the R package *'stats'*; R Core Team, 2018) to test if the observed network metrics (binary degree, weighted degree, and CV of edge weights) differed between skink demographics (i.e., adult females, adult males, and juveniles). To generate contrasts between all demographic classes from our linear models, we re-levelled the demographic variable and re-ran the models to extract coefficient estimates of the comparison between males and juveniles. The data used within these linear models was explored prior to statistical analyses to investigate normality, the presence of outliers, and collinearity. Additionally, the assumptions of normality of residuals and homogeneity of variance were verified for all linear models (Zuur et al., 2010).

Skink snout-vent length (SVL; reported as an estimated marginal mean ± standard error calculated using the function *'emmeans'* from the *'emmeans'* R package) (Lenth, 2020) was confounded with their age and sex classes: females (99 ± 1 mm) and males (101 ± 1 mm) did not significantly differ in SVL (*'eemeans'* contrasts [β] = -1.61, SE = 1.36, t = -1.18, p = 0.24). However, juveniles (67 ± 2 mm) were significantly smaller than females (*'eemeans'* contrasts [β] = 32.55, SE = 1.76, t = 18.48, $p < 0.01$) and males (*'eemeans'* contrasts [β] = -34.16, SE = 1.94, t = -17.64, $p < 0.01$). Differences in SVL were assessed using a linear model, and then post-hoc multiple comparisons between demographic classes were completed using the function *'emmeans'* from the *'emmeans'* R package with no p-value adjustment (Lenth, 2020). Due to the relationships between skink SVL and their age and sex, we opted to only include the latter in models.

We used the double permutation approach described in Farine and Carter (2020) for hypothesis testing regarding these network metrics. This is necessary because of non-independence of the data from social networks. This approach uses pre-network permutations to calculate the deviation of the network metrics from their expected random values given the structure of the observed data (i.e., the median value of the same network metric over 10,000 permuted networks); this is the equivalent to a residual value. These 'residual' network metrics were then analyzed using the linear models described above. We then calculated the significance of each effect (p_{rand}) by comparing model coefficients (β_{corr}) to the distribution of model coefficients (β_{rand}) based on randomized data (Farine and Whitehead, 2015). The randomized data we used for our calculation of significance was based on our original association matrix, which was randomized 10,000 times by randomly swapping individuals between groups (Farine and Whitehead, 2015). This permutation technique maintains the structure of our observed dataset: the same number of dyads observed, number of times an

individual is sighted, and number of individuals recorded during each sampling period as our observed data (Whitehead, 2008; Croft et al., 2009; Farine and Whitehead, 2015). From this randomized data, we then reconstructed a social network, calculated the same three network metrics, and conducted the same linear models as we did for the observed data. We considered effects to be significant if observed values fell outside the 95% range of the random coefficient distributions. Results from these analyses are reported in the main manuscript "Results" section and Table 1.

1.3.3 Spatial Overlap Across Years

Using the same methods as described in the manuscript, we calculated home- and core-range overlap separately for both field seasons (2014/15 n_{ind} = 118; 2015/16 n_{ind} = 109). Then, to assess if Tree Skink spatial overlap was stable across seasons, we used separate MQRAPs to test for correlations between home- and core-range overlap between field seasons. These matrices contained data from 82 skinks whose spatial data was sufficiently observed (i.e., more than 5 locations) in both active seasons. The results from our analyses indicate that spatial overlap between Tree Skinks is highly correlated between active seasons. Specifically, home-range overlap was significantly, positively related across seasons (MQRAP estimate [r] = 0.122, p = 0.015, R^2_{adj} = 0.004), and the same significant trend was found in core-range overlap from different seasons (MQRAP estimate [r] = 0.199, p = 0.002, R^2_{adj} = 0.016).

1.4 Genetic Analyses

1.4.1 DNA Extraction, Single Nucleotide Polymorphism (SNP) Sequencing, and Bioinformatics

DNA was extracted from skink tissue samples using GenCatch™ Blood and Tissue Genomic Mini Prep Kits (Epoch Life Science, Inc., Sugarland, Texas) in accordance with manufacturer instructions. Aliquots of all DNA samples were electrophoresed on 0.8% agarose gels pre-stained with GelRed™ (Biotium, Inc., Fremont, California; Huang et al. 2010) to confirm they contained high molecular weight DNA. After extraction, DNA samples were sent to a commercial genotyping service: Diversity Arrays Technology Pty Ltd (Canberra, Australia). This company has developed a widely used technique called DArTseq™ that identifies SNPs. Detailed descriptions of the DArTseq™ process of SNP identification are provided in Jaccoud et al. (2001) and Sansaloni et al. (2011). Using this process, we obtained a dataset of 15,187 SNPs with an average call and reproducibility rate of 95.16 ± 0.09% (mean ± standard error) and 99.45 ± 0.01%, respectively.

We filtered this SNP dataset using the R packages '*Radiator*' (Gosselin, 2017) and '*adegenet*' (Jombart, 2008; Paradis, 2010), and ended with a final filtered dataset consisting of 2105 SNPs. During the filtering process, we removed any sequence clusters that were monomorphic. In cases where multiple polymorphisms were found within the same sequence length, only one SNP was retained and all other duplicates were removed in order to avoid bias due to physical linkage (Lemay and Russello, 2015). We only retained loci with a call rate ≥ 95% and a reproducibility rate of ≥ 99%. We screened the data for allele coverage and removed any SNPs displaying a read depth of less than 8 and greater than 30 (Lemay and Russello, 2015). We also filtered SNPs for minor allele frequencies < 2%, because low frequency SNPs can create biases in the data (Roesti et al., 2012). At this stage of filtering, we used the '*hw.test*' function in the R package '*pegas*' (Paradis, 2010) to assess if any SNPs significantly departed from Hardy-Weinberg equilibrium (HWE) and linkage disequilibrium using data from only adult skinks within our population. Loci that significantly departed from HWE were removed from the dataset. We are confident that the final filtered dataset consists of loci that are unlinked and conform to the expectations of HWE. After our SNP data was filtered, we ensured data integrity by identifying duplicate individuals using a combination of a likelihood method via the program COLONY (Jones and Wang, 2010) and

relatedness estimates (R) using the program COANCESTRY (Wang, 2011), as well as correcting any labeling errors as appropriate.

1.4.2 Relatedness Estimator Determination

We used the program COANCESTRY (Wang, 2011) to determine the appropriate relatedness estimator to use, because relatedness estimator performance relies on understanding the underlying true population genetic structure (Van de Casteele, 2001; Wang, 2011). In COANCESTRY we simulated multilocus genotype data, based on the allele frequencies of our observed dataset, for 100 individuals assuming predefined relationships as: unrelated ($R = 0$), first cousins ($R = 0.125$), half siblings/avuncular/grandparent-grandchild ($R = 0.25$), full siblings ($R = 0.5$), parent-offspring ($R = 0.5$), twins/clones ($R = 1$). We then calculated pairwise relatedness for this simulated data using seven relatedness estimators (two likelihood estimators: dyadic and triodic likelihood estimators from Milligan (2003) and Wang (2007), respectively, as well as five moment estimators: Ritland (1996), Lynch and Ritland (1999), Li et al. (1993), Wang (2002), and Queller and Goodnight (2002). We assessed correlation between relatedness estimates and expected relatedness using Pearson correlation coefficients (R^2 using the R function '*cor*'; R Core Team, 2018). Based on this analysis, we selected the dyadic likelihood relatedness estimator because it yielded the strongest correlation between estimated and expected values ($R^2 = 0.9986$, see Figure S2 and Table S2 for all comparisons).

1.5 Relationships between Social Associations and Spatial Overlap

Tree Skink social associations and spatial overlap were significantly related, which we tested using MRQAPs using the same methods as describe above. Specifically, overall association strength and home-range overlap matrices were significantly, positively related (MQRAP estimate [r] = 0.000005, $p < 0.001$, $R^2_{adj} = 0.004$), as well as overall association strength and core-range overlap matrices (MQRAP estimate [r] = 0.00008, $p < 0.001$, $R^2_{adj} = 0.011$). Preferred Tree Skink association strengths and home-range overlap (MQRAP estimate [r] = 0.000005, $p < 0.001$, $R^2_{adj} = 0.004$), as well as core-range overlap (MQRAP estimate [r] = 0.00008, $p < 0.001$, $R^2_{adj} = 0.011$), were also significantly, positively related. Thus, we separately analyzed the relationship between relatedness vs. social association strength and spatial overlap, as to avoid any confounding effects of including both these matrices (r ranged between 0.063 to 0.104, as assessed using the function '*mantel'* in the R package '*vegan'* using 1000 permutations; Oksanen et al., 2019) in the same MRQAP (Dekker et al., 2007).

1.6 Analysis of whether Demography and Size are Driving Skink Social Associations

Using the same methods as described above, we used a MRQAP, and data from 164 skinks, to test if skink demographics and size affected Tree Skink social association strength. In this analysis, the overall association strength matrix was the dependent matrix, and three predictor matrices were as follows:

1. The genetic relatedness matrix that contained relatedness estimates (R) between all skink dyads,
2. A demographic similarity matrix that was set to 0 if dyads differ in demographics (e.g., an adult female and adult male), and to 1 if dyad demographics agree (e.g., both juveniles), and
3. A SVL similarity matrix consisting of the difference in SVL (mm) between members of a dyad.

Predictor matrices were not strongly related to each other ($r < |0.05|$ in all cases), as assessed via pairwise comparisons with a Mantel test (function '*mantel'* in the R package '*vegan'* using 1000 permutations; Oksanen et al., 2019). Thus model outputs contain measures of how each factor

affects skink social associations while controlling for the others. From this analysis we determined that demographic (i.e., age class and sex) and size similarity did not affect Tree Skink social associations, and instead the only significant driver in this analysis was genetic relatedness (Table S5).

1.7 Comparison of Spatial Autocorrelation Distance Classes

We found evidence for strong positive genetic-spatial autocorrelation over short distances, and our results largely agreed across distance classes. We analyzed data at 3 m, 5 m, and 10 m intervals, as well as a combination of four distance classes (i.e., pairwise comparisons at 0.0-3.0 m, 3.1-10.0 m, 10.1-50.0 m, and 50.1-127.0 m; as presented within the manuscript), and similar findings were clear across all analyses.

For the 10 m distance class, *r* values were positive and significant at 10 m ($p_F = 0.000$, $p_J = 0.000$), 20 m ($p_F = 0.000$, $p_J = 0.002$), and 30 m ($p_F = 0.032$, $p_J = 0.012$) for females and juveniles. Male *r* values were positive and significant at 10 ($p_M = 0.000$) and 20 m ($p_M = 0.000$). The *x*-intercept was 40 m, 56 m, and 58 m for females, males, and juveniles, respectively.

For the 5 m distance class, *r* values were positive and significant at 5 m ($p_F = 0.000$, $p_M = 0.004$), 10 m ($p_F = 0.000$, $p_M = 0.010$), 15 m ($p_F = 0.000$, $p_M = 0.003$), 20 m ($p_F = 0.003$, $p_M = 0.000$), and 25 m ($p_F = 0.000$, $p_M = 0.027$) for both females and males. The *x*-intercept value for females and males were 29 and 30 m, respectively. The results were the same for juveniles, with the exception of 15 m ($p_{5m} = 0.000$, $p_{10m} = 0.000$, $p_{15m} = 0.199$, $p_{20m} = 0.001$, $p_{25m} = 0.003$), and an *x*-intercept value of 29 m.

For the 3 m distance class, *r* values were positive and significant at 3 m ($p = 0.000$), 6 m ($p = 0.000$), 9 m ($p = 0.000$), 12 m ($p = 0.026$), 15 m ($p = 0.001$), 18 m ($p = 0.034$), 21 m ($p = 0.002$), and 24 m ($p = 0.001$) for females (Figure 4). The female *x*-intercept was 27 m. Males had similar results, but with non-significance at 6 and 12 m ($p_{3m} = 0.002$, $p_{6m} = 0.310$, $p_{9m} = 0.006$, $p_{12m} = 0.433$, $p_{15m} = 0.000$, $p_{18m} = 0.000$, $p_{21m} = 0.004$, $p_{24m} = 0.051$) and an *x*-intercept of 12 m. The results were also similar between females and juveniles, with non-significance at 15 m and 24 m ($p_{3m} = 0.000$, $p_{6m} = 0.001$, $p_{9m} = 0.000$, $p_{12m} = 0.001$, $p_{15m} = 0.205$, $p_{18m} = 0.005$, $p_{21m} = 0.000$, $p_{24m} = 0.149$) and an *x*-intercept of 26 m.

1.8 Mating System

While we maintained females temporarily in captivity at Macquarie University to monitor birth, they were individually housed in a climate-controlled room (maintained at 24ºC) within opaque plastic tubs (350 mm W x 487 mm L x 260 mm H). We lined these tubs with newspaper, and placed tree bark, a water dish, and a refuge (120 mm W x 175 mm L x 38 mm H) in each. A UV lamp provided light for each skink's tub, and each tub had an under-cage heating wire, restricted to one side. We cleaned tubs once weekly. We fed skinks 3 adult house crickets (*Acheta domesticus*) dusted with calcium and vitamins twice a week and puréed fruit (1.25 ml of Heinz® fruit baby food: mango, apple, and pear) once a week.

To assess parentage of Tree Skink litters, we used a combination of three programs and assessed agreement between the results. We used (1) COLONY (Jones and Wang, 2010) and (2) CERVUS (Marshall et al., 1998) to estimate paternity, as well as then (3) verified paternity using our relatedness estimates that were calculated in COANCESTRY (Wang, 2011). First, we used COLONY's maximum-likelihood method to assign parentage and sibship groups and to reconstruct genotypes of fathers (Jones and Wang, 2010). COLONY conducts simultaneous inference of multiple relationships among individuals and as such performs with greater statistical power compared to pairwise parentage analysis (Sieberts et al., 2002, Walling et al., 2010). Additionally,

COLONY assesses statistical confidence at an individual-level from the proportion of iterations that a specific relationship occurs and by the probability of configurations (Wang and Santure, 2009). Female and offspring genotypes were entered into COLONY, as well as known maternity and maternal sibships. A polygamous mating system was assumed for both sexes, thus permitting the assignment of half-siblings. An estimate of genotyping error (for all loci = 0.01) was included in the COLONY input, and the program was set to estimate and update allele frequencies throughout the analysis. The COLONY output clustered offspring into full- and half-sibling groups, as well as identifies fathers. The output from COLONY also contained reconstructed paternal genotypes, in the case that a father was not identified in the list of potential fathers, using the most-likely minimum-father combination (Wang, 2004; Phillips et al., 2013).

Second, we used CERVUS to find highly likely paternal assignments. CERVUS bases their confidence levels on simulated populations (specified to be 10,000 offspring genotypes in our case), which can increase the total number of parentage assignments at the possible cost of a larger number of inaccurate assignments (Walling et al., 2010). Assignments to potential fathers was carried out using a strict 95% confidence interval, and all adult males from our main site in Albury, New South Wales were included as candidate fathers. Mothers were known. The probability of a candidate father being present in the sample population was set at 0.9, because we sampled 203 out of a possible 240 individuals (estimated population size for Albury; see above). The genotyping error rate we assumed was 0.01 per locus for typing errors.

Finally, to determine paternity of Tree Skink litters, we assessed if the COLONY results identifying paternity of litters and sibship of juveniles within litters (i.e., half or full siblings) agreed with the father assigned with 95% confidence from CERVUS. We similarly verified these results using relatedness estimates (*R*). In the majority of cases, the results from all three methods agreed.

1.9 Summary of Tree Skink Habitat Use

We summarized the following variables using data from skinks with more than 10 spatial observations ($n = 132$). The ratio of observations on rocks:trees was, on average, 5:1 and this ratio reflects the presence of both habitat types on the landscape (i.e., there were more rocks than trees). The majority of Tree Skinks (63.6% or 84/132) were observed on both rock and tree habitats during our two-year study. Only 29.5% (39/132) and 6.8% (9/132) of individuals were observed solely on rock and tree habitats, respectively. The individuals that were restricted to only one habitat type (rocks or trees) spanned all life-stages and sexes.

1.10 Summary of Group Composition and Stability

Using our definition (≥ 2 individuals on the same rock or tree), we found that, in 1007/3593 of our observations, Tree Skinks were aggregating. In total, we observed 438 aggregations across our study's two active seasons. Of these 438 aggregations, we found that 190 were unique (i.e., consisting of a distinctive set of individuals). We used this observational data to summarize group size and composition and it was also what we used to construct our social networks and quantify Tree Skink social associations.

Tree Skink aggregation size varied between 2 to 5 individuals; although the most commonly observed size was 2 skinks (Table S3). The demographic composition of aggregations was highly variable (Table S4). The most commonly observed group composition was one male and one female (33%; Table S4). Between adults, mixed-sex groups were the most common ($n = 84$ of 142 adult-only groups; Table S4). Most adult groups had either one ($n = 62$) or multiple females (2-4 individuals; $n = 19$) and only one male. In groups with multiple females, relatedness was higher among females ($R_{2F \& 1M} = 0.209 \pm 0.206$; $R_{3F \& 1M} = 0.305 \pm 0.198$; $R_{4F \& 1M} = 0.322 \pm 0.167$) than between males and females ($R_{2F \& 1M} = 0.102 \pm 0.182$; $R_{3F \& 1M} = 0.138 \pm 0.210$; $R_{4F \& 1M} = 0.035 \pm$

0.070). Same-sex aggregations were more often observed between females (varied in size from 2 to 4 individuals) than males (only observed in groups of 2), and an aggregation consisting of two adult females was the second-most commonly observed composition (22%; Table S4).

Aggregations with adults and juveniles (n = 33/190) generally had higher within-group relatedness than adult-only groups (Table S4). Juveniles were more likely to be in groups with only females (n = 31), than males (n = 10) and adults of mixed sexes (n = 6). Juveniles were rarely observed aggregating with one another (n = 1) without adults also present (Table S4).

1.11 Anecdotal Observation of Parent-Offspring Interactions

In addition to the observations we made during this study about Tree Skink aggregations, we also had the opportunity to observe other unique behaviors of Tree Skinks. These accounts are anecdotal, but we have included them and our speculations about them to inspire future research. On three occasions at our study site in Albury, New South Wales, we observed behavior that may reflect adult skinks acting as a 'look-out' or 'sentinel' as juveniles foraged nearby and using tactile signals to communicate the presence of predators. Of course, this behavior of lizards positioning themselves upon a high vantage is common, especially in territorial species (Fox et al., 2003), but it is rarer in Tree Skinks that typically cryptically bask within or at the edge of, their crevices, only quickly darting in-and-out for prey as they are sit-and-wait foragers (Riley, 2017). We observed this behavior when a predator approached, often a researcher (JLR) but sometimes a bird of prey, and adults, before retreating to the crevice themselves, would move towards a juvenile and repeatedly 'nudge' the juvenile's back with their snout, as if to motivate them to move back the crevice (J Riley, pers. obs.). Thus, we think Tree Skinks may be an interesting model to investigate and quantify direct parental care and communication (i.e., visual and/or tactile) within a family group.

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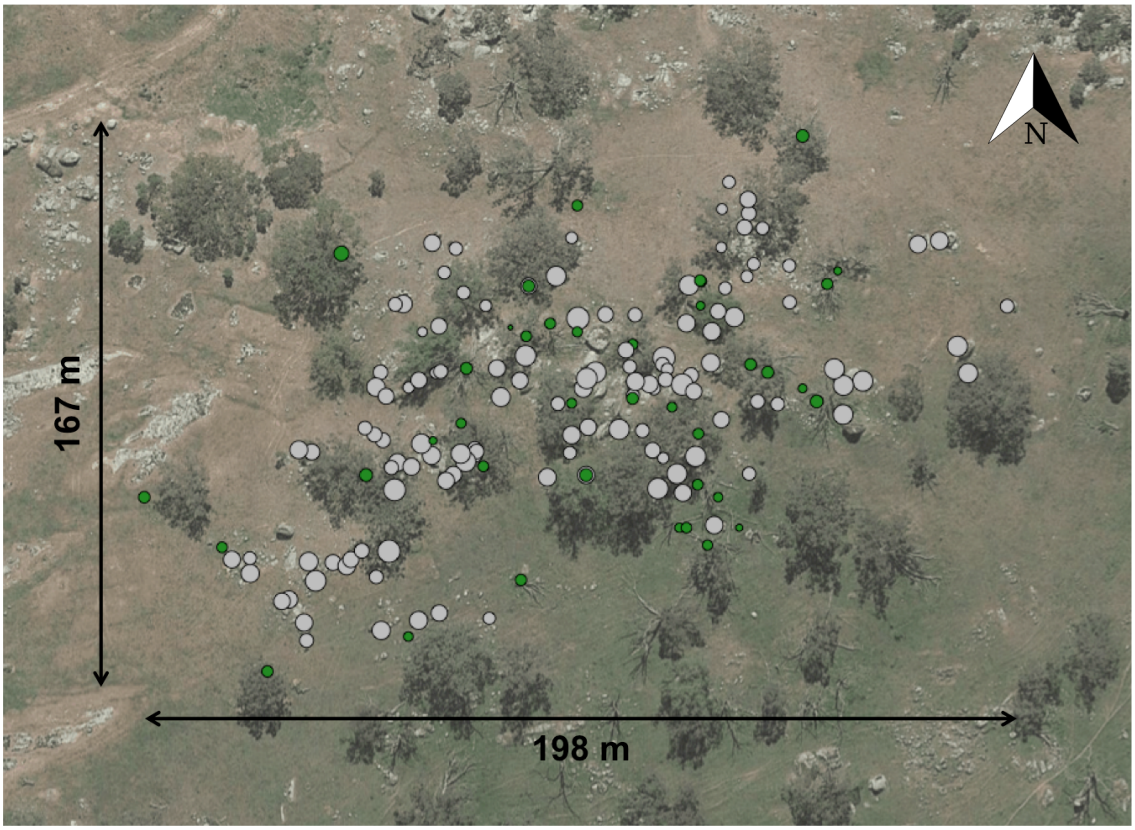
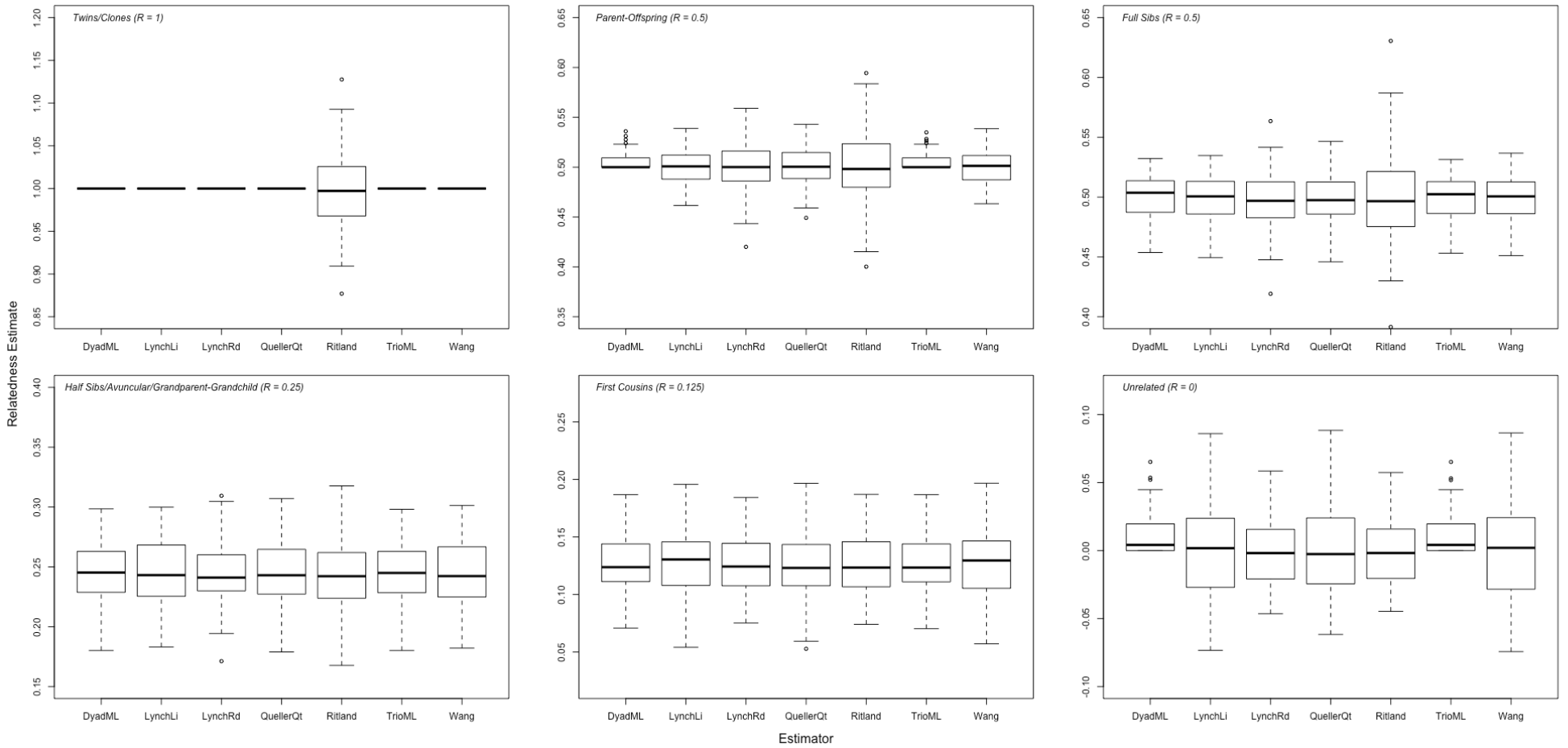
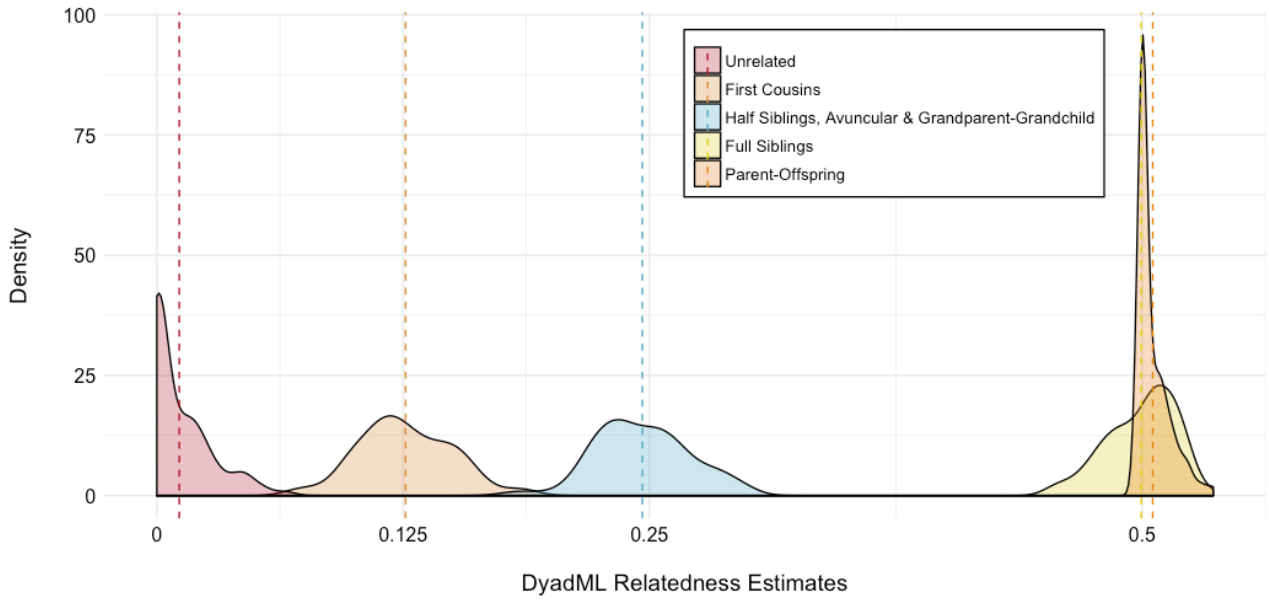
3 Supplemental Figures



Supplemental Figure 1. Our Tree Skink (*Egernia striolata*) study site in Albury, NSW, Australia (-35.98°S, 146.97°E) with 166 marked trees and rocks (grey circles; size reflects tree or rock diameter) and trees (green circles) that were used by skinks as habitat (i.e., the majority of the rocks and trees that that were marked are ones we observed skinks using).



Supplemental Figure 2. Boxplots comparing relatedness estimates for seven relatedness estimators (two likelihood estimators: dyadic [dyadML] and triadic [TrioML] likelihood estimators from Milligan (2003) and Wang (2007) respectively, as well as five moment estimators: Ritland (1996) [Ritland], Lynch and Ritland (1999) [LynchRd], Li et al. (1993) [LynchLi], Wang (2002) [Wang], and Queller and Goodnight (2002) [QuellerQt]).



Supplemental Figure 3. Density of the relatedness estimates for our Albury, NSW population of Tree Skinks (*Egernia striolata*) using the dyadic likelihood estimator (Milligan 2003).

4 Supplemental Tables

Supplemental Table 1. Age class structure of our population of Tree Skinks (*Egernia striolata*) across both study years (2014/2015; 2015/2016).

Time period	Adult Females *n* (%)	Adult Males *n* (%)	Juveniles *n* (%)	Total *n*
All surveys	115 (57)	53 (26)	35 (17)	203
2014/2015	94 (56)	49 (29)	26 (15)	169
2015/2016	82 (61)	39 (29)	13 (10)	134

Supplemental Table 2. Pearson correlations (R^2) between relatedness estimates, for each relatedness estimator simulated (n = 700) and expected values. The estimator with the highest correlation (dyadic likelihood estimator; Milligan 2003) was selected for our study.

Pearson R^2	Relatedness Estimator
0.99856	triadic likelihood estimator (Wang 2007)
0.99724	Wang (2002)
0.99728	Li et al. (1993)
0.99771	Lynch and Ritland (1999)
0.9949	Ritland (1996)
0.99745	Queller and Goodnight (1989)
0.99857	dyadic likelihood estimator (Milligan 2003)

Supplemental Table 3. Composition of Tree Skink (*Egernia striolata*) aggregations in Albury, NSW. This includes a summary of how many times unique social groups (n = 190) of each size (varied from 2 to 5 individuals) were observed (n), the number of observed, a summary of the demography of each group (ordered based on the number of times observed) and habitat. The size (circumference) of and the number of crevices occurring on the habitat was summarized by group size, which indicates that habitat size/availability of crevices does not appear to limit group size of Tree Skinks.

Aggregation Size	*n*	Number of Unique Aggregations	Demography			Habitat		Circumference of Habitat (m)	Number of Crevices
			Female	Male	Juveniles	Rocks	Trees		
5	11	3	4 (6) or 2 (5)	1 (11)	0 (6) or 2 (5)	11	0	13.64 ± 6.52	5.30 ± 2.26
4	31	14	3 (19), 4 (5), 2 (2) or 1 (2)	1 (13), 0 (13) or 2 (2)	0 (19) or 1 (9)	23	8	11.26 ± 5.98	6.55 ± 3.02
3	60	38	2 (25), 3 (13), 1 (12) or 0 (6)	0 (30), 1 (18) or 2 (8)	0 (30), 1 (20) or 2 (6)	47	13	11.54 ± 4.72	9.39 ± 3.38
2	326	135	1 (205), 2 (98) or 0 (23)	1 (191), 0 (131) or 2 (4)	0 (278), 1 (44) or 2 (4)	252	74	11.62 ± 5.90	6.90 ± 3.77

Supplemental Table 4. Within 190 unique social aggregations of Tree Skinks (*Egernia striolata*) 21 different compositions of adult (F = female and M = male) and juvenile (J) skinks were observed. The number (*n*) of times each of these compositions was observed is provided, and the unique pairwise pedigree relationships within these aggregations are identified. For each of these compositions, we also provide the average (± standard deviation with minimum and maximum values in brackets) of within-group relatedness. This table is presented over the following three pages.

Group Composition	Group Size	*n*	Pedigree Relationships	Within-Group Relatedness
1F 1M	2	62	7 parental/full sibling 0 half sibling/avuncular 4 first cousin 51 unrelated	0.072 ± 0.162 (0.000, 0.615)
2F	2	42	10 parental/full sibling 2 half sibling/avuncular 3 first cousin 27 unrelated	0.016 ± 0.199 (0.000, 0.528)
1F 1J	2	18	7 parental/full sibling 3 half sibling/avuncular 0 first cousin 8 unrelated	0.271 ± 0.204 (0.010, 0.523)
2F 1M	3	12	7 parental/full sibling 1 half sibling/avuncular 5 first cousin 23 unrelated	0.143 ± 0.196 (0.000, 0.500)
3F	3	11	13 parental/full sibling 2 half sibling/avuncular 2 first cousin 16 unrelated	0.252 ± 0.219 (0.000, 0.608)
1M 1J	2	8	4 parental/full sibling 0 half sibling/avuncular 1 first cousin 3 unrelated	0.248 ± 0.257 (0.002, 0.567)
3F 1M	4	6	10 parental/full sibling 1 half sibling/avuncular 3 first cousin 22 unrelated	0.192 ± 0.213 (0.000, 0.541)

2F 1J	3	6	8 parental/full sibling 1 half sibling/avuncular 0 first cousin 9 unrelated	0.300 ± 0.200 (0.010, 0.527)
3F 1J	4	4	12 parental/full sibling 3 half sibling/avuncular 1 first cousin 8 unrelated	0.321 ± 0.244 (0.000, 0.582)
2M	2	4	2 parental/full sibling 0 half sibling/avuncular 1 first cousin 1 unrelated 0 unrelated	0.181 ± 0.247 (0.000, 0.542)
1F 2J	3	3	4 parental/full sibling 1 half sibling/avuncular 1 first cousin 3 unrelated	0.442 ± 0.128 (0.252, 0.527)
2M 1J	3	2	2 parental/full sibling 0 half sibling/avuncular 2 first cousin 2 unrelated	0.154 ± 0.216 (0.012, 0.472)
1F 2M	3	2	0 parental/full sibling 0 half sibling/avuncular 1 first cousin 5 unrelated	0.039 ± 0.042 (0.000, 0.108)
1F 1M 1J	3	2	2 parental/full sibling 1 half sibling/avuncular 1 first cousin 2 unrelated	0.357 ± 0.191 (0.116, 0.514)
2F 1M 2J	5	2	6 parental/full sibling 0 half sibling/avuncular 0 first cousin 14 unrelated	0.203 ± 0.251 (0.000, 0.526)
4F	4	1	2 parental/full sibling 1 half sibling/avuncular 2 first cousin 1 unrelated	0.322 ± 0.167 (0.142, 0.506)

4F 1M	5	1	3 parental/full sibling 1 half sibling/avuncular 2 first cousin 4 unrelated	0.207 ± 0.198 (0.000, 0.506)
2F 1M 1J	4	1	2 parental/full sibling 0 half sibling/avuncular 0 first cousin 4 unrelated	0.013 ± 0.015 (0.000, 0.030)
2F 2M	4	1	3 parental/full sibling 0 half sibling/avuncular 1 first cousin 2 unrelated	0.260 ± 0.247 (0.000, 0.494)
1F 1M 2J	4	1	3 parental/full sibling 0 half sibling/avuncular 0 first cousin 3 unrelated	0.264 ± 0.283 (0.009, 0.526)
2J	2	1	1 parental/full sibling 0 half sibling/avuncular 0 first cousin 0 unrelated	0.418

Supplemental Table 5. Results of the MQRAP model examining if overall Tree Skink association strength was affected by demographic or size (based on snout-vent-length; SVL) similarity. Significant effects are bolded.

	Regression Coefficient (β)	*t-value*	*P*
Intercept	0.0004	1.4680	0.3699
Genetic Relatedness	**0.0622**	**21.0543**	**<0.0001**
Demographic Similarity	-0.0002	-0.3697	0.7564
SVL Similarity	-0.0000	-0.8747	0.5085

Multiple $R^2 = 0.032$