

1 **Bioturbation by bandicoots facilitates seedling growth by altering soil properties**

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16 **Abstract**

- 17 **1.** Animals that forage for food via bioturbation can alter their habitat, influencing soil turnover,  
18 nutrient cycling and seedling recruitment, effectively acting as ecosystem engineers. Many digging  
19 mammals forage for food by digging small pits and creating spoil heaps with the discarded soil.  
20 We examined how small-scale bioturbation, created by the foraging actions of an ecosystem  
21 engineer, can alter soil nutrients and subsequently improve growth of plants.
- 22 **2.** We investigated the microbial and chemical properties of soil disturbed by the foraging of an  
23 Australian marsupial bandicoot, quenda (*Isoodon fusciventer*). Soil was collected from the base of  
24 20 recent foraging pits (pit), the associated spoil heaps (spoil) and adjacent undisturbed soil  
25 (control) and analysed for nutrients (phosphorus, potassium, sulphur, organic carbon and  
26 conductivity) and microbial activity. Soil cores were collected from the same locations and seeds  
27 of the dominant canopy species, tuart (*Eucalyptus gomphocephala*), added to the soil under  
28 glasshouse conditions. The growth of seedlings were measured (height, maximum growth, basal  
29 stem width, shoot and root biomass) over a four-month period and arbuscular mycorrhizae (AM)  
30 fungi colonisation rates of seedling roots investigated.
- 31 **3.** Soil from the spoil heaps had the greatest levels of conductivity and potassium. Both the spoil and  
32 undisturbed soil had greater amounts of microbial activity and organic carbon. In contrast, the pits  
33 had less nutrients and microbial activity.
- 34 **4.** Seedlings grown in spoil soil were taller, heavier, with thicker stems and grew at a faster rate than  
35 seedlings in the pit or control soil. Colonisation with AM fungi was greatest for seedlings grown  
36 in pit soil. The best predictors of seedling growth were greater amounts of potassium, electrical  
37 conductivity and microbial activity. The best predictor of higher colonisation rates of AM fungi  
38 was less phosphorus.
- 39 **4.** Bioturbation by ecosystem engineers, like quenda, can alter soil nutrients and microbial activity,  
40 facilitating seedling growth. We propose this may be caused by enhanced litter decomposition  
41 beneath the discarded spoil heaps. As the majority of Australian digging mammals are threatened,

42 with many suffering substantial population and range contractions, the loss of these species will  
43 have long-term impacts on ecosystem processes.

44

45 Key Words: arbuscular mycorrhizal fungi; bandicoot; digging mammals; ecosystem engineer; plant-  
46 animal interactions; plant-animal-microbe interactions.

47

## 48 **Introduction**

49 Bioturbation by animals that dig, burrow or displace soil while searching for food can influence their  
50 environment in many ways (Whitford & Kay 1999). Digging animals alter the physical and chemical  
51 properties of soils, modify resource pathways and alter the availability of resources for other species;  
52 and; consequently many digging animals are considered ecosystem engineers (Davidson, Detling &  
53 Brown 2012; Coggan, Hayward & Gibb 2018). Species that dig when foraging for food create small-  
54 scale disturbances that may be quite ephemeral in nature; however, small-scale bioturbation actions  
55 may cumulatively impact ecosystems (Darwin 1881). When digging animals are numerous, the  
56 foraging pits they create can be plentiful and subsequently influence environmental processes (Alkon  
57 1999; Eldridge *et al.* 2012). Here, we examine how foraging pits created by quenda, *Isoodon*  
58 *fusciventer*, an Australian digging marsupial, may alter soil nutrients and consequently facilitate  
59 seedling growth.

60

61 By foraging in the soil, animals break through the soil crust, often mixing soil types and horizon  
62 layers (Alkon 1999). In arid environments, breaking the soil crust can reduce soil hydrophobicity,  
63 while simultaneously allowing moisture to infiltrate the top layer of soil (Garkaklis, Bradley &  
64 Wooller 1998; Valentine *et al.* 2017), at least initially. The pit created often acts as a sink for organic  
65 matter, trapping sediment, litter and seeds, altering soil fertility at local scales (Garkaklis, Bradley &  
66 Wooller 2003; Eldridge & Mensinga 2007; James, Eldridge & Hill 2009; Hagenah & Bennett 2013).  
67 When a foraging pit is created, it usually has an associated spoil heap of evacuated soil, also known as  
68 ejecta mounds (Whitford & Kay 1999). The combination of digging and discarding soil disrupts the

69 microhabitat layer by exposing soil at the digging site, and burying organic matter and litter under the  
70 spoil heap; subsequently altering surface litter composition and potentially contributing to litter  
71 decomposition (Valentine *et al.* 2017). The burial of litter is an important component in litter  
72 decomposition (Beare *et al.* 1992; Austin, Araujo & Leva 2009) and the digging or raking activities of  
73 some animals, such as heteromyid rodents, the short-beaked echidna (*Tachyglossus aculateatus*) and  
74 malleefowl (*Leipoa ocellata*) enhance litter decomposition in arid environments (Eldridge *et al.* 2012;  
75 Smith, Avitabile & Leonard 2016; Travers & Eldridge 2016).

76

77 The engineering activities of animals that enhance litter decomposition can facilitate a change in soil  
78 nutrients (see Platt *et al.* 2016 for review); although these are often inconsistent, varying among  
79 organisms, bioturbation type and intensity of digging (Yu *et al.* 2017). For example, the burrows of  
80 mole-rats (Bathyergidae) have more nitrogen compared to undisturbed soil (Hagenah & Bennett  
81 2013); while mounds of pocket gophers (*Thomomys talpoides*) are predominantly associated with  
82 lower levels of nitrogen (Yurkewycz *et al.* 2014). Foraging pits created by badgers (*Meles meles*)  
83 have more potassium (Kurek, Kapusta & Holeksa 2014) as do those made by burrowing bettongs  
84 (*Bettongia lesuer*) and greater bilbies (*Macrotis lagotis*) (James, Eldridge & Hill 2009), although there  
85 appears to be no effect on potassium or phosphorus levels in foraging pits created by the woylie (*B.*  
86 *penicillata*)(Garkaklis, Bradley & Wooller 2003).

87

88 As many nutrients (e.g. nitrogen, phosphorus and potassium) are essential for adequate plant growth,  
89 burrowing or foraging that encourages litter decomposition may subsequently lead to enhanced  
90 seedling recruitment and/or growth. Greater seedling recruitment was observed in areas with digging  
91 marsupials (James, Eldridge & Moseby 2010) and in experiments using artificial diggings compared  
92 to undisturbed areas (Valentine *et al.* 2017). Glasshouse trials also indicate that when grass seedlings  
93 are grown in the soil of foraging tracks created by echidna, the seedlings grew taller than seedlings  
94 grown in undisturbed soil, especially under challenging conditions (Travers *et al.* 2012).

95 Furthermore, the composition of many vegetation communities are considered to be influenced by the

96 presence (or the removal) of digging animals (Whitford & Kay 1999; Davidson, Detling & Brown  
97 2012).

98

99 Digging activities of animals are also linked to changes in soil microbial communities, with foraging  
100 activities of echidnas influencing ecosystem function, measured by enzyme concentrations, compared  
101 to undisturbed soils (Eldridge *et al.* 2016). Digging mammals can also be key dispersers of  
102 mycorrhizal fungi, via consumption of the fruiting bodies and subsequent defecation of viable spores  
103 (Johnson 1996; Tay *et al.* 2018). Mycorrhizae are specialised structures arising from the association  
104 of plant roots and fungi, that allow plants greater access to limited soil nutrients (e.g. nitrogen and  
105 phosphorus) and water (Smith & Smith 2011), with an estimated 72% of vascular plants forming  
106 symbiotic associations with arbuscular mycorrhizae (AM) (Brundrett & Tedersoo 2018). Indeed, the  
107 presence of small mammals positively influenced AM colonisation of roots in semi-arid Chilean  
108 shrubland (Aguilera *et al.* 2016), while in Western Australia woodlands mycorrhizal communities  
109 differ in areas with abundant digging mammals (Dundas *et al.* in press).

110

111 Many of the world's digging mammals are threatened (Davidson, Detling & Brown 2012). The loss  
112 of these ecosystem engineers may lead to a subsequent loss of the ecological processes they perform  
113 and important plant-animal interactions. Globally, conservation efforts include reintroductions of  
114 threatened species, increasingly not only for the conservation of species themselves, but also in  
115 attempts to restore lost ecosystem functions (e.g. Law *et al.* 2017); and greater understanding on the  
116 role of digging mammals in ecosystem function is therefore required (Coggan, Hayward & Gibb  
117 2018). Australia has the world's highest record of mammal extinction in the last 200 years  
118 (Woinarski, Burbidge & Harrison 2015) and a large proportion of extant digging marsupials are  
119 threatened or have suffered severe range contractions (Fleming *et al.* 2014). Many of these species are  
120 within the critical weight range category (35–5500 g) and are highly susceptible to predation by  
121 introduced red foxes (*Vulpes vulpes*) and feral cats (*Felis catus*), in addition to habitat loss and  
122 inappropriate fire regimes (Johnson & Isaac 2009; Woinarski, Burbidge & Harrison 2015).

123

124 We examined the role of quenda foraging in facilitating plant growth. Previous research indicates this  
125 species is an important ecosystem engineer, with an individual quenda creating ~45 pits each night  
126 and displacing nearly four tonnes of soil annually per individual (Valentine *et al.* 2013). The foraging  
127 pits of quenda can also reduce soil water repellency, increase soil moisture and reduce litter size  
128 within a few months of creation (Valentine *et al.* 2017). In addition, seedling recruitment of co-  
129 occurring native tree species (e.g. *Eucalyptus gomphocephala* and *Acacia saligna*) is greater in  
130 artificially dug soil compared to undisturbed soil (Valentine *et al.* 2017). Our research further  
131 explores the role of quenda in manipulating soil and plant properties by examining: *i*) whether soil  
132 nutrients are different between recently created quenda foraging pits (both the foraging pit and  
133 associated spoil heap) and undisturbed soil; *ii*) difference in growth of seedlings and AM fungi  
134 colonisation of seedling roots grown in quenda-manipulated soil and undisturbed soil and, *iii*) whether  
135 soil nutrients and microbial activity can predict seedling growth and AM colonisations.

#### 136 **Methods:**

137 The quenda is a medium-sized (weighing 800–1200 g) omnivorous marsupial that searches for food  
138 (e.g. invertebrates, tubers and fungi) by digging foraging pits (Valentine *et al.* 2013). Previously  
139 considered a subspecies of the threatened southern brown bandicoot (*Isoodon obesulus*) (Travouillon  
140 & Phillips 2018), the quenda has similarly suffered population decline, principally as a result of  
141 introduced predators and habitat loss, throughout its range in south-western Australia. The quenda  
142 persists in forest remnants and peri-urban reserves where vegetation cover is sufficient to provide  
143 protection from predators (Bryant *et al.* 2017), although these small meta-populations are vulnerable  
144 to disturbances (Ramalho *et al.* 2018). While digging for food, quenda create conical-shaped foraging  
145 pits (~100 mm across and 70 mm deep), with soil ejected from the pit forming a spoil heap (ejecta  
146 mound) that covers the undisturbed ground surface and any litter present (Valentine *et al.* 2013).

147

148 Yalgorup National Park (32°50'54.52"S; 115°40'08.72"E) within the Swan Coastal Plain bioregion  
149 (Thackway & Cresswell 1995) in south-western Australia, supports a naturally-occurring population  
150 of quenda. The region has a Mediterranean-type climate with hot, dry summers and mild, wet winters

151 with average annual rainfall of 864 mm (Bureau of Meteorology, station # 009679). Our work was  
152 conducted on the Spearwood Dune system (predominantly yellow-phase Karrakatta sands) where the  
153 habitat was open woodland dominated by *Eucalyptus gomphocephala* (tuart), with scattered *E.*  
154 *marginata* (jarrah) and *Corymbia calophylla* (marri) and a mid-storey *Banksia* spp. (for detailed  
155 vegetation description, see Valentine *et al.* 2013; Valentine *et al.* 2017). The dominant eucalypt, tuart,  
156 has been the focus of restoration trials within sections of Yalgorup National Park (see Ruthrof *et al.*  
157 2016). South-western Australian soils are old, leached and nutrient deficient (McArthur & Bettenay  
158 1960; Henderson & Johnson 2016), and consequently mycorrhizal fungi play an important role in  
159 maintaining plant health.

160

#### 161 *Soil nutrients*

162 We identified 20 recent foraging pits created by quenda, within the previous 1 – 2 months, at Martin's  
163 Tank, Yalgorup National Park (29/10/2012). Samples from three locations along the foraging pit  
164 profile were collected: *i*) the base of the foraging pit (hereafter called pit), *ii*) the spoil heap or ejecta  
165 mound (spoil), and *iii*) adjacent undisturbed ground, located within 0.5 m of the foraging pit (control).  
166 From each location, we collected soil samples (~ 150 g) for nutrient analyses. Standard soil nutrient  
167 analyses, undertaken by CSBP Soil and Plant Analysis Laboratory (Bibra Lake, Western Australia),  
168 examined nutrient quantities that may be important for plant growth: nitrate nitrogen (mg/kg),  
169 ammonium nitrogen (mg/kg); phosphorus (mg/kg; Colwell), potassium (mg/kg; Colwell), sulphur  
170 (mg/kg; KCl 40), organic carbon (carbon, %; Walkley-Black), as well electrical conductivity (dS/m;  
171 which provides an indication of the level of nutrient salts present (Landis 1989) and pH level (CaCl<sub>2</sub>  
172 and H<sub>2</sub>O).

173

#### 174 *Microbial activity*

175 To estimate the overall microbial activity in each sample, we undertook a fluorescein diacetate (FDA)  
176 hydrolysis assay, which measures the enzyme activity (including lipases, esterases and proteases) of  
177 microbial populations (using methods following: Schnürer & Rosswall 1982; and Adam & Duncan  
178 2001). We collected soil samples (~5 g) from the top 5 cm of soil from the three locations: pit, spoil

179 and control. Activity of the enzymes results in the hydrolytic cleavage of FDA (colourless) into  
180 fluorescein (fluorescent yellow-green). Enzyme activity is quantified by assessing the intensity of  
181 colour using spectrophotometry (490 nm). A range of fluorescein dilutions was used (n = 5) to  
182 generate a standard curve and optical densities converted to  $\mu\text{g}$  fluorescein produced per gram of soil.

183

#### 184 *Plant growth and colonisation of arbuscular mycorrhizal fungi*

185 To examine growth of seedlings, we collected 60 soil cores from the three locations (pit, spoil, and  
186 control from 20 replicate foraging pits) using a cylindrical corer (plastic PVC pipe inner diameter: 27  
187 x 10 cm L x W) and carefully transferred the soil to standard, free-draining pots of similar dimensions  
188 to the corer with minimal disturbance of soil. Pots were placed in a glasshouse, seeded with 10 *E.*  
189 *gomphocephala* seeds into each pot (3/11/2012) and watered automatically once daily. Germination  
190 was successful with all pots containing seedlings (median 8 seedlings per pot) and were thinned to the  
191 largest single seedling per pot (at 7 weeks, 21/12/ 2012). We measured seedling height (cm) every 7–  
192 12 days, with a total of 13 measurements over a 3-month period. Prior to harvesting (25/03/2013), we  
193 measured the final height and stem width (mm, using digital callipers, 1 cm from the soil surface).  
194 Shoots were harvested using secateurs to cut the shoot off at 5 mm from the soil surface and were  
195 dried at 70°C for 3 days, before weighing (g).

196

197 To collect root material, we gently removed roots from the pots and washed the root mass to remove  
198 excess soil, then gently dried with paper towels. Fine roots were identified using visual inspection  
199 and a small sample (~0.5 g) was carefully removed into a fine sieve (0.5 mm) to examine AM  
200 colonisation. Fine root samples were stored in 70% ethanol, with remaining root material dried at  
201 70°C for 3 days before weighing (g). Fine roots (<1 mm in diameter) were later fixed in formalin  
202 acetic acid (FAA) solution (13 ml formalin + 5 ml acetic acid + ethyl alcohol) and cut into 1-cm-long  
203 segments. Mycorrhizal colonization was assessed according to methods described by Brundrett et al.  
204 (1984). The root segments were washed with water and placed in 20-ml vials containing 10% KOH  
205 solution and incubated for 30 min at 90°C. Roots were washed with water and dyed with 0.05%  
206 trypan blue solution (lactic acid : glycerol : distilled water = 1 : 2 : 2) and maintained at 50°C



207 overnight. Ten randomly selected root segments per plant replicate were mounted on each of three  
208 microscope slides and examined for mycorrhizal colonisation under an Olympus BX50 transmitted  
209 light bright field microscope (Olympus, Japan). The number of colonised root sections was counted  
210 and summed across the three slides and converted to a proportion of the 30 root sections examined.

211

### 212 *Statistical analyses*

213 Individual seedling trajectories were fitted by modelling seedling height using a Gamma distribution  
214 as a smooth function of time since sowing via the gamm4 package (Wood & Scheipl 2013) in R (R  
215 Core Team 2016). The resulting smoothed model trajectories were used to calculate rate of maximum  
216 growth for each seedling ( $\text{mm day}^{-1}$ ). We used a hierarchical mixed modelling approach to examine  
217 the strength of the effect of the foraging pit location (pit, spoil, control) on both soil characteristics  
218 (conductivity, nutrients and FDA) as well as the plant growth response variables. The variables final  
219 height, max growth, dry shoot biomass, dry root biomass and stem width were modelled using a  
220 gamma distribution, and the proportion of AM in roots were modelled using a binomial distribution  
221 based on the 30 observations. As soil characteristic variables were used as predictors of the plant  
222 growth response variables in subsequent analyses (see below) they were transformed (where  
223 necessary) to optimize spread across the predictor range and improve scaling relationships. The  
224 nutrients phosphorus, potassium and sulphur were natural log transformed, FDA was cube-root (cbt)  
225 transformed and conductivity was square-root (sqrt) transformed. Following transformations all soil  
226 characteristic variables were modelled via a Gaussian distribution. Each variable was modeled using a  
227 Generalized Linear Mixed Model (GLMM), including foraging pit identifier as a random intercept to  
228 account for non-independence of the three locations (pit, spoil and control) sampled at each foraging  
229 pit replicate. Initial models were fit using the function glmer from the lme4 library (Bates *et al.* 2015)  
230 in R, with resulting model output used to calculate AICc and a pseudo  $R^2$ . Equivalent models were fit  
231 in a Bayesian context based on uninformative priors using the INLA package (Lindgren & Rue 2015)  
232 in R and the inla.posterior.sample used to generate 95% credible bounds for model parameters that  
233 were used to interpret significant differences among locations. Two models were fitted for each  
234 variable: the null model including only an intercept and the foraging pit identifier and a model

235 including foraging pit location (pit, spoil, control). Differences in the AICc and pseudo  $R^2$  values  
236 between the location and null models were used to evaluate the strength of the effect of foraging pit  
237 location for each variable.

238

239 Differences in the growth trajectories of seedlings among the three foraging pit profile locations were  
240 assessed using Generalized Additive Mixed Models (GAMMs) based on a Gamma distribution with a  
241 log link function, with foraging pit identifier included as a random intercept term as in the GLMM  
242 above, but an additional seedling identifier random intercept to account for repeated measurement on  
243 individual seedlings over time.

244

245 We explored the relative importance of the relationship among the soil characteristics [phosphorus  
246 (mg/kg), potassium (mg/kg), sulphur (mg/kg), carbon (%), pH (CaCl<sub>2</sub>), electrical conductivity (dS/m)  
247 and FDA ( $\mu\text{g}$  hydrolysed FDA / g of dry soil)] as predictors of the plant growth variables [response  
248 variables: final height (mm); stem width (mm); maximum growth (cm/day); dry shoot biomass (g);  
249 dry root biomass (g); AM colonisation (%)] using a full sub-sets GAMM approach via the function  
250 `full.subsets.gam` described in Fisher *et al.* (2018) in R using the default argument settings, with the  
251 exception that maximum model size was limited to two simultaneous predictors. This approach  
252 constructs a complete model set excluding any models containing correlated  $> 0.28$  Pearson  
253 correlation and compares these using Akaike Information Criterion (AICc), Bayesian Information  
254 Criterion (BIC) and AIC weight ( $\omega_i$ ) values (Burnham & Anderson 2002). The simplest model within  
255 2 AICc of the model with the lowest AICc was assumed to be the optimal model, with the relative  
256 importance of each predictor across the whole model set calculated as summed model weights. All  
257 models were fit using GAMMs, via the `gamm4` function from the `gamm4` package (Wood & Scheipl  
258 2013) in R using the appropriate statistical distribution and random structure as described for the  
259 GLMs above.

## 260 **Results**

### 261 *Soil nutrients*

262 Many of the soil physiochemical properties (e.g. conductivity, Fig. 1a and potassium, Fig. 1c) were  
263 significantly greater in the spoil soil than either the pit or control soil. Carbon was least in the pit  
264 compared to either spoil or control soil (Fig. 1d). Soil location significantly influenced conductivity,  
265 potassium and carbon, with models including foraging pit location having substantially smaller AICc  
266 values than the null models (Fig. 1). Although there was a trend for higher levels of phosphorus and  
267 sulphur in the spoil compared to pit soil (based on 95% CI; Fig. 1b and 1e), the AICc, models  
268 including location had very little support, indicating that differences were not strong. The pH level  
269 (both CaCl<sub>2</sub> and H<sub>2</sub>O) did not vary among the foraging pit locations, and is not considered in any  
270 further analyses (not shown on Fig. 1).

271

#### 272 *Soil microbial activity*

273 There was more microbial activity in the spoil and control soil, indicating the pit soil was  
274 comparatively sterile, and soil microbial activity, indicated by hydrolysed FDA (Fig. 1f), showed  
275 strong support for the inclusion of soil location in a model.

276

#### 277 *Plant growth and colonisation of arbuscular mycorrhizal fungi*

278 There was no difference in the number of seedlings that germinated among foraging pit locations at  
279 seven weeks post-sowing in pots in the glasshouse trial (location mean seedlings  $\pm$ 95% CI; Pit =  $7.8 \pm$   
280  $1.1$ ; Spoil =  $7.8 \pm 0.7$ ; Control =  $7.5 \pm 0.8$ ). Location along the foraging pit had a strong influence on  
281 seedling growth over time with seedlings grown in the spoil soil taller than seedlings grown in pit or  
282 control soil (location model AICc: 2778.3 versus null model AICc: 2815.3; Fig. 2). Seedlings in the  
283 spoil soil were already slightly taller than seedlings in the pit soil at the first measurement (49 days  
284 since sowing) and by the third measurement (62 days since sowing) differences in the heights of  
285 seedlings among foraging pit locations were distinct (Fig. 2). Seedlings grown in the spoil soil grew  
286 more rapidly than seedlings grown in either the pit (2.8 times faster) or control (~2 times faster) soils  
287 (Fig. 3b), especially in the first 40 days of measurements (Fig. 2). At the time of harvest (142 days  
288 since seeding), seedlings from the spoil soil were double the height of pit seedlings and 1.5 times  
289 taller than the control seedlings (Fig. 3a). At harvest, seedlings grown in the spoil soil had the greatest

290 shoot biomass (4 times heavier than seedlings from the pit; Fig 3c), stem width (Fig. 3d) and root  
291 biomass (3.5 times heavier than seedlings from the pit; Fig. 3e). By contrast, seedlings grown in the  
292 pit soil were consistently the shortest seedlings (Fig. 2 & 3). Seedlings in the pit soil had the  
293 narrowest stems (Fig. 3d) and smallest shoot biomass (Fig. 3c), while their root biomass was not  
294 different to the seedlings grown in the control soil (Fig. 3e). The seedlings grown in the pit soil,  
295 despite being typically the smallest seedlings observed, exhibited the greatest proportion of AM  
296 colonization (4 times greater than for seedlings from the pit; Fig. 3f).

297

### 298 *Predictors of seedling growth*

299 Potassium, phosphorus, FDA and electrical conductivity were the strongest predictor variables for the  
300 six seedlings response variables examined (Fig. 4). For each seedling response variable there was  
301 only one preferred model (all other models had  $\Delta AICc > 2$ ), with each model for the seedling  
302 response variable containing two predictor variables (Table 1). Seedling final height, stem width and  
303 root biomass were positively correlated with the amount of potassium in soil samples. Maximum  
304 growth per day and shoot biomass of seedlings was positively correlated with the amount of electrical  
305 conductivity of the soil (Table 1; Fig. 4; Figure S1 in Supporting Information). The percentage  
306 colonisation of AM was negatively influenced by the amount of phosphorus in the soil (Table 1; Fig.  
307 4; Fig. S1). All seedling response variables were correlated with FDA readings, with bigger seedlings  
308 tending to have greater levels of FDA (Table 1; Fig. 4; Fig S1).

### 309 **Discussion**

310 We have demonstrated that foraging activities of quenda alter soil properties, including nutrient  
311 concentrations and microbial activity, which facilitates greater plant growth of young seedlings. The  
312 differences in soil properties were most evident in spoil soils (the soil ejected from the foraging pits)  
313 where the subsequent growth of seedlings was 1.5–2 times greater than seedlings grown in control  
314 (undisturbed) or foraging pit soils. Seedling growth response variables were best predicted by greater  
315 amounts of microbial activity and some soil nutrients (potassium and electrical conductivity), which  
316 were often greatest in the spoil soils. While it has been demonstrated that quenda foraging alters the

317 heterogeneity of soil properties at micro-scales, such as increasing water infiltration and decreasing  
318 hydrophobicity (Valentine *et al.* 2017), our current results illustrate that digging activities of quenda  
319 also significantly increases native plant growth.

320

321 Soil disturbance by animals that dig or burrow can have a great impact on soil chemical properties,  
322 (Platt *et al.* 2016; Yu *et al.* 2017), with most studies comparing soil from burrows or mounds with  
323 nearby undisturbed soil (Coggan, Hayward & Gibb 2018). Far fewer studies examine the more  
324 ephemeral foraging pits, although in Australia there has been some research in this field (e.g.  
325 Garkaklis, Bradley & Wooller 2003; James, Eldridge & Hill 2009; Travers *et al.* 2012). Our study is  
326 the first to compare soil nutrients at different locations along the foraging pit profile and our findings  
327 clearly show that digging animals are creating significant nutrient patchiness at a micro-site scale.

328

329 Our study demonstrated that the spoil soil of quenda foraging had greater levels of electrical  
330 conductivity and potassium than either the undisturbed soil or the pit themselves. Similarly, the  
331 burrow spoils of wedge-tailed shearwaters (*Puffinus pacificus*) were greater in electrical conductivity  
332 than soil from the bird colonies or surrounding undisturbed vegetation mounds (Bancroft, Garkaklis &  
333 Roberts 2005). Although not an active dig, hip holes created by Australian kangaroos (*Macropus*  
334 spp.) while they rest, have greater electrical conductivity, which decreases with distance from the hip  
335 hole (Eldridge & Rath 2002). Very little is known about how electrical conductivity affects tree  
336 species, although seedlings seem sensitive to small changes (Allen, Chambers & Stine 1994). Growth  
337 of container-grown seedlings of *Pinus resinosa* from north-eastern North America was greatest at  
338 electrical conductivity between 1.8-2.2 dS/m; followed by toxicity at 2.5 dS/m (Timmer & Parton  
339 1984). The ancient, low-nutrient soil of south-western Australia typically has low levels of electrical  
340 conductivity (Henderson & Johnson 2016), and small changes in these amounts, such as those  
341 observed in this paper (e.g. control soil = 0.16 dS/m *c.f.* spoil soil = 0.22 dS/m), may facilitate  
342 seedling growth in the early establishment phase.

343

344 In our study, potassium was one of the best predictors of seedling growth. Changes in soil potassium  
345 levels have been observed in the burrows created by many digging animals (see Platt *et al.* 2016 for  
346 review), although there is little consistency in the direction of change. For example, burrows created  
347 by badgers and foxes had more potassium (Kurek, Kapusta & Holeksa 2014) whilst mounds of pocket  
348 gophers (*T. talpoides*) had less potassium than undisturbed surface soil (Mielke 1977). In contrast,  
349 potassium quantities at foraging pits created by woylies were similar to undisturbed soil (Garkaklis,  
350 Bradley & Wooller 2003), and the intensity of digging by plateau pika (*Ochotona curzoniae*) did not  
351 modify potassium levels (Yu *et al.* 2017). Potassium plays a key role in plant growth and  
352 development through the movement of water, nutrients and carbohydrates in plant tissue (Marschner  
353 1995). Potassium is considered to be an essential nutrient that can significantly ameliorate plant  
354 abiotic stress (Marschner 1995); and previous studies have associated greater levels of potassium with  
355 increases in tree growth, wood production, leaf gas exchange, stomatal sensitivity to water deficit, and  
356 water use efficiency (Battie-Laclau *et al.* 2016). The addition of potassium to soil can also result in a  
357 positive effect on the growth of tropical forest seedlings (Santiago *et al.* 2011), while potassium  
358 deficiency can result in reduced plant growth (Marschner 1995). Our research is one of the first  
359 studies that demonstrate a clear relationship between animal foraging activities, changes in nutrient  
360 levels and subsequent plant growth. Given that potassium is highly mobile and readily leached in  
361 soils, for the nutrient deficient soils of south-western Australia (McArthur & Bettenay 1960;  
362 Henderson & Johnson 2016), even small increases in potassium (such as those created in the wake of  
363 quenda digging activities) could make a difference to early seedling development.

364

365 Microbial activity (FDA) was significantly less in pit soil than for spoil and control soil. The depth of  
366 the foraging pit may contribute towards this observation, as microbial activity declines with  
367 increasing soil depth (Taylor *et al.* 2002). Quenda digs at Yalgorup National Park have a depth of ~  
368 70 mm (range 35 - 135 mm; Valentine *et al.* 2013). Consequently, the bottom of the pit (where pit soil  
369 was sampled) may have been below the level of high microbial activity. Previous research has  
370 indicated that burrowing by invertebrates (e.g. earthworms, Aira *et al.* 2010) can also increase FDA  
371 levels, but, this is the first study to show an increase in FDA through the digging actions of mammals.

372 Further research examining the influence of digging on the composition and function of microbial  
373 communities and how they impact seedling germination and establishment, would be valuable.

374

375 Mycorrhizal mutualisms are particularly important for plant growth; specifically, these fungi increase  
376 the ability of plants to take up phosphorus, nitrogen and micronutrients, and are a defence against  
377 plant pathogens (see review by Smith & Smith 2011). We found that AM colonisation was greater in  
378 seedlings grown in the pit soil, and that low levels of soil phosphorus were a predictor of high AM  
379 colonisation. Phosphorus is an important nutrient for plant growth, but can be challenging for plants to  
380 take up; AM fungi-plant mutualisms are an effective pathway for plants to acquire phosphorus, which  
381 can assist in root growth (Smith *et al.* 2011). The seedlings grown in the pit soil had ~one third of the  
382 root biomass compared to seedlings grown in the spoil heap, and it is possible that this greater root  
383 biomass reduced the ratio of AM root colonisation to non-colonisation (Smith & Smith 2011). In  
384 addition, it is unclear how the differences in AM colonisation of roots would affect seedling growth  
385 over longer time frames.

386

387 *Why does quenda digging facilitate seedling growth?*

388 In our study, seedling growth was substantially greater for seedlings grown in soil from the spoil heap  
389 created by quenda than either the foraging pit or adjacent undisturbed soil. Potential reasons for  
390 enhanced seedling growth may be due to reduced bulk density of soil in the spoil heaps and altered  
391 litter decomposition rates. Although we did not measure bulk density among the soil treatments,  
392 previous research has identified that spoil heaps created by digging animals often have lower bulk  
393 density than undisturbed soils (reviewed in Platt *et al.* 2016). In manipulative experiments, lower soil  
394 bulk density positively affected many growth parameters of Scots pine (*Pinus sylvestris*) and  
395 European beech (*Fagus sylvatica*) seedlings (Kormanek, Banach & Sowa 2015). In addition to the  
396 potential changes in soil density, we propose that foraging by quenda created an environment  
397 conducive for litter decomposition in the spoil heap that subsequently returned nutrients to the soil,  
398 making them available for plant up-take and therefore facilitating seedling growth. The facilitation of  
399 seedling growth by animal digging activities has previously been demonstrated with Australian grass

400 seedlings (*Dactyloctenium radulans*) grown in 18-month old echidna foraging pits and undisturbed  
401 surface soil in a glasshouse experiment (Travers *et al.* 2012). Seedlings grown in the echidna  
402 foraging pit soils had greater biomass, greater proportional reproductive effort and growth rate than  
403 those growing on surface soils.

404

405 Litter decomposition is a major determinant of nutrient cycles for many terrestrial ecosystems, with  
406 decomposition returning nutrients (including potassium) captured in plant material to the soil (Aerts  
407 1997). Decomposition rates are influenced by climate, litter chemistry (Aerts 1997), soil microbial  
408 and fungal communities (Beare *et al.* 1992) as well as litter position (above vs below ground) and  
409 microhabitat characteristics (Austin, Araujo & Leva 2009). Buried litter decomposes faster than  
410 surface litter (Austin, Araujo & Leva 2009), potentially due to the increased exposure to microbial  
411 and fungal communities (Beare *et al.* 1992), with microbial communities varying in association with  
412 animal foraging activities (Eldridge *et al.* 2016).

413

414 Even though we collected the soil, and sampled the nutrients, when the foraging pits were still  
415 relatively fresh (within ~2 months of creation), the greater levels in the spoil soil we observed is likely  
416 to have occurred due to greater rates of litter decomposition (with the spoil heap containing surface  
417 litter that was buried by the spoil heap). During the glasshouse trial, the litter in the spoil soil may  
418 have continued to decompose (especially given the constant supply of water), adding nutrients to the  
419 soil, and potentially accounting for the relatively steep growth rate of seedlings grown in the spoil  
420 heaps within 2 – 3 months since seeding (Fig. 1). In contrast, the pit had captured very little litter and  
421 had low levels of microbial activity potentially explaining the slow seedling development. In the  
422 field, we have observed the spoil heap partially degraded into the pit, and the foraging pits of digging  
423 mammals often becomes a reservoir that collects litter (and seeds) over time (James, Eldridge &  
424 Moseby 2010). The combination of increased nutrients, reduced soil bulk density and greater water  
425 infiltration (Valentine *et al.* 2017) provide important sites for seedling germination, establishment and  
426 growth.

427



428 **Conclusions**

429 The micro-scale disturbances created by digging mammals may be incredibly important for ecosystem  
430 functioning, facilitating changes in soil nutrients, microbial activity and plant growth. Our study  
431 clearly shows that foraging by quenda can alter soil nutrient and microbial activity that subsequently  
432 influences plant growth. Of concern in Australian ecosystems, is that the vast majority of digging  
433 mammals are threatened (Fleming *et al.* 2014) and many landscapes no longer contain these  
434 ecosystem engineers, or if they do, the animals are in substantially reduced numbers. The loss of  
435 digging mammals goes hand-in-hand with the loss of their functional role in maintaining landscapes.  
436 Consequently, our understanding of the biotic and abiotic ecological interactions of Australian  
437 landscapes may be impoverished by not accounting for their presence. Further research is needed to  
438 understand the role of digging mammals in landscapes, as well as whether the return of such species  
439 may aid, or hinder, landscape restoration processes.

440

441 **Authors' Contributions**

442 LV and KR conceived the ideas and designed methodology; LV, KR and RF collected the data; LV  
443 and RF analysed the data; LV and KR led the writing of the manuscript with contributions from GH,  
444 RH, RF and PF. All authors contributed critically to the drafts and gave final approval for publication.

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#### 456 **Data Accessibility**

457 Raw data used in this research article are accessible via the University of Western Australia Research  
458 Repository: <https://doi.org/10.4225/23/5b16364fb037e>.

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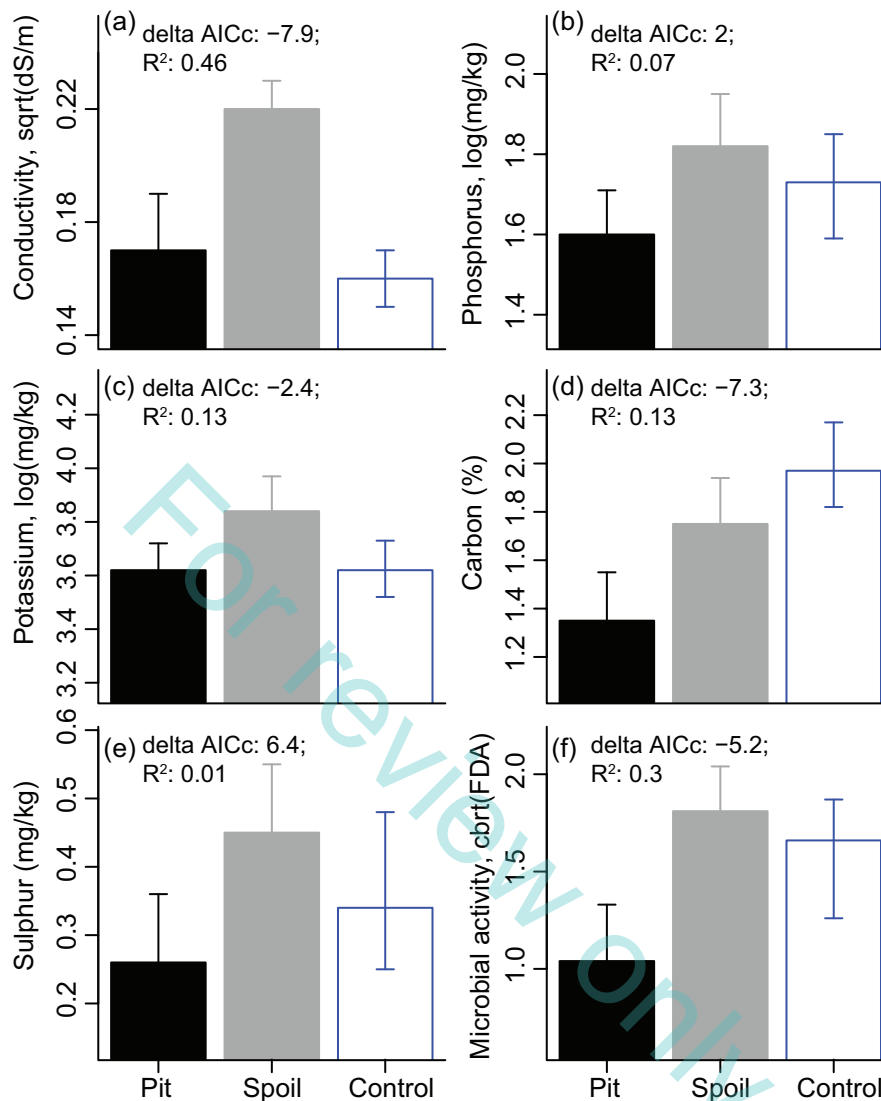
#### 624 **Supporting Information**

625 Additional supporting information may be found in the online version of this article.

626 Figure S1. GAMM fits for the top-ranking models for seedling response variables with predictor  
627 variables for seedlings grown in soil collected from different locations of a quenda (*Isoodon*  
628 *fusciventer*) foraging pit.

629



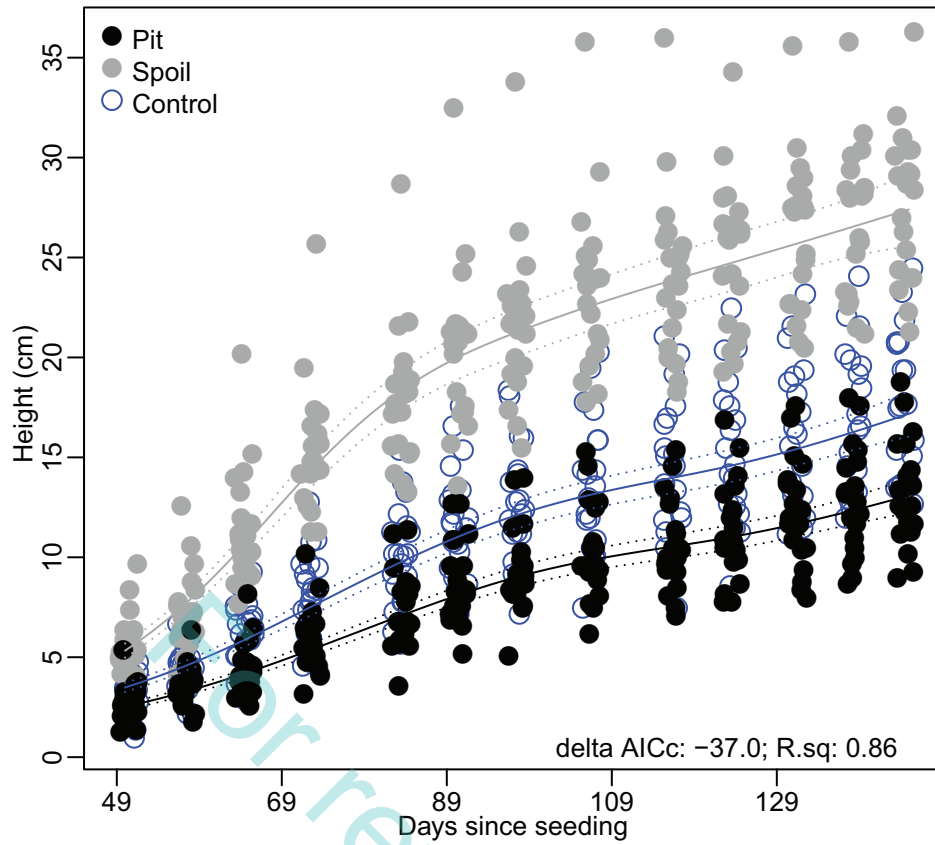


631

632 Fig 1. Conductivity (dS/m), nutrient levels (mg/kg) and microbial activity (FDA) of soil collected  
 633 from different locations of a foraging pit created by quenda (*Isoodon fusciventer*). Means ( $\pm 95\%$   
 634 Credible Intervals, based on estimated Bayesian posterior parameter estimates) are plotted. Delta  
 635 AICc and R.sq values show the difference in AICc and  $R^2$  values between GLMMs based on location  
 636 and null models respectively (e.g. location model AICc – null model AICc). Negative delta AICc  
 637 values indicate that the model containing location was a better fit than the null model (i.e. the AICc  
 638 value of the location model was less than the AICc of the null model).

639

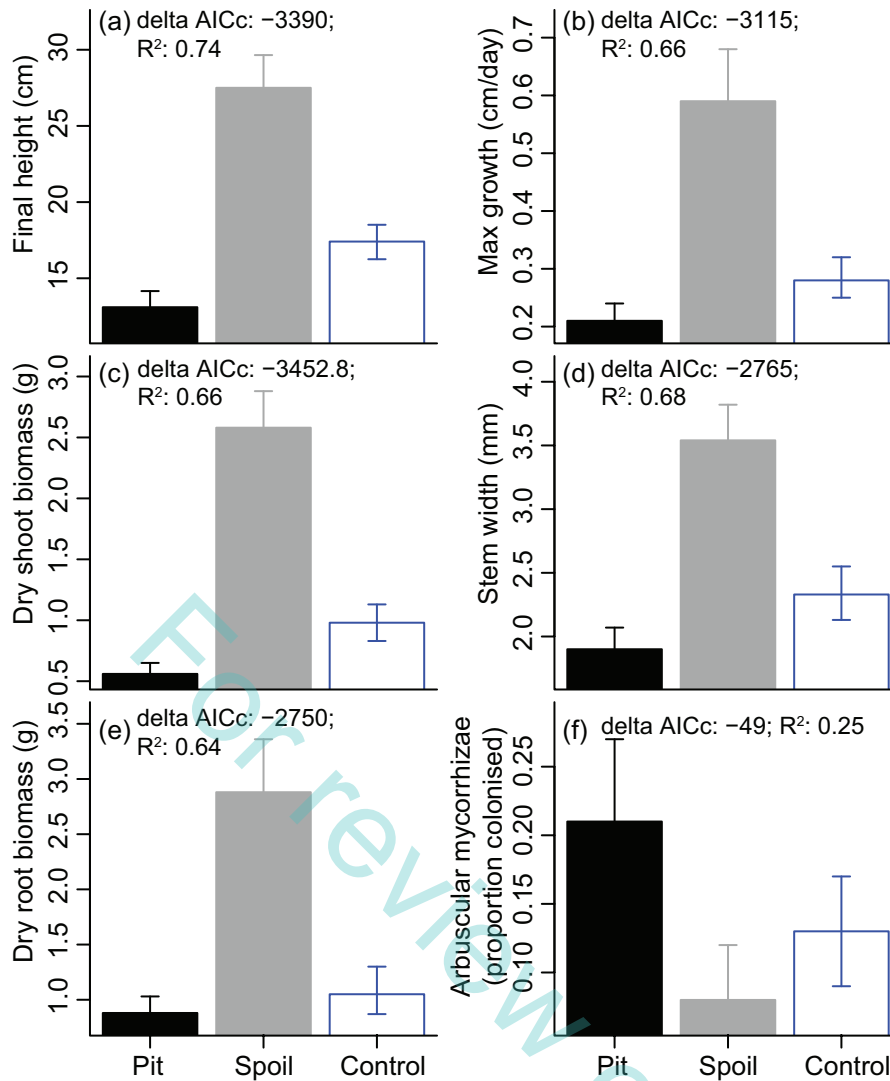
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641

642 Fig. 2. Growth of seedlings over time grown in soil collected from different locations of a foraging pit  
 643 (pit, spoil and control) created by quenda (*Isoodon fusciventer*). Solid lines show GAMM fits for  
 644 each treatment, dotted lines indicate estimated 95% Confidence Limits.

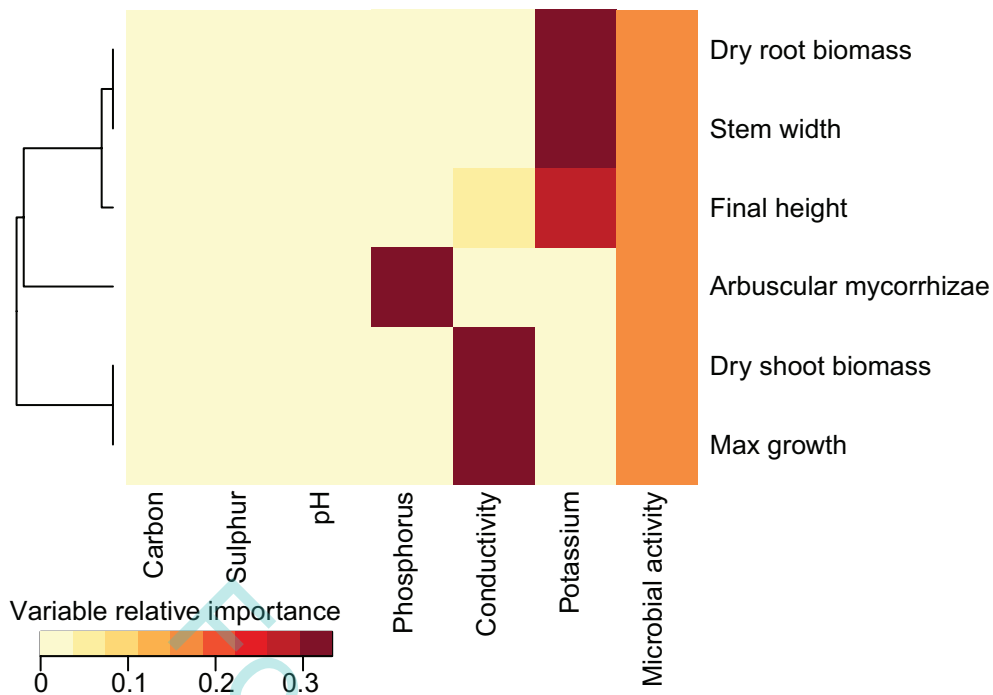
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646

647 Fig. 3. Seedling response variables and proportion of arbuscular mycorrhizal (AM) fungi colonisation  
 648 on roots from seedlings grown in soil collected from different locations of a foraging pit created by  
 649 quenda (*Isoodon fusciventer*). Plotted are means ( $\pm 95\%$  Credible Intervals, based on estimated  
 650 Bayesian posterior parameter estimates). Delta AICc and R.sq values show the difference in AICc  
 651 and R<sup>2</sup> values between GLMMs based on location and null models respectively (e.g. location model  
 652 AICc – null model AICc). Negative delta AICc values indicate that the model containing location was  
 653 a better fit than the null model (i.e. the AICc value of the location model was less than the AICc of the  
 654 null model).

655



656

657 Fig. 4. Heat-map indicating the relative importance (summed AICc weights/number of models) of  
 658 each predictor variable (FDA, potassium, electrical conductivity, phosphorus, pH, sulphur and  
 659 carbon) in contributing towards each seedling response variables (maximum growth, shoot biomass,  
 660 AM colonisation, final height, stem width and root biomass) of seedlings grown in soil from different  
 661 locations of a foraging pit created by quenda (*Isoodon fusciventer*). Dendrogram shows a Euclidian  
 662 hierarchical cluster analysis (complete linkage) of the seedling response variables based on the  
 663 relative importance of the different predictor variables.

664

665 **Tables**

666 Table 1. Top-ranking generalised additive mixed models (GAMM) for seedling response variables  
 667 with soil nutrients and microbial activity predictor variables from seedlings grown in soil collected  
 668 from different locations along the foraging pit profile created by the quenda (*Isoodon fusciventer*).  
 669 Models included are the top-ranking model (i.e.  $\Delta\text{AICc} = 0$ ) for each response variable.

Response variable	Model	df	Adjusted- R <sup>2</sup>	AICc weight
Final height (mm)	Potassium + microbial activity	8.74	0.26	0.88
Max. growth (mm/day)	Conductivity + microbial activity	8.38	0.41	1
Shoot biomass (g)	Conductivity + microbial activity	8.07	0.24	1
Stem width (mm)	Potassium + microbial activity	8.45	0.19	1
Root biomass (g)	Potassium + microbial activity	8.07	0.15	1
Arbuscular mycorrhizae (proportion colonised)	Phosphorus + microbial activity	4.58	0.18	0.92

670

671