

1 Journeying towards best practice data management 2 in biodiversity genomics

3 Running title

4 Biodiversity genomic data management

5 Authors

6 Natalie J. Forsdick*^{1,2}, Jana Wold*^{3,2}, Anton Angelo⁴, François Bissey⁵, Jamie Hart⁵, Mitchell
7 Head⁶, Libby Liggins^{7,2}, Dinindu Senanayake⁸, Tammy E. Steeves^{3,2}

8 Affiliations

9 1 Manaaki Whenua – Landcare Research, Auckland, New Zealand

10 2 Genomics Aotearoa, New Zealand

11 3 School of Biological Sciences, University of Canterbury, Christchurch, New Zealand

12 4 Library, University of Canterbury, Christchurch, New Zealand

13 5 Digital Services, University of Canterbury, Christchurch, New Zealand

14 6 Te Kotahi Research Institute, University of Waikato, Hamilton, New Zealand

15 7 School of Natural Sciences, Massey University, Auckland, New Zealand

16 8 New Zealand eScience Infrastructure, Auckland, New Zealand

17 * Co-first authors.

18 Corresponding author

19 NJF: forsdickn@landcareresearch.co.nz

20 Key words

21 CARE Principles for Indigenous Data Governance; data life cycle; data management plans;
22 digital sequence information; FAIR Guiding Principles; Indigenous data sovereignty

23 **Abstract**

24 Advances in sequencing technologies and declining costs are increasing the accessibility of
25 large-scale biodiversity genomic data sets. To maximise the impact of these data, a careful,

26 considered approach to data management is essential. However, challenges associated with the
27 management of such data sets remain, exacerbated by uncertainty among the research
28 community as to what constitutes best practices. As an interdisciplinary team with diverse data
29 management experience, we recognise the growing need for guidance on comprehensive data
30 management practices that minimise the risks of data loss, maximise efficiency for stand-alone
31 projects, enhance opportunities for data reuse, facilitate Indigenous data sovereignty and uphold
32 the FAIR and CARE Guiding Principles. Here, we describe four personas reflecting user
33 experiences with data management to identify data management challenges across the
34 biodiversity genomics research ecosystem. We then use these personas to demonstrate realistic
35 considerations, compromises, and actions for biodiversity genomic data management. We also
36 launch the Biodiversity Genomics Data Management Hub
37 (<https://genomicsaotearoa.github.io/data-management-resources/>), containing tips, tricks and
38 resources to support biodiversity genomics researchers, especially those new to data
39 management, in adopting best practice. We aim to support the biodiversity genomics community
40 in embedding data management throughout the research life cycle to maximise research
41 impacts and outcomes.

42 1. Introduction

43 The field of biodiversity genomics has undergone a fast-paced transformation over the last
44 decade. Once largely inaccessible for non-model organisms, advances in sequencing
45 technology have substantially reduced costs associated with generating these data, leading to
46 significant increases in the types and volumes of genomic data. Today, biodiversity genomics is
47 a highly dynamic research field that integrates methods pioneered in human health (e.g.,
48 genome-wide association studies; Ozaki et al., 2002), agricultural breeding programmes (e.g.,
49 inbreeding coefficients; Wright 1922), and principles from molecular ecology and evolution (e.g.,
50 identifying the genomic consequences of small population size; Duntsch et al. 2021; Khan et al.
51 2021; Liu et al. 2021; Robledo-Ruiz et al. 2022). The proliferation of data is being used to
52 address an ever-expanding array of research questions and is a challenge for existing data
53 management systems and research community practices.

54 To maximise the short- and long-term impacts of biodiversity genomic data, a considered and
55 careful approach to data management is essential. Good data management practices (see Box
56 1) can benefit research teams and institutions, the research community, and wider society when
57 biodiversity genomics data is used to address contemporary socio-environmental challenges.
58 For research teams, the positive impacts of data management can be particularly pronounced
59 for large and long-term projects where there is regular turnover of members and/or research
60 roles are highly partitioned. Effective data management benefits research groups through
61 ensuring efficient resource use (e.g., time, computational, financial), risk mitigation (e.g., data
62 loss, misinterpretation, misuse), signalling credibility through data reproducibility (Baker, 2016;
63 Eisner, 2018), and ease of data-sharing for enhanced collaboration (Lau et al., 2017; Möller et
64 al., 2017; Riginos et al., 2020). For research institutes and/or funding organisations there may

65 be legal obligations and long-term responsibilities (including social licence requirements) for
66 them as custodians to maintain the integrity of research data. These information-rich biodiversity
67 data sets have immense reuse value that can only be realised if the data-generating
68 researchers/institutions undertake careful data management (Toczydlowski et al., 2021). These
69 secondary use cases may diverge from the original purpose of data generation (Hoban et al.,
70 2022; Leigh et al., 2021), and can provide additional valuable insights (e.g., Crandall et al.,
71 2019), enhancing the value of these data to the research community and their potential impacts
72 on society (e.g., Beninde et al., 2022; Exposito-Alonso et al., 2022).

Box 1. Best practices vs good practices

Here we recognise there are different standards of data management. We acknowledge that achieving best practices is aspirational, and may not always be practicable within the constraints of a research project due to external factors (see section 2. *Exploring biodiversity genomic data management challenges*). Instead, we encourage researchers to pursue ‘good practices’ as part of their efforts to adopt best practices.

Despite the availability of data management knowledge and resources, we acknowledge (and have lived experience with) the array of challenges that exist within the institutional frameworks in which we operate. These challenges may restrict the ability of research groups to adhere to best practices we describe. For example, the prevalence of short-term research contracts, combined with a ‘publish or perish’ mindset, may result in the deprioritisation of data management for some researchers. Nonetheless, even incremental improvements to data management by individuals, within their own capacity, should be encouraged and supported.

73

74 The incentives to implement data management practices are clear, and although conceptual
75 guidance on best practices exists within the broader scientific community (e.g., the FAIR Guiding
76 Principles for scientific data management and stewardship, Wilkinson et al., 2016; and the
77 CARE Principles for Indigenous data governance, Carroll et al., 2020, 2021), implementation
78 remains challenging (Box 2). Contributing factors include the sheer volume of these information-
79 rich data sets and the associated resource requirements (i.e., the time and financial costs of
80 data curation, maintenance, and processing (Batley & Edwards, 2009; Chiang et al., 2011;

81 Grigoriev et al., 2012; Schadt et al., 2010), as well as the inability of existing data standards,
82 infrastructures, and repositories to keep pace with the needs of this research community (e.g.,
83 Crandall et al., 2023; Liggins et al., 2021). Best practices for biodiversity genomic data
84 management are an active area of discussion among the biodiversity genomics community
85 (Anderson & Hudson, 2020; Fadlelmola et al., 2021; Field et al., 2008; Liggins et al., 2021;
86 Yilmaz et al., 2011). However, these initiatives can be easily missed by biodiversity genomics
87 researchers because they are often disseminated as discipline-specific outputs (e.g.,
88 publications, conference presentations, blogs) or institution-specific internal documents. Thus,
89 there are opportunities to centralise these existing resources. There are also benefits for
90 research teams in extending their networks beyond the biodiversity genomics community to
91 leverage the wealth of knowledge available across disciplines and institutes.

92 By necessity, biodiversity genomics brings together diverse teams with broad interests. We are a
93 cross-institutional, interdisciplinary, multi-career stage collaborative team based in Aotearoa
94 New Zealand, including biodiversity genomics researchers (NJF, JW, LL, TES), institutional and
95 national eResearch and libraries staff (AA, FB, JH, DS), and those with broad interests in the
96 inclusion of Indigenous perspectives pertaining to biodiversity genomic data (NJF, JW, MH, LL,
97 TES). Our extensive experience includes: overseeing biodiversity genomic research projects,
98 curating and managing biodiversity genomic data sets, developing project-specific data
99 management plans (DMPs), and providing data management solutions to research groups. We
100 have lived experience with the caveats of applying data management theory to real-life research
101 situations.

102 Through this contribution we aim to provide support to biodiversity genomics researchers in
103 incorporating data management within their daily research practices by:

- 104 ● describing typical data management experiences of individuals across the research
105 ecosystem
 - 106 ● presenting ‘tips and tricks’ for documenting and managing genomic data sets and
107 suggesting simple tools to support researchers in adhering to the FAIR and CARE
108 Guiding Principles
 - 109 ● collating resources such as templates and workflows for data management that can be
110 readily adopted and/or adapted for wide usage in biodiversity genomics projects in the
111 Biodiversity Genomics Data Management Hub ([https://genomicsaotearoa.github.io/data-](https://genomicsaotearoa.github.io/data-management-resources/)
112 [management-resources/](https://genomicsaotearoa.github.io/data-management-resources/)).
- 113 We encourage researchers to view data management practices as behaviours intrinsic to the
114 research process, and to adopt a mindset of adaptability to the various hurdles that may be
115 encountered along the way. Through sharing these perspectives, we hope to support emerging
116 researchers and the biodiversity genomics community more broadly on their data management
117 journeys, and ultimately to amplify the real-world impacts of biodiversity genomics research. Our
118 Glossary defines and explains key terms and concepts used here.

Box 2. Ethical considerations for biodiversity genomic data management

The potential for data misuse (e.g., cherry-picking, data theft, unpermitted use, sharing, or misappropriation) is ever-present throughout the data life cycle (Cragin et al., 2010). Data misuse is harmful to the integrity of the research, science, and innovation sector, and has important social implications due in part to an erosion of public trust in science (Laurie et al., 2014). Misuse can have direct negative impacts for participants, communities, research partners, and end-users. This harm can further extend to the research group, collaborators, and their institutes in the form of serious legal implications, reputational risk, and negative impacts on career trajectories. There are clear ethical processes for other aspects of research (such as regulatory bodies for human and animal ethics) but such ethical frameworks may not yet be established for the generation and storage of biodiversity genomic data (especially eDNA, plants, invertebrates, fungi). Data management is a tool researchers can use to mitigate this risk and some institutes and communities are well versed in defining and implementing consistent and effective data management practices. We recognise that there remain gaps between knowing and doing, with different groups positioned at different points on their data management journeys. However, good data management minimises the risks of data misuse, loss, or theft, improves transparency, and ensures data FAIRness within established parameters specific to those data.

It also seeks to find balance between 'Open Data' and 'Accessible Data', the latter of which may be more appropriate for data pertaining to species and locations significant to Indigenous Peoples (e.g., Henson et al., 2021; Rayne et al., 2022). To facilitate Indigenous data sovereignty, data should be accompanied by metadata that includes details of appropriate

permissions, which may include access restrictions. Local Contexts Notices, including Traditional Knowledge and Biocultural Labels, offer one such framework to support this (Anderson & Hudson 2020; Liggins et al., 2021).

119

120 2. Exploring biodiversity genomic data management 121 challenges

122 In this section we present user experience personas to describe data management needs for
123 individuals in different career stages and roles. Using these personas, we aim to highlight some
124 of the many important considerations associated with genomic data management. While we
125 acknowledge that real life is not typically this tidy, we hope that researchers may see their own
126 experiences reflected through some combination of these personas. The layers of challenges
127 experienced by researchers may include the growing volume and types of genomic data and
128 metadata, rapid technological and methodological advances, ensuring interoperability with
129 metadata, and balancing openness and Indigenous data sovereignty.

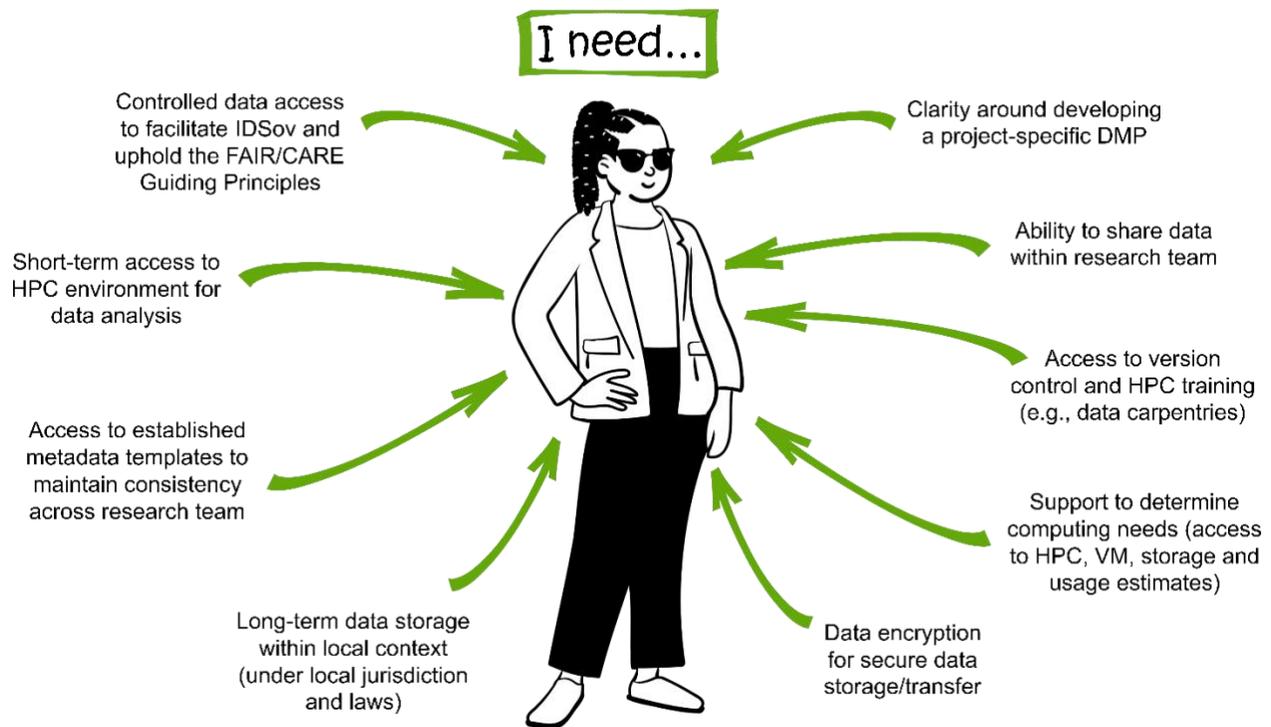
130 2.1. A student new to biodiversity genomics

131 New PhD student Taylor Smith (Figure 1) has started a research project that will generate
132 genomic data to inform conservation management for a culturally significant species (a recently
133 described species of endemic lizard). Their project involves data collection and generation,
134 analysis using the local compute infrastructure provided by their institute, and dissemination of
135 results to end users including conservation practitioners and local communities. They will be

136 operating under a DMP adapted from the template used across their research group, and they
137 have access to internal training and external support structures.

138 Their research group is in the process of developing a lab manual that includes daily data
139 management processes, along with on/offboarding procedures. Taylor is grateful for the
140 supportive research group environment, as they feel comfortable asking questions and sharing
141 thoughts to help develop these processes. While their data is yet to be generated, being
142 involved in these processes ensures they have a clear understanding of what will be involved in
143 managing their data.

144 Taylor's main concerns are ensuring their data management practices facilitate Indigenous data
145 sovereignty and uphold the FAIR and CARE Guiding Principles during the active lifespan of the
146 project. As the project has a defined end date, they also want to ensure that there is a
147 framework in place to maintain these practices into the future. Communication around data
148 management is primarily with their research group leader, Professor Nepia (Persona 3), who
149 maintains trust-based relationships with the Indigenous tribes that have strong cultural ties to the
150 focal species, and supported by the wider research team and eResearch and libraries staff.



151

152 Figure 1. Typical data management needs and concerns of emerging researchers starting their
 153 journey. Our persona, Taylor Smith, exemplifies some of these. DMP: Data Management Plan.
 154 HPC: High-performance computing. IDsov: Indigenous data sovereignty. VM: Virtual machine.

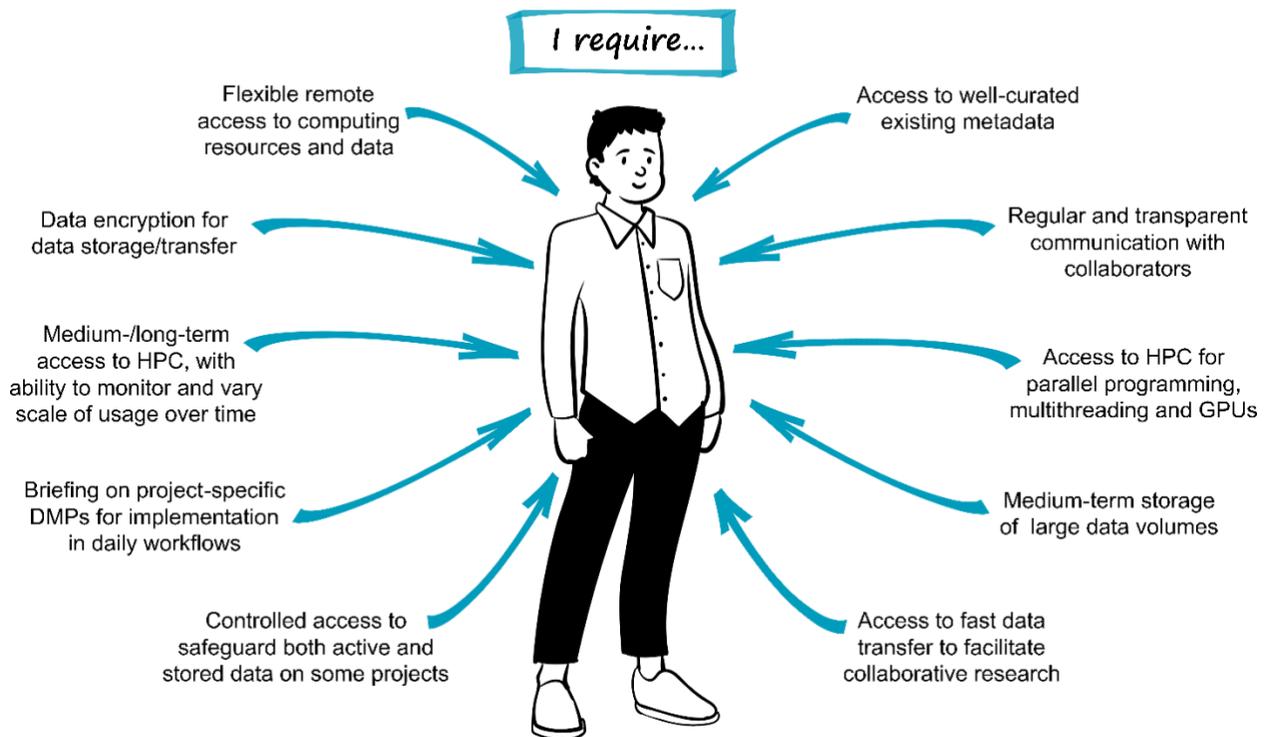
155 **Persona 2. An early career researcher working collaboratively**

156 Dr Atsushi Sato (Figure 2) is a postdoctoral researcher at a national research institute, and
 157 contributes to several large international biodiversity genomics collaborations (including with
 158 Professor Nepia, Persona 3). These projects vary in scale, longevity, and data management
 159 requirements. Each project Dr Sato is involved with has its own established DMP, so he must
 160 take care to ensure that the workflows he uses for each project align with the respective DMPs.
 161 Although he has some input into research planning and dissemination of results, his primary
 162 focus is on the analysis of large data sets, and specifically in incorporating environmental and
 163 climate data alongside genomic data. To do this, he relies on comprehensive and consistent
 164 metadata for each data set.

165 He is experienced in biodiversity genomics, and is able to clearly report his data management
166 needs to eResearch and libraries staff at his research institute. These needs predominantly
167 relate to short- or mid-term storage and access, as the long-term storage of most of the data
168 sets Dr Sato works with is the responsibility of researchers at other institutes. Dr Sato also seeks
169 support from eResearch staff that deliver the national high-performance computing (HPC)
170 infrastructure, where he can execute programs using multithreading and parallel-processing for
171 analysing these large data sets.

172 While Dr Sato's skills are in high demand, he has been persistently employed on precarious
173 short-term contracts. He finds this stressful, and is constantly looking for new opportunities that
174 may propel him towards his goal of attaining a permanent research position. These concerns
175 affect his research priorities, as he perceives trade-offs between time spent on data
176 management and that spent on data analysis that can produce results that contribute towards
177 his publication record. From Dr Sato's perspective, data management is an onerous task.

178



179

180 Figure 2. Typical data management requirements experienced by researchers in highly
 181 collaborative spaces. Our Dr Sato persona exemplifies these. DMPs: Data Management Plans.
 182 HPC: High-performance computing. GPUs: Graphics processing units, often used to accelerate
 183 data processing.

184 **Persona 3. A biodiversity genomics research team leader**

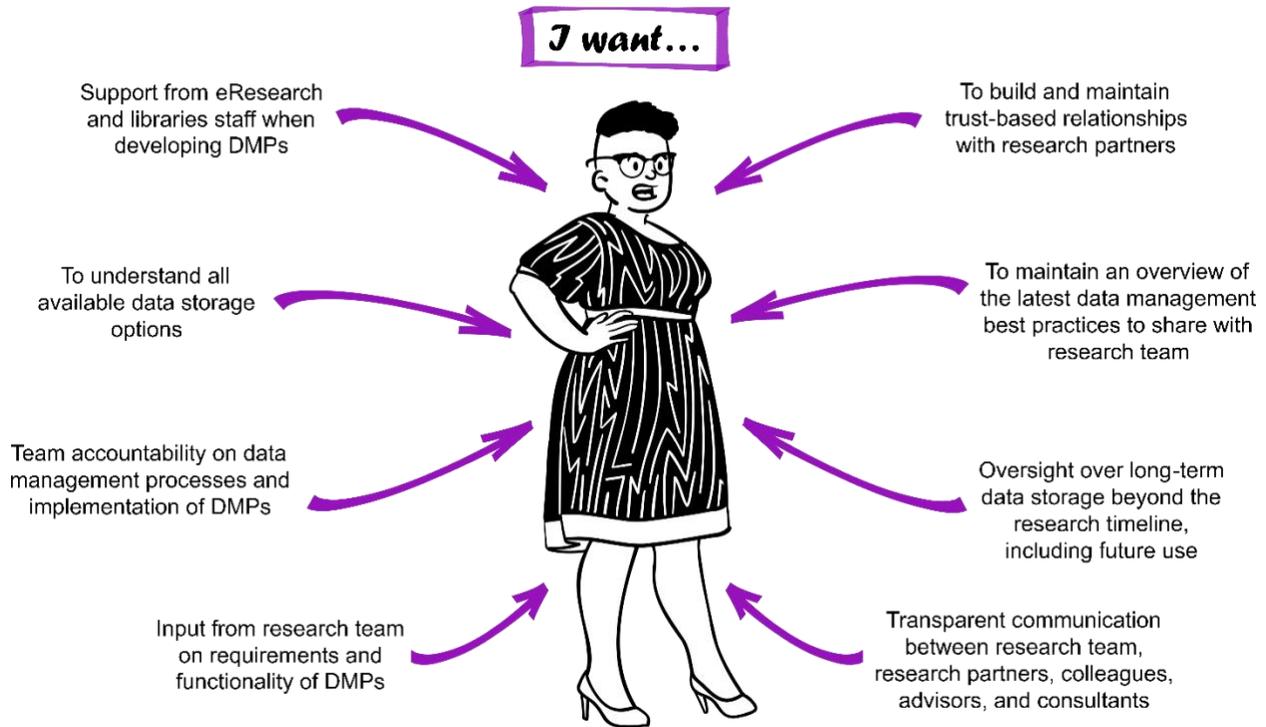
185 Professor Tehara Nepia (Figure 3) is a principal investigator at a university overseeing a
 186 conservation genomics research group including postgraduate students (including Taylor Smith,
 187 Persona 1), postdoctoral researchers, and research associates (including Dr Atsushi Sato,
 188 Persona 2). Her focus is on designing, facilitating, and disseminating research, and providing a
 189 supportive environment that produces highly-skilled emerging researchers well-equipped to
 190 contribute to the research, science, and innovation sector. Professor Nepia also places strong
 191 emphasis on building and maintaining trusted relationships with research partners, including
 192 Indigenous tribes. A substantial part of her role includes seeking and managing funding and

193 resources (including computing resources and data storage) for the research group.

194 As the volume of data generated by Professor Nepia's team is continually expanding, there is a
195 growing need to ensure a smooth transition of data (including metadata) between members of
196 her research group. While Professor Nepia has a responsibility to meet institutional
197 requirements, she is also committed to embedding data management practices that facilitate
198 Indigenous data sovereignty and uphold the FAIR and CARE Guiding Principles. She is working
199 towards a DMP template for use across all her research group's projects. To achieve this,
200 Professor Nepia encourages open two-way communication with her research group to gain their
201 perspectives on the needs and challenges associated with data management. She relies upon
202 her research group to adhere to the DMPs, to support and encourage each other to do this, and
203 to seek strategic advice from her when needed. Beyond the DMPs, Professor Nepia and her
204 group co-develop research group guidelines that include data management practices to
205 streamline group on/offboarding, allowing new members to quickly get up to speed, and
206 providing clear expectations of data management for those departing.

207 She also engages with colleagues in similar situations nationally and internationally, including
208 her disciplinary research community. Keeping abreast of evolving best practices in the
209 biodiversity genomics research community and updating the research group's DMP accordingly
210 is an added pressure on Professor Nepia's limited time; she never feels completely up to date
211 with the latest developments but understands she must be the one in the research group to lead
212 data management practices even if she is only able to support 'good' versus 'best' practice (Box
213 1). To help with this burden, Professor Nepia prioritises building strong relationships with local
214 eResearch and libraries staff (including Darryl, Persona 4) that are based on transparent, timely,
215 bi-directional communication. Through knowledge-sharing, eResearch and libraries staff help
216 her to understand local data management capacity and constraints, and to gain the necessary

217 understanding of the project-specific nuances that enable delivery of wrap-around solutions that
218 support the needs of the research group now and into the future.



219

220 Figure 3. Support and oversight desired by research project leaders developing data
221 management practices. Our Professor Nepia persona exemplifies these. DMPs: Data
222 Management Plans.

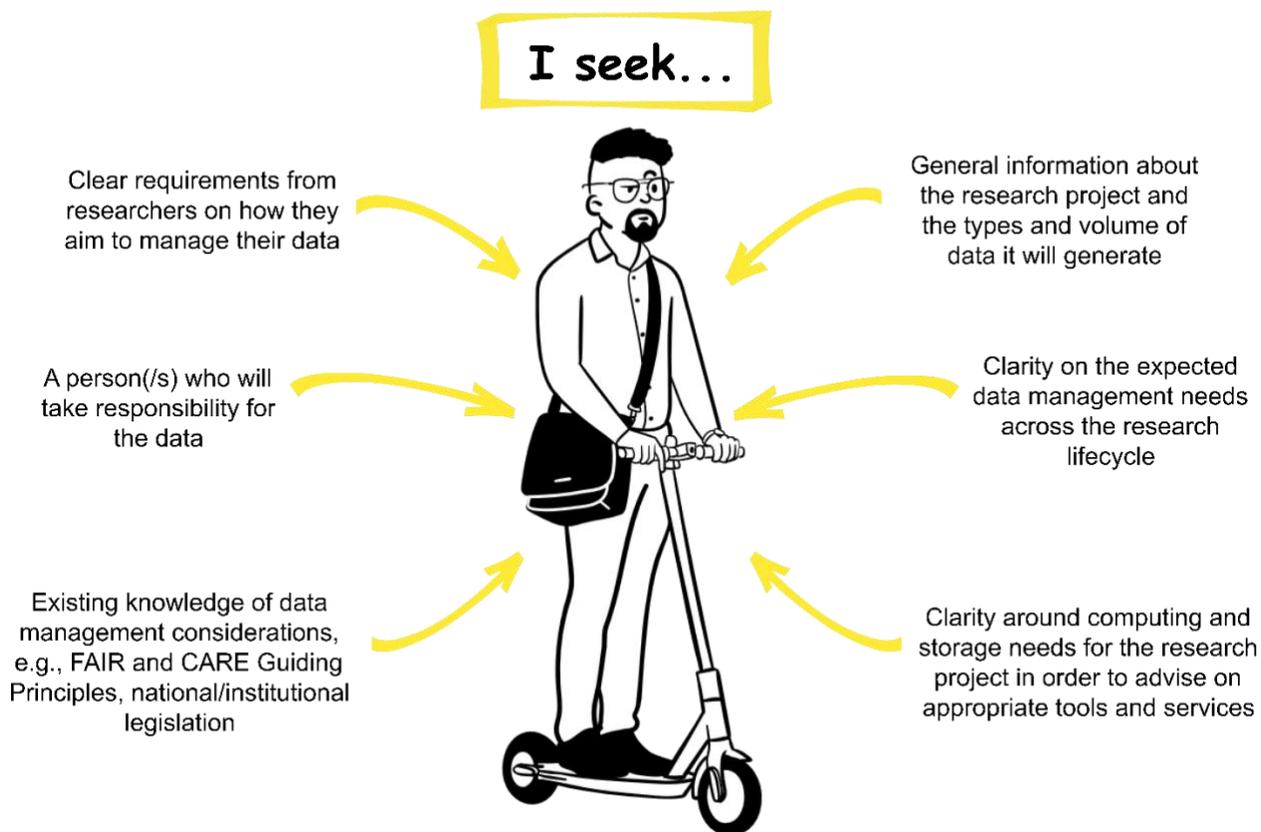
223 Persona 4. An eResearch staff member

224 Darryl Baker (Figure 4) is an eResearch Manager at a university, and provides eResearch
225 support to numerous research projects across all disciplines and departments, including
226 providing advice and services relating to compute and data storage facilities for biodiversity
227 genomic data. Darryl manages the resource that is the institutional compute and storage
228 facilities allocated to research. He keeps up to date with research-focussed technologies,
229 consults with research groups, and mentors researchers on the use of the available research

230 systems. In the last four years the storage facility of the institution has reached peak capacity,
231 requiring careful resource management. Darryl seeks budget approval to expand the current on-
232 premise storage facility. Based on quotes provided by vendors, purchasing additional storage
233 infrastructure proves to be expensive. Further, it would only provide a short-term fix as the
234 institution's research data is predicted to exceed the storage limit within five years.

235 Recently, Professor Nepia (Persona 3) contacted Darryl about eResearch services and support
236 for her biodiversity genomics research group. Professor Nepia's group generates a number of
237 projects, with rapidly increasing data management needs over the last 10 years. Darryl meets
238 with one of Professor Nepia's research students, Taylor Smith (Persona 1), to understand the
239 eResearch needs of an upcoming project about a new species of lizard. In a face-to-face
240 meeting, he gathers information about the data being produced. Early indications are that this
241 project will generate vast amounts of data and function under a DMP. Darryl wishes to
242 understand the project-specific needs in order to advise on appropriate storage and computing
243 solutions that will facilitate Indigenous data sovereignty and uphold the FAIR and CARE Guiding
244 Principles. Darryl holds a clear understanding of the constraints arising from the institutional
245 infrastructure, and the responsibilities of the researcher under national and institutional
246 legislation. Through conversations with researchers and research groups, Darryl can gain a
247 clear vision of what they are trying to achieve within these constraints, and provide advice and
248 solutions to overcome data management pain points that may arise.

249

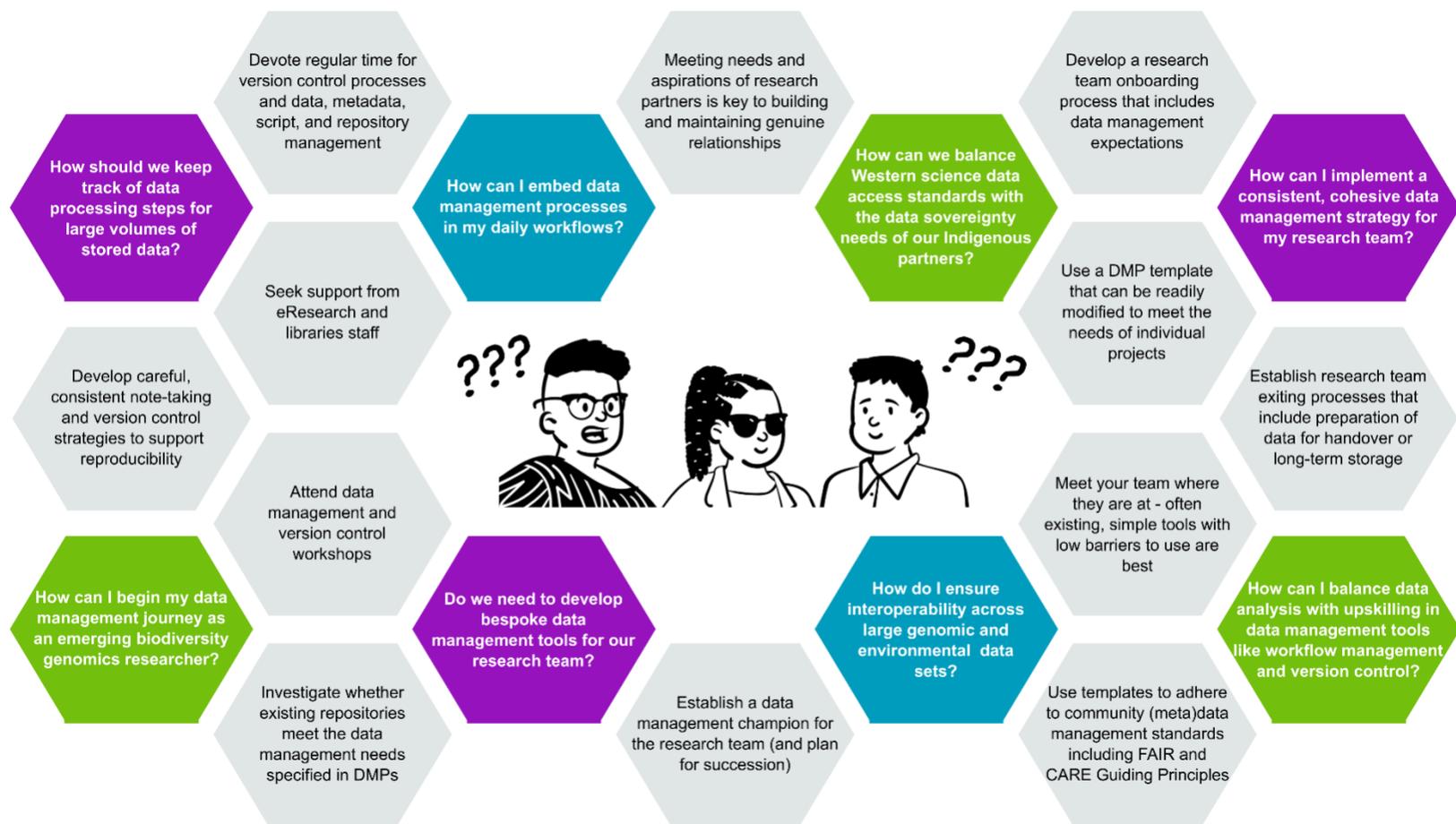


250

251 Figure 4. Typical eResearch and libraries staff needs for developing specialised data
 252 management solutions. Mr Baker's persona exemplifies meeting and delivering these needs for
 253 researchers and research groups.

254 3. Addressing the challenges

255 Following the description of these personas, we identified key data management questions that
 256 researchers across the biodiversity genomics research ecosystem may have, and propose
 257 solutions to support good data management practices (Figure 5). As every situation is different,
 258 we recognise that not all solutions will be immediately adaptable to specific challenges, but may
 259 spark ideas. Here we provide discussion of some potential solutions to these identified
 260 challenges, and supporting resources to implement effective data management practices.



262 Figure 5. Some key data management questions and solutions for biodiversity genomic researchers and teams. Potential
 263 questions (coloured hexagons) and potential (non-exhaustive) solutions (light grey hexagons) are shown. The colours of the
 264 question hexagons denote their relevance to the personas described above, though we note that different personas may share
 265 common questions, and that solutions may address multiple challenges.

266 3.1 Resources to support researchers in implementing effective data 267 management

268 To reduce the frustration often experienced by researchers on their journey towards best
269 practices in data management, we have established the Biodiversity Genomics Data
270 Management Hub (<https://genomicsaotearoa.github.io/data-management-resources/>) where we
271 connect the challenges described in the personas to modules that provide topic-specific tips,
272 tricks, and resources, including some from beyond the traditional biodiversity genomics
273 literature. Module content draws on the diversity of our experiences and knowledge, with topics
274 including: 'Hot, warm, and cold data storage', 'Data Management Plans in practice', and 'Helping
275 eResearch staff help you'. These tips and tricks are largely hard-won, through the trials and
276 tribulations experienced during our personal research journeys. We intend the Hub to be a living
277 resource that evolves over time, incorporating new tools and practices as these come to light.
278 We welcome suggestions of additional module topics, along with contributions of the latest
279 resources. We envision that the Hub will be of special interest for emerging researchers, and will
280 be useful as a teaching resource, instilling data management practices as part of daily workflows
281 from the beginning of the research journey. The Hub may also provide an opportunity for those
282 with an interest in data management outside genomics to have the opportunity to peek 'through
283 the looking glass' and gain insight into the similarities and differences with their own fields.

284 In assembling resources for the Hub to address challenges across personas, three overarching
285 actions stood out as immediately accessible steps toward best practices for the biodiversity
286 genomics community. Here, we elaborate on these.

287 3.2. Develop Data Management Plans

288 Biodiversity genomic data management tends to come into focus at the end rather than
289 throughout the research life cycle. Many journals that publish biodiversity genomic research
290 have open data policies (e.g., the Joint Data Archiving Policy; Dryad, 2020), and this may be the
291 first instance at which researchers are required to demonstrate data management. Indeed,
292 genomics broadly appears immature compared with other disciplines in terms of data
293 management. For example, DMPs are often perceived as 'nice to have' but are not yet widely
294 required. However, when working with the large volumes of data produced via genomic
295 sequencing, and/or in research teams distributed across multiple institutions, data management
296 can quickly degenerate leaving the data, researchers, and research partners vulnerable (Box 2).
297 We note that DMPs are one tool among many that will be needed to achieve the benefit-sharing
298 goals relating to genomic data as described in decisions 15/4 and 15/9 of the Kunming-Montreal
299 Global Biodiversity Framework (Convention on Biological Diversity, 2022).

300 DMPs are key tools for mitigating the risks of data loss and misuse. Where they do not already
301 exist, we anticipate a widespread shift towards the establishment of data management policies
302 within institutions and by research funding organisations (including the requirement of DMPs in
303 research funding applications) in the near future (Bloemers & Montesanti, 2020; Fadlilmola et
304 al., 2021; Jorgenson et al., 2021). The primary research funding body in Aotearoa New Zealand,
305 the Ministry of Business, Innovation and Employment, is shifting towards an open research
306 policy (MBIE 2022) as many of its contemporaries have done (e.g., the Australian Research
307 Council, the European Research Council, the National Institutes of Health), which may come to
308 include a requirement for DMPs. We foresee that some of the challenges associated with
309 requirements to provide DMPs during funding applications will lie in ensuring cohesive

310 frameworks for the development of DMPs that are fit for purpose, and more broadly in the
311 development and maintenance of trusted data repositories at scale (Lin et al. 2020).

312 The inclusion of an approval and/or compliance pathway may be recommended by international
313 funding bodies to ensure that DMPs lead to meaningful actions in the improvement of data
314 management in biodiversity genomics rather than becoming simple 'box-ticking' or thought
315 exercises. Specifically, approval pathways would require consideration of the DMP during the
316 funding application process to determine whether it is fit for purpose. In comparison, a
317 compliance pathway requires researchers to demonstrate that data management actions have
318 been carried out in accordance with the DMP provided. DMP approval and compliance with
319 regard to the FAIR Guiding Principles would require consideration by external assessment
320 panels with discipline-specific knowledge and expertise. For data and metadata associated with
321 species or locations significant to Indigenous Peoples (see Box 2), decisions around auditing
322 and assessment of DMPs in relation to the CARE Guiding Principles can only be made by the
323 associated Indigenous Peoples, so Indigenous leadership will be required in the development of
324 any such systems.

325 While compliance is one method of ensuring that data management actions are implemented,
326 research projects tend to change course over time, and a DMP designed during the planning
327 stage may not provide the flexibility required to meet changing data needs later in the research
328 life cycle. Rather than using approvals or compliance processes to ensure appropriate data
329 management actions are taken, a more appropriate approach could be to recognise a DMP as a
330 live document throughout the research process, allowing for updates as the project changes. In
331 this scenario, version control methods should be used to track changes throughout the project.
332 During any process of revision of the DMP, it will be important to maintain regular and
333 transparent communication with relevant research partners whenever changes are being

334 considered. This will ensure that changes are fit for purpose, while continuing to accommodate
335 the needs and interests of all parties. At the end of the project, the research team could
336 complete a self-reflective retrospective process, identifying which aspects went according to
337 plan, where needs changed over time, and whether there were any limitations or challenges due
338 to institutional or infrastructure constraints. This could help researchers to better understand the
339 capabilities and capacities of their teams and systems, and inform future research design that
340 includes DMP development. Feeding back the learnings derived through this retrospective to
341 associated eResearch and libraries staff will also help to close the loop.

342 3.3 Seek support from eResearch and libraries staff

343 We challenge researchers to look beyond their immediate research community for assistance –
344 help may be closer at hand than expected. Here we highlight the benefits of engaging with
345 eResearch and libraries staff within or beyond your institute from an early stage in the research
346 life cycle. These professional staff are a supporting network who hold knowledge and expertise
347 in crafting solutions to data management challenges (Andrikopoulou et al., 2022). Researchers
348 benefit from developing these relationships with staff who cultivate institutional knowledge and
349 solutions that may not be captured in the traditional or domain-specific scientific literature. In
350 addition, eResearch and libraries staff can provide guidance and targeted support in the co-
351 development of project-specific data management strategies that take into account institutional
352 operating requirements and the capacity and capability of existing infrastructure, and in
353 incorporating data management practices into day-to-day research workflows.

354 At times, eResearch and libraries staff may be overlooked as a consequence of disciplines
355 becoming siloed. This can result in researchers being unaware of how these staff can provide
356 support, and unclear as to what their mandates are; and in eResearch and libraries staff

357 consequently being unaware of the data management needs and challenges experienced by
358 research teams. Further, eResearch and libraries staff are often spread thinly across institutions,
359 with high demand for their services but limited capacity to provide much-needed support. For all
360 these reasons, building channels of communication between research groups and support
361 teams is key, and both parties must be willing to come to the table to share and learn from one
362 another.

363 Developing strong working relationships requires reciprocity, with an emphasis on mutual benefit
364 (which may include academic acknowledgement) and respect for expertise on both sides. The
365 eResearch and libraries staff often require information about the research context and learned
366 experiences from researchers so they can provide and/or procure the necessary services and
367 support, and researchers can also endeavour to engage with the technicalities and concepts
368 necessary for full and fruitful discussions. We recommend that researchers meet early and often
369 with eResearch and libraries staff to discuss their data management needs. Investing in these
370 relationships ultimately means that researchers will get the wrap-around support they require,
371 and eResearch and libraries staff will be kept apprised of their changing needs, facilitating the
372 development of future-focussed solutions.

373 3.4 Establish a research data management culture in your group

374 It is vital to ensure the continuity of data management throughout the research life cycle and
375 beyond. We strongly encourage researchers to step up and take an active leadership role in
376 situations where there is an absence of clear and consistent guidelines. However, data
377 management is most effective when pursued as a team, with a consistent and cohesive plan
378 and division of labour. A little effort early in the process can go a long way, and so we
379 recommend that research teams develop clear documentation around on/offboarding

380 procedures and daily data management practices. This will streamline the process of joining the
381 team, and provide guidance on the options for and constraints around data transfer, storage,
382 and access; it also provides a clear pathway to follow when departing that may include ongoing
383 access to data, or the packaging of data and metadata for long-term storage.

384 To ensure consistency despite the potential for frequent turnover within the group, we suggest
385 that research teams establish a data management champion to oversee the onboarding and
386 training of new members and ensure the implementation of consistent data management
387 practices across the research team. While anyone can take on this transferable role, a data
388 management champion will ideally have a mid- to long-term position within the research team,
389 hold a deep understanding of the unique characteristics of each research project, and have the
390 necessary level of autonomy to operate independently as a leader in this role. Succession
391 planning for this role will be essential to ensure consistency and continuity. This person can also
392 operate as a conduit between the research team and eResearch and libraries staff, and so
393 excellent people skills will be advantageous. By engaging regularly and often with their institute's
394 support structures, they can ensure that eResearch and libraries staff are kept up to date with
395 the changing needs of the team, and ensure access to the latest services and support.

396 4. Continuing the data management journey

397 In this contribution, we have presented tips and tricks to support biodiversity genomics
398 researchers in the development of good data management practices, though we acknowledge
399 that any level of data management is better than none. Data management is a journey, and we
400 are all on an aspirational path striving towards best practice. We trust our contribution will be a
401 helpful guide for researchers new to biodiversity genomics, and a useful prompt for existing
402 researchers to embed good data management practices into their daily research routines.

Glossary

- Accessible data. Data accessible under well-defined conditions, as per the FAIR Guiding Principles (Mons et al., 2017; Wilkinson et al., 2016).
- CARE Principles for Indigenous Data Governance. Designed to complement the FAIR Guiding Principles, these people- and purpose-oriented principles and supporting concepts (Collective benefit, Authority to control, Responsibility, Ethics) reflect the crucial role of data in advancing innovation, governance, and self-determination among Indigenous Peoples (Carroll et al. 2020; 2021). See <https://www.gida-global.org/care>.
- Data life cycle. The steps in the research process specifically relating to data, including planning, collection and generation, analysis and collaboration, evaluation, storage, dissemination, access, and reuse, which can contribute to the planning for new data generation. The data and research life cycles are distinct but interrelated.
- Data management. The processes and practices associated with the documentation and storage of and access to data and associated metadata throughout the research life cycle.
- DMP. Data management plan. Also known as a data management and sharing plan, though in our definition of data management, data sharing is inherently included in data access. A document describing the data that will be generated during a research project, and how it will be used, accessed, and stored during the research life cycle.

- eResearch. The use of digital tools and techniques to advance research.
- eResearch and libraries staff. A broad group that includes research software engineers, research infrastructure developers, data scientists, data stewards, and other professional services staff that deliver library, IT, bioinformatics, and high-performance compute support.
- FAIR Guiding Principles. Guidelines for scientific data management and stewardship intended to improve the Findability, Accessibility, Interoperability, and Reuse of digital assets (Wilkinson et al. 2016). See <https://www.go-fair.org/fairprinciples/>.
- Indigenous data. The tangible and/or intangible cultural materials, belongings, knowledge, digital data, and information about Indigenous Peoples or that to which they relate (Lovett et al., 2019; Rainie et al., 2019).
- Indigenous data sovereignty. The expression of a legitimate right of Indigenous Peoples to control the access, the collection, ownership, application and governance of their own data, knowledge, and/or information that derives from unique cultural histories, expressions, practices, and contexts. See <https://localcontexts.org/indigenous-data-sovereignty/>.
- Metadata. Data that provides information about other data. For biodiversity genomic data, metadata can provide information regarding context (e.g., taxonomic, spatial, temporal, and associated permissions) as well as used technologies/methodologies.
- Open data. Data anyone can use and share, typically publicly accessible and with an open licence.

- Research life cycle. The steps in the process of scientific research from inception (research planning, design, and funding) to completion (dissemination of results and real-world impact), which often leads back to development of new related projects. The research and data life cycles are distinct but interrelated.
- VM: Virtual machine. A software-based computer system emulating that of a different physical machine, often used to run a different operating system than that of the primary system of the physical computer

403

404 5. Acknowledgements

405 We wish to thank the following people for their thoughtful advice, insights, and friendly feedback
406 during the development of this project: Mik Black, Thomas Buckley, Eric D. Crandall, Tom
407 Etherington, Stephanie Galla, Tipene Merritt and the University of Canterbury (UC) eResearch
408 Co-Design Group, David Medyckyj-Scott, Nick Spencer, Matt Stott, and the UC ConSERTeam.

409 6. References

- 410 Anderson, J., & Hudson, M. (2020). The Biocultural Labels Initiative: Supporting indigenous
411 rights in data derived from genetic resources. *Biodiversity Information Science and*
412 *Standards*, 4, Article e59230. <https://doi.org/10.3897/biss.4.59230>
- 413 Andrikopoulou, A., Rowley, J., & Walton, G. (2022). Research Data Management (RDM) and the
414 evolving identity of academic libraries and librarians: A literature review. *New Review of*
415 *Academic Librarianship*, 28(4), 349–365.
416 <https://doi.org/10.1080/13614533.2021.1964549>
- 417 Baker, M. (2016). 1,500 scientists lift the lid on reproducibility. *Nature*, 533(7604), Article 7604.
418 <https://doi.org/10.1038/533452a>
- 419 Batley, J., & Edwards, D. (2009). Genome sequence data: Management, storage, and
420 visualization. *BioTechniques*, 46(5), 333–336. <https://doi.org/10.2144/000113134>
- 421 Beninde, J., Toffelmier, E., & Shaffer, H. B. (2022). A brief history of population genetic research

422 in California and an evaluation of its utility for conservation decision-making. *Journal of*
423 *Heredity*, 113(6), 604–614. <https://doi.org/10.1093/jhered/esac049>

424 Bloemers, M., & Montesanti, A. (2020). The FAIR Funding Model: Providing a Framework for
425 Research Funders to Drive the Transition toward FAIR Data Management and
426 Stewardship Practices. *Data Intelligence*, 2(1–2), 171–180.
427 https://doi.org/10.1162/dint_a_00039

428 Carroll, S. R., Garba, I., Figueroa-Rodríguez, O. L., Holbrook, J., Lovett, R., Materechera, S.,
429 Parsons, M., Raseroka, K., Rodriguez-Lonebear, D., Rowe, R., Sara, R., Walker, J. D.,
430 Anderson, J., & Hudson, M. (2020). The CARE Principles for Indigenous Data
431 Governance. *Data Science Journal*, 19(1), Article 1. <https://doi.org/10.5334/dsj-2020-043>

432 Carroll, S. R., Herczog, E., Hudson, M., Russell, K., & Stall, S. (2021). Operationalizing the
433 CARE and FAIR Principles for Indigenous data futures. *Scientific Data*, 8(1), Article 1.
434 <https://doi.org/10.1038/s41597-021-00892-0>

435 Chiang, G.-T., Clapham, P., Qi, G., Sale, K., & Coates, G. (2011). Implementing a genomic data
436 management system using iRODS in the Wellcome Trust Sanger Institute. *BMC*
437 *Bioinformatics*, 12(1), Article 361. <https://doi.org/10.1186/1471-2105-12-361>

438 Convention on Biological Diversity (2022). Kunming-Montreal Global Biodiversity Framework.
439 <https://www.cbd.int/decisions/cop/?m=cop-15>

440 Cragin, M. H., Palmer, C. L., Carlson, J. R., & Witt, M. (2010). Data sharing, small science and
441 institutional repositories. *Philosophical Transactions of the Royal Society A:*
442 *Mathematical, Physical and Engineering Sciences*, 368(1926), 4023–4038.
443 <https://doi.org/10.1098/rsta.2010.0165>

444 Crandall, E. D., Riginos, C., Bird, C. E., Liggins, L., Trembl, E., Beger, M., Barber, P. H., Connolly,
445 S. R., Cowman, P. F., DiBattista, J. D., Eble, J. A., Magnuson, S. F., Horne, J. B.,
446 Kochzius, M., Lessios, H. A., Liu, S. Y. V., Ludt, W. B., Madduppa, H., Pandolfi, J. M., ...
447 Gaither, M. R. (2019). The molecular biogeography of the Indo-Pacific: Testing
448 hypotheses with multispecies genetic patterns. *Global Ecology and Biogeography*, 28(7),
449 943–960. <https://doi.org/10.1111/geb.12905>

450 Crandall, E. D., Toczydlowski, R. H., Liggins, L., Holmes, A. E., Ghoojaei, M., Gaither, M. R.,
451 Wham, B. E., Pritt, A. L., Noble, C., Anderson, T. J., Barton, R. L., Berg, J. T., Beskid, S.
452 G., Delgado, A., Farrell, E., Himmelsbach, N., Queeno, S. R., Trinh, T., Weyand, C., ...
453 Toonen, R. J. (2023). Importance of timely metadata curation to the global surveillance of
454 genetic diversity. *Conservation Biology*, Jan 27:e14061. doi: 10.1111/cobi.14061. Epub
455 ahead of print.

456 Dryad (2020). Joint Data Archiving Policy.
457 <https://datadryad.org/docs/JointDataArchivingPolicy.pdf>

458 Duntsch, L., Whibley, A., Brekke, P., Ewen, J. G., & Santure, A. W. (2021). Genomic data of
459 different resolutions reveal consistent inbreeding estimates but contrasting homozygosity
460 landscapes for the threatened Aotearoa New Zealand hihi. *Molecular Ecology*, 30(23),
461 6006–6020. <https://doi.org/10.1111/mec.16068>

462 Eisner, D. A. (2018). Reproducibility of science: Fraud, impact factors and carelessness. *Journal*
463 *of Molecular and Cellular Cardiology*, 114, 364–368.
464 <https://doi.org/10.1016/j.yjmcc.2017.10.009>

465 Exposito-Alonso, M., Booker, T. R., Czech, L., Gillespie, L., Hateley, S., Kyriazis, C. C., Lang, P.
466 L. M., Leventhal, L., Nogues-Bravo, D., Pagowski, V., Ruffley, M., Spence, J. P., Toro
467 Arana, S. E., Weiß, C. L., & Zess, E. (2022). Genetic diversity loss in the Anthropocene.
468 *Science*, 377(6613), 1431–1435. <https://doi.org/10.1126/science.abn5642>

469 Fadlelmola, F. M., Zass, L., Chaouch, M., Samtal, C., Ras, V., Kumuthini, J., Panji, S., & Mulder,
470 N. (2021). Data Management Plans in the genomics research revolution of Africa:

471 Challenges and recommendations. *Journal of Biomedical Informatics*, 122, 103900.
472 <https://doi.org/10.1016/j.jbi.2021.103900>

473 Field, D., Garrity, G., Gray, T., Morrison, N., Selengut, J., Sterk, P., Tatusova, T., Thomson, N.,
474 Allen, M. J., Angiuoli, S. V., Ashburner, M., Axelrod, N., Baldauf, S., Ballard, S., Boore,
475 J., Cochrane, G., Cole, J., Dawyndt, P., De Vos, P., ... Wipat, A. (2008). The minimum
476 information about a genome sequence (MIGS) specification. *Nature Biotechnology*,
477 26(5), Article 5. <https://doi.org/10.1038/nbt1360>

478 Grigoriev, I. V., Nordberg, H., Shabalov, I., Aerts, A., Cantor, M., Goodstein, D., Kuo, A.,
479 Minovitsky, S., Nikitin, R., Ohm, R. A., Otilar, R., Poliakov, A., Ratnere, I., Riley, R.,
480 Smirnova, T., Rokhsar, D., & Dubchak, I. (2012). The Genome Portal of the Department
481 of Energy Joint Genome Institute. *Nucleic Acids Research*, 40(D1), D26–D32.
482 <https://doi.org/10.1093/nar/gkr947>

483 Henson, L., Balkenhol, N., Gustas, R., Adams, M., Walkus, J., Housty, W., Stronen, A., Moody,
484 J., Service, C., Reece, D., vonHoldt, B., McKechnie, I., Koop, B., & Darimont, C. (2021).
485 Convergent geographic patterns between grizzly bear population genetic structure and
486 Indigenous language groups in coastal British Columbia, Canada. *Ecology and Society*,
487 26(3). Article 7. <https://doi.org/10.5751/ES-12443-260307>

488 Hoban, S., Archer, F. I., Bertola, L. D., Bragg, J. G., Breed, M. F., Bruford, M. W., Coleman, M.
489 A., Ekblom, R., Funk, W. C., Grueber, C. E., Hand, B. K., Jaffé, R., Jensen, E., Johnson,
490 J. S., Kershaw, F., Liggins, L., MacDonald, A. J., Mergeay, J., Miller, J. M., ... Hunter, M.
491 E. (2022). Global genetic diversity status and trends: Towards a suite of Essential
492 Biodiversity Variables (EBVs) for genetic composition. *Biological Reviews*, 97(4), 1511–
493 1538. <https://doi.org/10.1111/brv.12852>

494 Jorgenson, L. A., Wolinetz, C. D., & Collins, F. S. (2021). Incentivizing a new culture of data
495 stewardship: The NIH policy for data management and sharing. *JAMA*, 326(22), 2259–
496 2260. <https://doi.org/10.1001/jama.2021.20489>

497 Khan, A., Patel, K., Shukla, H., Viswanathan, A., van der Valk, T., Borthakur, U., Nigam, P.,
498 Zachariah, A., Jhala, Y. V., Kardos, M., & Ramakrishnan, U. (2021). Genomic evidence
499 for inbreeding depression and purging of deleterious genetic variation in Indian tigers.
500 *Proceedings of the National Academy of Sciences*, 118(49), e2023018118.
501 <https://doi.org/10.1073/pnas.2023018118>

502 Lau, J. W., Lehnert, E., Sethi, A., Malhotra, R., Kaushik, G., Onder, Z., Groves-Kirkby, N.,
503 Mihajlovic, A., DiGiovanna, J., Srdic, M., Bajcic, D., Radenkovic, J., Mladenovic, V.,
504 Krstanovic, D., Arsenijevic, V., Klisic, D., Mitrovic, M., Bogicevic, I., Kural, D., ... Seven
505 Bridges CGC Team. (2017). The cancer genomics cloud: Collaborative, reproducible,
506 and democratized—a new paradigm in large-scale computational research. *Cancer*
507 *Research*, 77(21), e3–e6. <https://doi.org/10.1158/0008-5472.CAN-17-0387>

508 Laurie, G., Jones, K. H., Stevens, L., & Dobbs, C. (2014). *A review of evidence relating to harm*
509 *resulting from uses of health and biomedical data*. Nuffield Council on Bioethics.
510 [https://www.pure.ed.ac.uk/ws/portalfiles/portal/19402878/Review_of_Evidence_Relating_](https://www.pure.ed.ac.uk/ws/portalfiles/portal/19402878/Review_of_Evidence_Relating_to_Harms_Resulting_from_Uses_of_Health_and_Biomedical_Data_FINAL.pdf)
511 [to_Harms_Resulting_from_Uses_of_Health_and_Biomedical_Data_FINAL.pdf](https://www.pure.ed.ac.uk/ws/portalfiles/portal/19402878/Review_of_Evidence_Relating_to_Harms_Resulting_from_Uses_of_Health_and_Biomedical_Data_FINAL.pdf)

512 Leigh, D. M., van Rees, C. B., Millette, K. L., Breed, M. F., Schmidt, C., Bertola, L. D., Hand, B.
513 K., Hunter, M. E., Jensen, E. L., Kershaw, F., Liggins, L., Luikart, G., Manel, S., Mergeay,
514 J., Miller, J. M., Segelbacher, G., Hoban, S., & Paz-Vinas, I. (2021). Opportunities and
515 challenges of macrogenetic studies. *Nature Reviews Genetics*, 22(12), Article 12.
516 <https://doi.org/10.1038/s41576-021-00394-0>

517 Liggins, L., Hudson, M., & Anderson, J. (2021). Creating space for Indigenous perspectives on
518 access and benefit-sharing: Encouraging researcher use of the Local Contexts Notices.
519 *Molecular Ecology*, 30(11), 2477–2482. <https://doi.org/10.1111/mec.15918>

520 Lin, D., Crabtree, J., Dillo, I., Downs, R. R., Edmunds, R., Giaretta, D., De Giusti, M., L'Hours,
521 H., Hugo, W., Jenkyns, R., Khodiyar, V., Martone, M. E., Mokrane, M., Navale, V.,
522 Petters, J., Sierman, B., Sokolova, D. V., Stockhouse, M., & Westbrook, J. (2020). The
523 TRUST Principles for digital repositories. *Scientific Data*, 7(1), Article 1.
524 <https://doi.org/10.1038/s41597-020-0486-7>

525 Liu, L., Bosse, M., Megens, H.-J., de Visser, M., A. M. Groenen, M., & Madsen, O. (2021).
526 Genetic consequences of long-term small effective population size in the critically
527 endangered pygmy hog. *Evolutionary Applications*, 14(3), 710–720.
528 <https://doi.org/10.1111/eva.13150>

529 Lovett, R., Lee, V., Kukutai, T., Cormack, D., Rainie, S. C., & Walker, J. (2019). Good data
530 practices for Indigenous data sovereignty and governance. In *Good data* (pp. 26–36).
531 Institute of Network Cultures Inc.

532 MBIE (2022). Open Research policy. New Zealand Ministry of Business, Innovation &
533 Employment. [https://www.mbie.govt.nz/science-and-technology/science-and-](https://www.mbie.govt.nz/science-and-technology/science-and-innovation/agencies-policies-and-budget-initiatives/open-research-policy/)
534 [innovation/agencies-policies-and-budget-initiatives/open-research-policy/](https://www.mbie.govt.nz/science-and-technology/science-and-innovation/agencies-policies-and-budget-initiatives/open-research-policy/)

535 Möller, S., Prescott, S. W., Wirzenius, L., Reinholdtsen, P., Chapman, B., Prins, P., Soiland-
536 Reyes, S., Klötzl, F., Bagnacani, A., Kalaš, M., Tille, A., & Crusoe, M. R. (2017). Robust
537 cross-platform workflows: how technical and scientific communities collaborate to
538 develop, test and share best practices for data analysis. *Data Science and Engineering*,
539 2(3), 232–244. <https://doi.org/10.1007/s41019-017-0050-4>

540 Mons, B., Neylon, C., Velterop, J., Dumontier, M., da Silva Santos, L. O. B., & Wilkinson, M. D.
541 (2017). Cloudy, increasingly FAIR; revisiting the FAIR Data guiding principles for the
542 European Open Science Cloud. *Information Services & Use*, 37(1), 49–56.
543 <https://doi.org/10.3233/ISU-170824>

544 Ozaki, K., Ohnishi, Y., Iida, A., Sekine, A., Yamada, R., Tsunoda, T., Sato, H., Sato, H., Hori, M.,
545 Nakamura, Y., & Tanaka, T. (2002). Functional SNPs in the lymphotoxin- α gene that are
546 associated with susceptibility to myocardial infarction. *Nature Genetics*, 32(4), Article 4.
547 <https://doi.org/10.1038/ng1047>

548 Rainie, S. C., Kukutai, T., Walter, M., Figueroa-Rodríguez, O. L., Walker, J., & Axelsson, P.
549 (2019). Indigenous data sovereignty. In *The state of open data: Histories and horizons*
550 (pp. 300–319). African Minds and International Development Research Centre.

551 Rayne, A., Blair, S., Dale, M., Flack, B., Hollows, J., Moraga, R., Parata, R. N., Rupene, M.,
552 Tamati-Elliffe, P., Wehi, P. M., Wylie, M. J., & Steeves, T. E. (2022). Weaving place-
553 based knowledge for culturally significant species in the age of genomics: Looking to the
554 past to navigate the future. *Evolutionary Applications*, 15(5), 751–772.
555 <https://doi.org/10.1111/eva.13367>

556 Riginos, C., Crandall, E. D., Liggins, L., Gaither, M. R., Ewing, R. B., Meyer, C., Andrews, K. R.,
557 Euclide, P. T., Titus, B. M., Therkildsen, N. O., Salces-Castellano, A., Stewart, L. C.,
558 Toonen, R. J., & Deck, J. (2020). Building a global genomics observatory: Using GEOME
559 (the Genomic Observatories Metadatabase) to expedite and improve deposition and
560 retrieval of genetic data and metadata for biodiversity research. *Molecular Ecology*
561 *Resources*, 20(6), 1458–1469. <https://doi.org/10.1111/1755-0998.13269>

562 Robledo-Ruiz, D. A., Gan, H. M., Kaur, P., Dudchenko, O., Weisz, D., Khan, R.,
563 Lieberman Aiden, E., Osipova, E., Hiller, M., Morales, H. E., Magrath, M. J. L., Clarke, R.
564 H., Sunnucks, P., & Pavlova, A. (2022). Chromosome-length genome assembly and
565 linkage map of a critically endangered Australian bird: The helmeted honeyeater.
566 *GigaScience*, 11, Article giac025. <https://doi.org/10.1093/gigascience/giac025>

567 Schadt, E. E., Linderman, M. D., Sorenson, J., Lee, L., & Nolan, G. P. (2010). Computational
568 solutions to large-scale data management and analysis. *Nature Reviews Genetics*, 11(9),

569 Article 9. <https://doi.org/10.1038/nrg2857>
570 Toczydlowski, R. H., Liggins, L., Gaither, M. R., Anderson, T. J., Barton, R. L., Berg, J. T.,
571 Beskid, S. G., Davis, B., Delgado, A., Farrell, E., Ghoojarei, M., Himmelsbach, N.,
572 Holmes, A. E., Queeno, S. R., Trinh, T., Weyand, C. A., Bradburd, G. S., Riginos, C.,
573 Toonen, R. J., & Crandall, E. D. (2021). Poor data stewardship will hinder global genetic
574 diversity surveillance. *Proceedings of the National Academy of Sciences*, 118(34), Article
575 e2107934118. <https://doi.org/10.1073/pnas.2107934118>
576 Wilkinson, M. D., Dumontier, M., Aalbersberg, I. J., Appleton, G., Axton, M., Baak, A., Blomberg,
577 N., Boiten, J.-W., da Silva Santos, L. B., Bourne, P. E., Bouwman, J., Brookes, A. J.,
578 Clark, T., Crosas, M., Dillo, I., Dumon, O., Edmunds, S., Evelo, C. T., Finkers, R., ...
579 Mons, B. (2016). The FAIR Guiding Principles for scientific data management and
580 stewardship. *Scientific Data*, 3(1), Article 1. <https://doi.org/10.1038/sdata.2016.18>
581 Wright, S. (1922). Coefficients of inbreeding and relationship. *The American Naturalist*, 56(645),
582 330–338. <https://doi.org/10.1086/279872>
583 Yilmaz, P., Kottmann, R., Field, D., Knight, R., Cole, J. R., Amaral-Zettler, L., Gilbert, J. A.,
584 Karsch-Mizrachi, I., Johnston, A., Cochrane, G., Vaughan, R., Hunter, C., Park, J.,
585 Morrison, N., Rocca-Serra, P., Sterk, P., Arumugam, M., Bailey, M., Baumgartner, L., ...
586 Glöckner, F. O. (2011). Minimum information about a marker gene sequence
587 (MIMARKS) and minimum information about any (x) sequence (MIxS) specifications.
588 *Nature Biotechnology*, 29(5), Article 5. <https://doi.org/10.1038/nbt.1823>

589

590 7. Data Accessibility and Benefit Sharing statements

591 7.1 Data Accessibility Statement

592 No data were produced or analysed in the development of this manuscript.

593 7.2 Benefit-Sharing Statement

594 Benefits Generated: A cross-institutional, interdisciplinary research collaboration was developed
595 with all collaborators included as co-authors. Benefits from this collaboration accrue through the
596 provision of the Biodiversity Genomic Data Management Hub, which is shared with the
597 biodiversity genomics community to support researchers in improving data management
598 practices across the data life cycle. This research is timely given predicted changes in research
599 funding requirements to include Data Management Plans.

600 8. Author Contributions

601 NF, JW and TES conceived the research. All authors provided input into the research direction
602 and contributed through robust discussion towards the development of the manuscript and the
603 Biodiversity Genomic Data Management Hub. JH provided illustrations. NF and JW wrote the
604 first draft of paper, and led the writing of subsequent drafts. All authors provided feedback and
605 approved the final manuscript.