

1 **How to Walk on Statistical Mandalas as a Population Ecologist**
2 Yukihiko Toquenaga
3 Faculty of Life and Environmental Sciences, University of Tsukuba, 1-1-1 Tennodai, Tsukuba,
4 Ibaraki 305-8572, Japan
5 Corresponding author, e-mail: toque@biol.tsukuba.ac.jp

6

7 **Manuscript Information:**

8 Number of pages: 16
9 Number of figures: 3

10

11

12 **Abstract**

13

14 We population ecologists who are believed to be good at dealing with statistics often get confused
15 about what kinds of statistical methods we should apply to our nuisance data. There are a couple
16 of conflicting paradigms and many associated methods in statistics. Classical frequentists'
17 approaches that have dominated in science have been severely criticized by the newcomers:
18 Bayesian and evidential statistics. But, both newcomers also have weak points. Researchers
19 devoted to different statistical approaches are seeking soft landing places where they can
20 compromise each other. Key aspects of statistical inference are discriminating model selection
21 and parameter estimation. Likelihood and Fisher information play important roles in both
22 processes. As an overview of the compromise processes, here I will introduce three contributing
23 papers by M. L. Taper, J. M. Ponciano, R. M. Dorazio, and K. Yamamura for the special issue
24 entitled "Bayesian, Fisherian, error, and evidential statistical approaches for population ecology."
25 This special feature is based on a symposium held in Tsukuba, Japan, on 11 October 2014.

26

27 **Keywords**

28

29 Bayesian • Evidential • Fisherian • Frequentist • Model selection • Parameter estimation

30

31 **Introduction**

32

33 When a non-native-English-speaking scientist submits his/her manuscript to an international
34 ecological journal, he/she often asks English proofreading of a professional or of his/her
35 native-English-speaking colleague. However, interestingly, there are few authorized systems to
36 encourage proofreading of statistical methods. One reason for this trend might be that statistical
37 methods have no authorized standards as does scientific English. Statistical practices, and in some
38 cases paradigms, are quite different among scientific fields. Population ecologists, who are
39 believed to be relatively better at statistics than ecologists specializing in other fields, also have to
40 consider which statistical methods and paradigms they should apply to their own researches. Are
41 we population ecologists actually good at statistics? I would say no. Most of us only specialize
42 in specific statistical methods and paradigms.

43 That would be why Dr. Takashi Saitoh who was the president of the Society of
44 Population Ecology asked Dr. Kohji Yamamura and myself to organize a special issue on statistics
45 of population ecology from a broad perspective. In this introductory review, I briefly list
46 questions and concerns about statistics that I have felt during my career as a population ecologist.
47 I first discuss the dominance of classical frequentist approaches in chronological order for which
48 they appeared for me personally, then I briefly discuss the two newcomers, Bayesian and evidential
49 statistics, and finally, I introduce the three contributing articles for this special issue. This special
50 feature is based on a symposium held in Tsukuba, Japan, on 11 October 2014.

51

52 **Dominance of classical frequentist approaches**

53

54 The vast majority of textbooks on statistics in the library of my university in the middle of the
55 1980s were, and might still be, classified as classical frequentist statistics. Here “classical
56 frequentist” refers to non-Bayesian or non-evidential, and mainly consists of null-hypothesis testing
57 and P -value worship approaches that assume normal distributions of original or transformed target
58 variables. As other students of population ecology, I had to start learning classical statistics when
59 I was a graduate student. I have always wondered why regressions and ANOVA-type methods
60 have two steps: significance tests of explanatory variables for the data variation as a whole
61 followed by significance tests for parameters or means of sub-units. Even for a simple one-way
62 ANOVA test for three categories, once we detect a significant difference among the three categories,
63 we cannot simply claim that the largest mean value for a category is larger than those of the other
64 two categories. I was taught that we had to perform appropriate *post hoc* tests even when the plot
65 of mean values clearly showed the difference.

66 The former step is model fitting, and the latter one is parameter estimation. These two
67 steps sometimes invoke different statistical methods, e.g., model fitting with information criteria,
68 such AIC or BIC, and parameter estimation with Bayesian methods. The former requires *post hoc*
69 tests to compare parameters of the best models, but the latter can spontaneously compare multiple
70 parameters after obtaining their posterior probabilities by checking the overlap of their posterior
71 distributions. *Post hoc* tests are a variant of multiple comparison (Hsu 1998). Multiple
72 comparison per se does not inherently mean post hoc tests, and there are relevant *a priori* tests of
73 multiple comparison. The difference between *post hoc* and *a priori* comparison is the
74 epistemological attitude towards data collection by researchers. If one designed the comparison

75 before his/her data collection, the test is *a priori* but it should be treated as *post hoc* if one did the
76 comparison after his/her data collection. This epistemological difference would affect the
77 complicatedness of calculating appropriate variances in the comparison. Much simpler methods
78 of *post hoc* comparison, for example the Bonferroni test or its variants (Holm 1979; Moran 2003),
79 often require some kind of programming skills, so one would preferably be able to claim, “I did
80 design the comparison beforehand!”

81 My supervisor, Dr. Koichi Fujii, mastered statistics under Dr. Robert R. Sokal who is the
82 author of the famous textbook, Biometry (Sokal and Rohlf 1981), which has a good flavor of
83 classical statistics. My friends believed that I would become an obedient successor of this
84 “normal distribution empire.” Then Dr. Nobuhiro Minaka who taught statistics at various
85 institutes and universities at that time, secretly sent me his image of a statistical mandala at the end
86 of the 1980s (Fig. 1). I was very excited about this mandala because with it I learned that there
87 were options other than the “normal distribution empire.” Moreover, those other options were
88 extremely attractive. After that, Dr. Mark L. Taper visited my laboratory as a post-doctoral fellow
89 of the National Science Foundation, U.S.A., and introduced me to the *bossa nova* of statistics. At
90 the time, besides discriminating egg shapes of two bean beetle species (Taper and Ponciano 2015),
91 Dr. Taper was struggling with quantitative genetic problems using MANOVA (Taper 1990). He
92 was always aware of the statistical power of constructed statistical models. He often questioned
93 me about how many replicates we needed to obtain significant differences among treatments
94 considering statistical power. He recommended that I read a textbook by Dr. Jerrold H. Zar (Zar
95 1984) rather than Biometry (Sokal and Rohlf 1981). Zar’s book (2nd ed.) was, as far as I knew,
96 the only book that started the first chapter with frequency data analysis, which taught me the

97 meaning of degrees of freedom.

98 At the beginning of the 1990s, there was a small boom of randomization statistics
99 (Noreen 1989; Good 1993; Edgington 1995; Manly 1997) among young behavioral ecologists in
100 Japan. Dr. Eiichi Kasuya and his collaborators claimed, “from now on, randomization will take
101 over those classical statistics such as ANOVA and multiple regressions.” They emphasized that
102 randomization methods were custom made, so we could adjust statistics so as to ask any question
103 and judge any problems. Randomization tests were first innovated by Dr. Ronald A. Fisher
104 (Salsburg 2001) and extensively developed by Dr. Bradley Efron (Efron 1982; Hall 1992) as the
105 Jackknife, bootstrap, and other resampling methods for reconstructing parameter distribution of
106 populations. One can reconstruct the background distribution believed to exist by simply or
107 honestly resampling obtained data. It is just like believing that nature is full of fractals (Peitgen
108 1992). Resampling plans need sophisticated stratification of variables if you have problems with
109 multiple variables. I was not sure how to apply randomization tests to all of the statistical
110 problems illustrated in Dr. Minaka’s mandala (Fig. 1).

111 In the middle of the 1990s, many population ecologists in Japan routinely used
112 generalized linear models (GLM; e.g., Dunteman 1984; Dobson 1990; Crawley 1993) for their
113 analyses. They fit models to their data, and examined parameter values for the models. Some
114 models showed quite low powers of explanation, or had low adjusted or generalized determination
115 coefficient (R^2) values (Nagelkerke 1991), but their discussions were based on highly significant
116 parameters of the models. Some researchers applied information criteria, such AIC and its
117 variants, but again they derived conclusions from significant parameters even though there might
118 have been alternative models with similar AIC values. Model selection and the following

119 parameter summarization were somehow estranged from one another.

120 Significance tests for parameters often ask whether the parameter values are greater or
121 less than zero. We all know the criticisms against the silly null hypothesis that reflect a lack of
122 thinking about plausible alternatives, so finding little/no support for the nulls does little to provide
123 evidence for the alternatives (Burnham et al. 2011). So we perhaps forget the criticisms when we
124 perform GLMs. Earnest population ecologists are aware of random effects as well as fixed effects,
125 but decisions on whether factors are fixed or random effects are often arbitrary (Royle and Dorazio
126 2008). Not a few articles encourage scientists to get rid of *P*-values and testing between null-model
127 and non-null-model hypotheses (e.g., Anderson et al. 2000; Stephens et al. 2005). Recently the
128 scientific journal, “Basic and Applied Social Psychology,” has gone so far as to ban *P*-value
129 significance tests (Trafimow and Marks 2015)! But many scientific articles still adopt classical
130 statistical methods. This situation resembles that of Mac and Linux users blaming Windows
131 because of its inability to stop malware proliferation, while at the same time, Windows users make
132 up the vast majority of the world’s computer-using population.

133

134 ***Bossa-nova* statistics from bayesian and evidential approaches**

135

136 Bayesian approaches are the most recent trend for population ecology (e.g., Ellison 2004; Qian and
137 Shen 2007). As for randomization methods, evangelists of Bayesian statistics claimed that
138 “everything is solved with Bayesian” (e.g., Albert 2007; McCarthy 2007; Gill 2008). Several
139 Bayesian introductory textbooks criticize classical approaches, sometimes even consuming an
140 entire chapter, and introduce Bayesian methods as a replacement for all of them (e.g., McCarthy

141 2007; McGrayne 2011). Some extremist opinions claim that Bayesian philosophy cannot coexist
142 with classical philosophy (e.g., Ellison 2004). There was, in fact, stubborn resistance against
143 Bayesian approaches from old schools of thought (e.g., Yamamura 2015). Students would ask,
144 “well, we can obtain posterior distribution of target parameters, but how can we say those
145 parameters are significantly different from zero?” Some textbooks even introduce significance
146 tests in terms of Bayesian approaches (e.g., Albert 2007). “Then which model should we select?”
147 is another question. Bayes factor, DIC and BIC have been proposed, but there exist *pros* and *cons*
148 for each of them (Ward 2008; Spiegelhalter et al. 2014; Hooten and Hobbs 2015). On the other
149 hand, there are more moderate Bayesian evangelists that would not mind combining Bayesian with
150 other, even classical, approaches (e.g., Bolker 2008; Royle and Dorazio 2008; Qian 2010).

151 As the rise of randomization approaches heavily depended on advances in computer
152 sciences, new and practical Bayesian approaches, such Markov chain Monte Carlo (MCMC,
153 Dorazio 2015) and Hamiltonian Monte Carlo (Stan Development Team 2015) have been enabled by
154 progress in calculation techniques with computers. Development of Bayesian-statistics-oriented
155 languages, such OpenBUGS, WinBUGS, JAGS, and Stan, also accelerated the spread of Bayesian
156 approaches (Kruschke 2011; Kery and Schaub 2012; Stan Development Team 2015). After
157 copying BUGS scripts from books, adjusting parameters for prior probability of one's data, and
158 then calculating the statistical scripts, posterior distributions are returned. It is often
159 recommended to check states of convergence of the posterior distribution by trace plots or \hat{R}
160 values (Gelman and Rubin 1992), but those checks do not guarantee parameter convergence
161 (Dorazio 2015).

162 Evidential statistical approaches appear more modest in propagation than Bayesian and

163 other approaches (Taper and Lele 2004). They mainly rely on the invariant characteristic of
164 maximum likelihood or variants of information criteria, and provide simple but clear ways to tell
165 which models should be selected. Interestingly, all the following tools were invented by Dr.
166 Fisher: *P*-value, randomization test, ANOVA, and maximum likelihood estimates. Dr. Fisher
167 himself strongly criticized Bayesian approaches (e.g., McGrayne 2011), but evidential approaches
168 seek a harmonious collaboration with Bayesian methods as well as with classical methods. So far
169 there seems not to have been any big booms in evidential approaches in Japan or in other regions of
170 the world.

171

172 **Walking through Bayesian, Fisherian, error, and evidential statistical approaches**

173

174 Dr. Minaka's mandala (Fig. 1) shows us nearly the whole scope of statistics that we population
175 ecologists should be aware of. I felt that a more simplified version of the mandala could be drawn.
176 A similar trial was done by Dr. Efron who categorizes himself as a Fisherian (Efron 1998, Fig. 2),
177 but here I would like to propose an even simpler mandala (Fig. 3). The horizontal line in Fig. 3
178 shows the one-dimensional problem space of statistics. The shaded rectangle shows the domain
179 of classical methods, or "normal distribution empire." Yes, there are many problems outside of
180 the rectangle: On the left-hand side, the amount of data is too small to apply a *t*-test or an ANOVA.
181 On the right-hand side, we have plenty of data, but they are too entangled to apply a simple
182 ANOVA or even a MANOVA. So, for situations represented by the left-hand side, proper
183 guidance would be, "collect more data!" How much data is necessary to shift into the gray
184 rectangle region? And, what about situations in which, we cannot collect more data?

185 Non-parametric methods, and sometimes Bayesian methods, are often invoked to support small
186 sample sizes (e.g., Hinton 2004). Note that neither non-parametric nor Bayesian methods were
187 invented for that purpose (Neave and Worthington 1988; Noether 1991; Sprent 1993; Salsburg
188 2001).

189 The problem is more serious if your data are located on the right-hand side of the shaded
190 rectangle in Fig. 3. Explanatory variables are complicatedly correlated, and variables to be
191 explained are also highly entangled. Applying classification methods, such cluster analyses and
192 correspondence analyses, may reveal distant relationships among the variables, but some criteria
193 for grouping them are necessary. The proper guidance for such situations is merely “muddle
194 through whatever tools you have!” (Taper and Ponciano 2015). One way of “muddling through”
195 might be to construct hierarchical models with the Bayesian method or variants of GLM methods.
196 But still one should be aware of the non-identifiability problem (Raue et al. 2013). MCMC
197 methods are so powerful, and output tentative posterior probability of parameters; however this
198 may be scientifically nonsensical (see Dorazio 2015; Taper and Ponciano 2015).

199 This Special Feature is another, albeit non-visualized and rather verbal, mandala. You
200 have to read through it, but after that, you will be able to visualize your own image in order to solve
201 your statistical problems. In this Special Feature, we have three contributing papers by four
202 statistics experts from different disciplines: Dr. Mark L. Taper and Dr. José M. Ponciano from
203 evidential statistics, Dr. Robert M. Dorazio from Bayesian statistics, and Dr. Kohji Yamamura from
204 Fisherian statistics.

205 Dr. Taper and Dr. Ponciano first overview different statistical approaches: Fisherian,
206 Bayesian, error, and evidential, in terms of population ecology. Their long introduction shows

207 conflicts among the approaches from methodological as well as philosophical points of view.
208 Then, they discuss the evidential statistical approach in depth. This explanation might be a good
209 place to start for those have never heard the name, “evidential statistical approach.” The final
210 section is a detailed list of misunderstandings and confusion of statistics in general, with which
211 population ecologists will no doubt be confronted at some point in their research. Readers might
212 be willing to compare these comments with previous ones from different points of view (e.g.,
213 Burnham et al. 2011).

214 Dr. Dorazio demonstrates contemporary views and attitudes of Bayesian approaches.
215 Based on the learning aspects of Bayesian approaches, he tries to persuade us that “hierarchical
216 modeling” is an engine for current research in the field of population ecology. He strongly
217 recommends Bayesian approaches as a first-choice method. He is not a fanatical Bayesian
218 evangelist at all, and discusses the *pros* and *cons* of Bayesian approaches. In particular, he admits
219 that the weakness in choosing prior probability and model comparison has not yet been solved
220 solely within Bayesian approaches, and hence, he recommends combinations with other statistical
221 approaches for those issues. He also provides brief but lucid explanations of MCMC techniques,
222 which most users of Bayesian software packages leave them as black-boxes. His examples are
223 very useful and practical even for Bayesian beginners.

224 Dr. Yamamura describes himself as a Fisherian rather than a frequentist. He has
225 repeatedly claimed in academic meetings that “Bayesian estimates can be used as an approximation
226 to maximum likelihood (ML) estimates,” which becomes the title of his article. His main
227 criticism of Bayesian approaches is the mal-effects of inappropriate prior probabilities of
228 parameters. He then proposes a Bayesian approximation of objective ML with appropriate

229 transformation that makes the posterior distribution close to a normal one. He explains his idea,
230 named as “empirical Jeffreys prior,” with a practical example of sika deer populations in Hokkaido,
231 Japan. The approximation method is, as Dr. Taper has repeatedly indicated, believed to have a
232 tight relationship with data cloning (Lele et al. 2007).

233 After reading through the above three articles, I am convinced that readers will have a
234 better understanding of what model selection is and of what parameter estimation is, as well as
235 learn what kinds of tools, such ML and Bayesian procedures, have been implemented for those
236 purposes. Discriminating as well as properly combining (not confusing) these two aspects will
237 work as a compass as readers “muddle through” the mandalas of statistics.

238

239 **Acknowledgement**

240

241 I thank Mark L. Taper, Robert M. Dorazio, and K. Yamamura for their contributions for this Special
242 Feature. I thank E. Kasuya for his helpful comments on an earlier manuscript. I thank N.
243 Minaka and B. Efron for allowing me to modify and reuse their mandalas. This study was
244 supported in part by Grant-in-Aids for Scientific Research (26440233) to YT from JSPS.

245

246 **References**

247

248 Albert J (2007) Bayesian computation with R. Springer, New York

249 Anderson DR, Burnham KP, Thompson W (2000) Null hypothesis testing: Problems, prevalence,
250 and an alternative. *J Wildlife Manage* 64:912-923

251 Bolker BM (2008) Ecological models and data in R. Princeton, New Jersey

252 Burnham KP, Anderson DR, Hyuvaert KP (2011) AIC model selection and multimodel inference in
253 behavioral ecology: some background, observations, and comparisons. *Behav Ecol Sociobiol*
254 65:23-35

255 Crawley MJ (1993) GLIM for ecologists. Blackwell Scientific Publications, Oxford

256 Dobson AJ (1990) An introduction to generalized linear models. Chapman & Hall, London

257 Dorazio RM (2015) Bayesian data analysis in population ecology: Motivations, methods, and
258 benefits. *Popul Ecol* doi:10.1007/s10144-015-0503-4

259 Dunteman GH (1984) Introduction to linear models. Sage, Beverly Hills

260 Edgington ES (1995) Randomization tests. Marcel Dekker, New York

261 Efron B (1982) The jackknife, the bootstrap and other resampling plans. SIAM, Philadelphia

262 Efron B (1998) R. A. Fisher in the 21st century. *Stat Sci* 13:95-122

263 Ellison AM (2004) Bayesian inference in ecology. *Ecol Lett* 7:509-520

264 Gelman A, Rubin DB (1992) Inference from iterative simulation using multiple sequences. *Stat Sci*
265 7:457-472

266 Gill J (2008) Bayesian methods: a social and behavioral sciences approach. Chapman & Hall/CRC,

- 267 Boca Raton
- 268 Good P (1993) Permutation tests: a practical guide to resampling methods for testing hypotheses.
- 269 Springer-Verlag, New York
- 270 Hall P (1992) The bootstrap and edgeworth expansion. Springer-Verlag, New York
- 271 Hinton PR (2004) Statistics explained, 2nd ed. Routledge, London
- 272 Holm S (1979) A simple sequentially rejective multiple test procedure. Scand J Stat 6:65-70
- 273 Hooten MB, Hobbs NT (2015) A guide to Bayesian model selection for ecologists. Ecol Monogr
274 85:3-28
- 275 Hsu JC (1998) Multiple comparisons: theory and methods. Chapman & Hall, London
- 276 Kéry M, Schaub M (2012) Bayesian population analysis using WinBUGS: a hierarchical
277 perspective. Academic Press, Burlington
- 278 Kruschke JK (2011) Doing Bayesian data analysis: a tutorial with R and BUGS. Academic Press,
279 Burlington
- 280 Lele SR, Dennis B, Lutscher F (2007) Data cloning: easy maximum likelihood estimation for
281 complex ecological models using Bayesian Markov Chain Monte Carlo methods. Ecol Lett
282 10:551-563
- 283 Manly BF (1997) Randomization, bootstrap and Monte Carlo methods in biology, 2nd edn.
- 284 Chapman & Hall, Boca Raton
- 285 McCarthy MA (2007) Bayesian methods for ecology. Cambridge University Press, Cambridge
- 286 McGraw SB (2011) The theory that would not die. Yale University Press, New Haven
- 287 Moran MD (2003) Arguments of rejecting the sequential Bonferroni in ecological studies. Oikos
288 100:403-405

- 289 Nagelkerke NJD (1991) A note on a general definition of the coefficient of determination.
- 290 Biometrika 78:691-692
- 291 Neave HR, Worthington PL (1988) Distribution-free tests. Routledge, London
- 292 Noether GE (1991) Introduction to statistics: the nonparametric way. Springer-Verlag, New York
- 293 Noreen EW (1989) Computer intensive methods for testing hypotheses: an introduction. Wiley,
- 294 New York
- 295 Peitgen HO, Jürgens H, Saupe D (1992) Chaos and fractals: new frontiers of science.
- 296 Springer-Verlag, New York
- 297 Qian SS (2010) Environmental and ecological statistics with R. Chapman and Hall/CRC Press,
- 298 Boca Raton
- 299 Qian SS, Shen Z (2007) Ecological applications of multilevel analysis of variance. Ecology
- 300 88:2489-2495
- 301 Raue A, Kreutz C, Theis F, Timmer J (2013) Joining forces of Bayesian and frequentist
- 302 methodology: a study for inference in the presence of non-identifiability. Philos T Roy Soc A
- 303 371:20110544
- 304 Royle JA, Dorazio RM (2008) Hierarchical modeling and inference in ecology. Academic Press,
- 305 Amsterdam
- 306 Salsburg D (2001) The lady tasting tea: how statistics revolutionized science in the twentieth
- 307 century. Owl Books, New York
- 308 Sokal RR, Rohlf FJ (1981) Biometry, 2nd ed. W. H. Freeman & Company, San Francisco
- 309 Spiegelhalter DJ, Best NG, Carlin BP, van der Linde A (2014) The deviance information criterion:
- 310 12 years on. J Roy Stat Soc B 76:485-493

- 311 Sprent P (1993) Applied nonparametric statistical methods, 2nd ed. Chapman & Hall, London
- 312 Stan Development Team (2015) Stan modeling language users guide and reference manual, ver.
- 313 2.7.0
- 314 Stephens PA, Buskirk SW, Hayward GD, del Rio CM (2005) Information theory and hypothesis
- 315 testing: a call for pluralism. *J Appl Ecol* 42:4-12
- 316 Taper ML (1990) Experimental character displacement in the adzuki bean weevil, *Callosobruchus*
- 317 *chinensis*. In: Fujii K, Gatehouse AMR, Johnson CD, Mitchel R, Yoshida T (eds) Bruchids and
- 318 Legumes: Economics, Ecology and Coevolution. Kluwer Academic, Dordrecht, pp 289-301
- 319 Taper ML, Lele SR (eds) (2004) The nature of scientific evidence: statistical, philosophical, and
- 320 empirical considerations. University of Chicago Press, Chicago
- 321 Taper ML, Ponciano JM (2015) Evidential statistics as a statistical modern synthesis to support 21st
- 322 century science. *Popul Ecol* doi:
- 323 Trafimow D, Marks M (2015) Editorial. *Basic App Soc Psych* 37:1-2
- 324 Ward EJ (2008) A review and comparison of four commonly used Bayesian and maximum
- 325 likelihood model selection tools. *Ecol Model* 211:1-10
- 326 Yamamura K (2015) Bayes estimates as an approximation to maximum likelihood estimates. *Popul*
- 327 *Ecol* doi:10.1007/s10144-015-0526-x
- 328 Zar JH (1984) Biostatistical analysis, 2nd ed. Prentice-Hall Inc., Englewood Cliffs
- 329

330 **Figure Legends**

331

332 Figure 1. Minaka's statistical mandala. This image is recreated from Dr. Nobuhiro Minaka's
333 original one posted at <http://cse.niaes.affrc.go.jp/minaka/R/images/Mandala2004-large.jpg>.

334

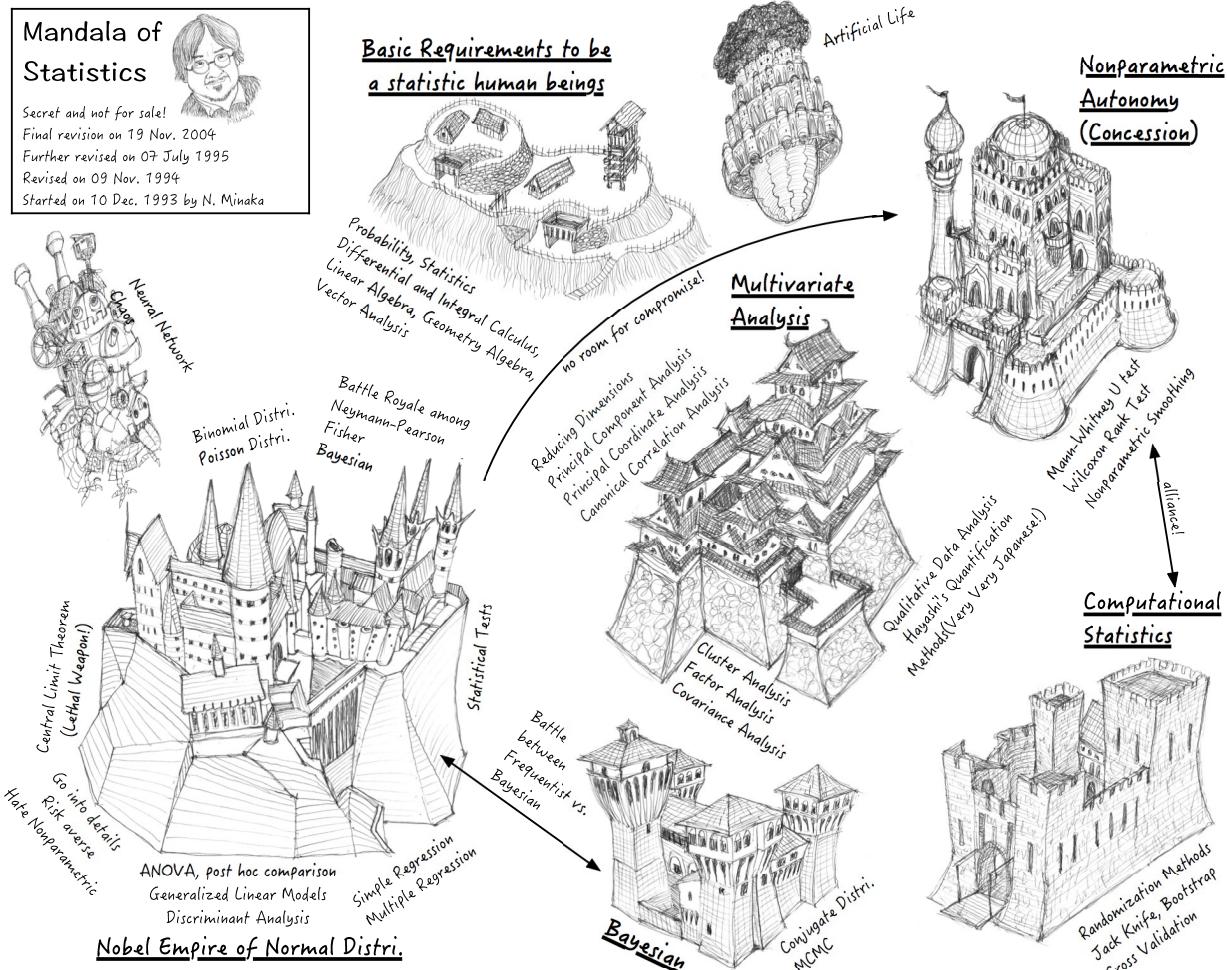
335 Figure 2. Efron's statistical mandala. For each aspect, the sitting place of Dr. Fisher indicates
336 the position of the Fisherian between Bayesian and frequentist. This image is recreated from Fig.
337 1 in Efron (1998).

338

339 Figure 3. A simplified statistical mandala. The horizontal axis indicates a statistical space that
340 ranges from small/simple to large/complex. The shaded rectangle shows the domain of the
341 normal distribution empire. Statistical problems often lie outside of the shaded rectangle.

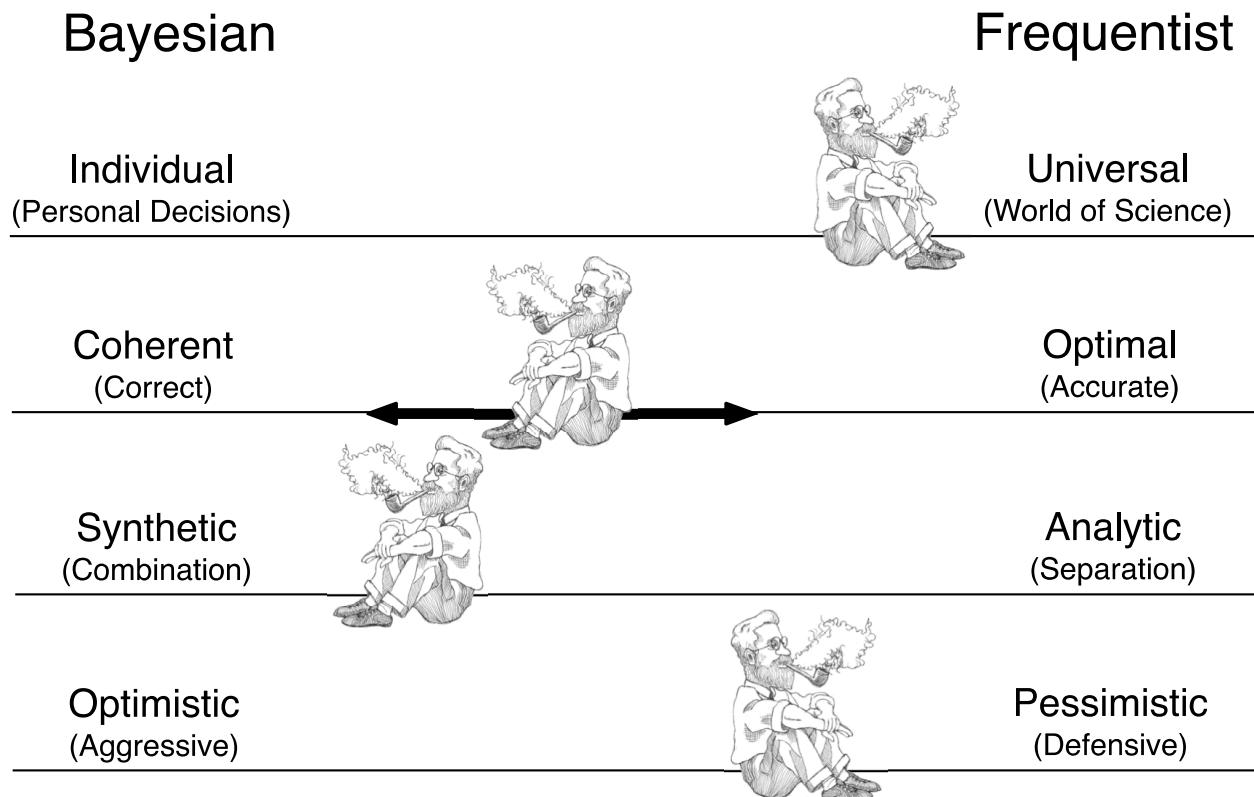
342

343 Figure 1



344

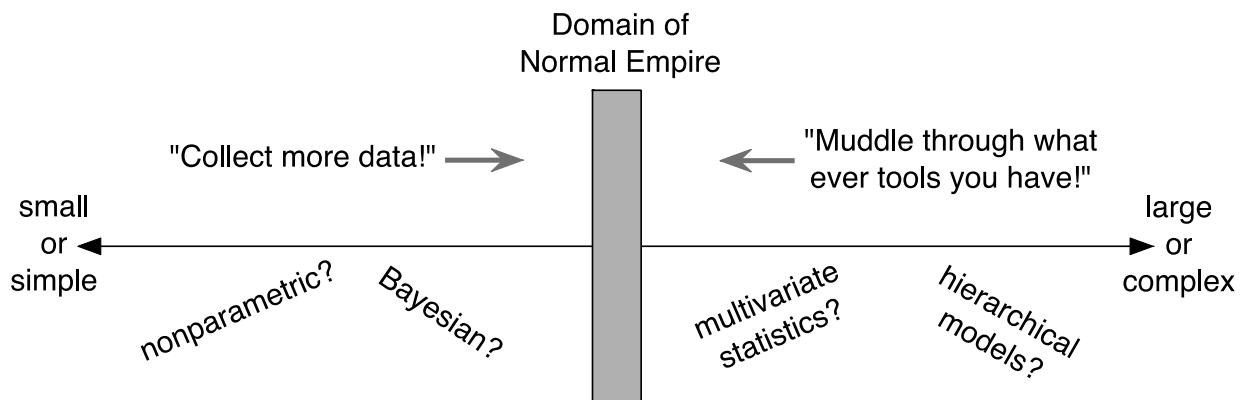
345 Figure 2



346

347

348 Figure 3



349