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Estimating abundance of Galliformes: tools and application

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ABSTRACT

A large number of techniques are available for assessing populations of vertebrates. However, application of many of those techniques to Galliformes is hampered by a variety of constraints. These problems are often magnified by poor understanding of the biology of many species of concern, and an absence of valid estimates of abundance and demographic parameters. Researchers interested in developing estimates of Galliformes populations must address a number of key issues before collecting field data, to avoid biases in the resulting population estimates. General guidance exists for the identification of appropriate population estimation techniques, and a dichotomous key has been developed for abundance estimation of other vertebrates, such as mammals. First, we review some of the basic principles of abundance estimation, with the goal of identifying sources of bias, and avoiding these in field surveys. We then develop specific guidelines for Galliformes, and a key to abundance estimation for field researchers. Based on our knowledge of the general biology of Galliformes, the most applicable techniques for estimating abundance are based on variations of distance sampling techniques, mark-resighting techniques, and removal techniques. Use of indices should be considered only when more quantitative analyses are logistically or biologically impossible. However, their use can be made more valuable by employing double sampling or other methods that directly link indices to unbiased estimates of abundance.

INTRODUCTION

Over the last 20 years, Galliformes biologists from around the world have been successful in establishing research projects on the many species with conservation status outlined in the various Action Plans (McGowan *et al.*, 1995; McGowan & Garson, 1995; Fuller & Garson, 2000; Fuller *et al.*, 2000). In gaining a useful understanding of the conservation status of particular species, we must have information on the distribution of the species, occupancy of available habitat, relative population estimates, and possible threats. Unfortunately for many of our species we are able to obtain these types of information with various levels of confidence in quality. However, these data often represent a "snapshot" of the population, but do not provide more useful information on population densities, rates of population increase or decrease, or causal factors affecting changes in population.

There is obviously a wide-range of biological, logistical, and financial constraints that limit our ability to understand populations of many species. Nonetheless, conservation decisions for these species must be made with incomplete data. We suggest that a hierarchical approach to understanding populations and demographics is necessary in order to make the best possible conservation decisions, given this incomplete understanding, and within the inevitable logistical and financial constraints. Such an approach must also allow us to assess the quality of our conservation decisions. Assuming that many of our species are relatively unstudied, we propose that even basic, descriptive models of populations are an important starting point. However, in our experience, once a species is judged to merit conservation status, evaluation of population status frequently comes to a stop. We believe that this failure to adequately understand population dynamics and causal factors will unnecessarily put many of our species at additional conservation risk.

We present an approach for developing a more structured approach to understanding populations and population dynamics of Galliformes. This approach suggests that many of the typical population estimation techniques should be looked at not as an endpoint, but as a step needed to better develop conservation assessments and strategies.

LEVELS OF POPULATION ANALYSIS

As suggested above, there are several levels at which population analysis can be initiated, depending on existing knowledge and the immediate and long-term needs of conservation. Often, little is known about the distribution, basic life history, and habitat affinities of the species, and this information is a prerequisite to further understanding. Beyond such basic information, conservation biologists will desire, if possible, estimates of abundance or density, or

if not, at least of relative abundance over the range. However, assessments such as these of the "status" of the species typically will be inadequate for management. At a minimum, biologists will wish to know whether the population is generally increasing or decreasing, the geographic areas (and habitats) in which increases or decreases are most pronounced.

As we shall see, defensible information on population status, trends, or both may or may not be readily attainable, but even if it is, is usually insufficient for management, without at least partial understanding as to why these patterns occur. Thus, for instance, animals may exist at higher densities in certain habitats, not because the habitats are particularly good, but because of demographic processes such as source-sink (Pulliam, 1988). Ideally, then, information on demography should also be available, as well as on patterns of abundance. Beyond simply quantifying abundance or demographic rates, however, we really need to know something about what factors may be affecting these rates, in particular so that negative impacts can be controlled, mitigated, or both. As a first step, measurement of habitat and environmental factors such as pollution should be taken, so that these may be compared to patterns in abundance and/or vital rates. Ideally, one would go beyond this correlative approach, to active control and assessment of the impacts of factors, via either direct experimentation or by adaptive management (Johnson *et al.*, 1997; Walters, 1986).

Again, we recognize that many or perhaps most conservation analyses will fall short of the above ideals. However, regardless at which level of analysis, it is absolutely essential that sound estimates of abundance, or at least relative abundance or density, are available. Without these, even basic comparisons over time, among habitats, or in relation to possible impacts will be suspect, and appropriate conservation decisions may be unsupportable (Conroy and Smith, 1994; Conroy and Noon, 1996). We believe that inattention to these details has plagued many otherwise laudable conservation efforts, and therefore devote the remainder of this paper to a discussion of approaches to sound estimation for the Galliformes.

GENERAL GUIDELINES FOR ESTIMATING ABUNDANCE

Any endeavor to estimate abundance, whether for Galliformes or for other taxa, should follow basic principles, which we outline below.

1. Objectives. It is essential that one properly define the objectives of the analysis. Is the purpose to estimate total abundance, or is it to estimate abundance for different portions of the range, or in different habitats? Is the principal purpose to make comparisons, for example among areas managed differently? Is one attempting to assess dynamics (trends), so that estimates of abundance through time, and rates of change, are needed? Is one attempting to ascertain causal relationships, either via correlational study, experimentation, or adaptive management (Walters, 1986)?

2. Sampling. Sampling from biological populations involves selection of elements of the population or study area (known as the target), taking measurements (e.g., a count) on those elements (α if known or if estimated), and then extrapolating back to the target population using inferential statistics. In doing so it is absolutely critical to keep several things in mind, if the sample estimates are to have biological meaning. First, it is important to carefully define the target population of interest. In most instances this should be straightforward (that is, we have a fairly good idea of what it is we are interested in), but it is surprising how often field sampling occurs without such a target in mind. Assume here, though, that we've done a good job of defining our target population as the population of some species of pheasant or quail that inhabits a 10,000ha reserve. Now we must be sure that our sample measurements about that population actually represent this target in a statistical sense. Fairly obviously, a survey along a single 1km stretch of road in the southwest corner of the reserve will do a terrible job of representing the reserve.

There are a number of methods that can be used to assure that the sample is statistically representative of the target population, including random or systematic sampling. Often, subdividing the target into sub-areas or strata can be used to improve the efficiency in which we apply our field effort prior to sampling, particularly if these are related to variation in abundance or density (or even complete absence) of the species of interest. For example, suppose that our target species is known to favor, in decreasing order, fields, forest edges, and forest interior, and all three types of habitats exist in our study area. If these habitats are mapped, we can stratify the study area by habitat and either randomly or systematically select sample points within each of the strata. This accomplishes two things: first, it assures that sampling is spread over the entire area, rather than clumped in a few non-representative areas, as may occur by chance with small random samples. Second, it utilizes our knowledge of the species and its habitats to "soak up" a certain amount of variability in the strata, resulting in more precise estimates than if samples were selected according to a simple random sample.

Sometimes biologists lose track of the reasons for sampling, and assume that more samples are always better. Clearly, the mistake of this point of view would be to "sample" (i.e., enumerate or count every single individual) the

entire population. This is what is technically meant by the term "census", although in practice a true census almost never occurs for any population, including humans. In fact, a complete population enumeration is often *less* reliable than a properly executed sample estimate, and is nearly always less efficient. On the other hand, a "sample" of a size one would nearly always be very unreliable. The goal of sampling should be to use sufficient sampling effort to assure statistically reliable estimates. Insufficient sampling effort will result in estimates of poor reliability that may be of little use to conservation; excessive sampling is a misallocation of resources that could be better utilized elsewhere (monitoring a different species, conserving habitats, etc.).

3. Detectability (β) control and estimation. In populations, reliable abundance estimates will not be assured just by increasing the number of spatial sampling replicates: attention must be paid to the issue of detectability at each of the points in space. Counts or other observations at each of these points must bear some relationship, either known or estimable, to abundance in the vicinity of the points, or sample-based estimates will be unreliable measures of abundance. This is true regardless of sampling intensity, and would apply whether 1% or 100% of the sample area is sampled. Take for instance a situation in which a 1000 ha study area is completely covered by 100 10-ha sample plots, so that 100% of the area is sampled. Let us suppose that we count c_i birds at each of the plots, for a total of $C = 125$. It appears that our best estimate of the population is $\hat{N} = 125$. However, unknown to us, on average we missed 30% of the birds actually present on each sample plot, or conversely that we found only 70% of the birds actually present. This means that our estimate of the population is 30% lower than the true population $N = 179$.

In general, since we don't know β , we'll need a sample-based estimate of it. Ordinarily this requires collecting additional data beyond just the sample counts, as discussed further below. This is, in fact, the basic approach used in most of the abundance estimation procedures that take into account detectability, although usually the estimation formulas and models will be a bit (sometimes a lot) more complicated.

Sometimes biologists will try to avoid the issue of detectability, by claiming that after all what is of interest is an estimate of relative abundance (i.e., an index). These claims would be legitimate, if it could be affirmed that detectability is uniform over time and space, in which case relative changes in the counts alone would suffice. However, there are many biological and logistical reasons to suppose that in general such a claim would be false. For example, observers with different levels of ability or experience may be involved in conducting surveys from year to year, resulting in counts that represent differing fractions of the population actually present. Counts could differ from year to year solely on account of this observer effect, even if abundance did not change. Comparisons over space may be faulty as well. For example, birds may be visually or aurally detected at different rates in habitats with differing amounts of vegetative cover, or having different topographies.

Ideally, detectability (β) should be estimated as part of the counting procedure. In practice this may be difficult to do at all sample locations. At least two alternatives exist. One is to conduct experiments in a variety of habitats, different observers and weather conditions, etc., in which the counts are compared to known values or unbiased estimates of abundance. The result of this would be estimates of β and a model of variation in β that presumably could be used to adjust the counts C in subsequent monitoring. A better approach would be to incorporate double sampling into the sampling design. We describe double sampling in more detail later.

From the previous discussion it is clear that sampling and estimation involve; 1) inference from a relatively small sample fraction (α) of the study area to the entire area, and 2) correction of the biased count on this area by detection probability (β). Again, often our sampling design and statistical models will be much more complex than these simple constants.

4. Estimates of estimate confidence Almost never will the estimate be exactly equal to population size or other measure of interest. We can only make probability statements about what the data suggests the true population size. Simple or point estimates of abundance are by themselves of limited value, unless we have some measure of their statistical reliability. Basically the idea is: how likely would we be to obtain the same (or similar) value for the abundance estimate, if we were able to repeat the sampling and estimation many times? This is the idea of *precision*, or conversely variance: estimates with high repeatability have low variance, and are said to be precise. Under certain assumptions (e.g., normality) we can also compute confidence intervals, which give us a probabilistic representation of precision: essentially, how likely is it that the confidence interval will contain the true parameter value?

APPLICATION TO GALLIFORMES

Objectives

The Galliformes are a unique group among the birds in that they include some species that are among the most intensively and extensively studied in the world (e.g. ring-necked pheasant *Phasianus colchicus* and northern bobwhite quail *Colinus virginianus*), yet many species are virtually unstudied. This situation creates many

challenges and opportunities for development of population analyses for conservation purposes. Many opportunities arise from intensive population studies on common species because of technique development that can then be applied to rare and unstudied species. This can be valuable both in terms of techniques selected and costs associated with development. However, there are limitations to transference of this knowledge to lesser-studied species. In addition, the goals of population analysis for common species is often different from studies of rare species.

In any case we must keep in mind that our data collection should provide defensible assessments of the conservation status of our species. This becomes particularly important when limited resources are available for undertaking conservation management of threatened species and decisions must be made to shift resources from one to another. In addition, when conservation management conflicts with other land use and human influences.

Sampling approaches

In assessing field methods for population assessment we need first to determine the strengths and limitations of each of the methods available in the context of logistical and financial constraints. In Appendix A we have used a hierarchical approach to provide guidance to field researchers. This approach uses two basic criteria, the first being that there is a great diversity of research goals requiring different levels of data precision and quality, and second, is that there is large diversity among Galliformes species in biology and habitat. What we do not do with this paper is address specific variations of these generalized methods that might need to be employed for a particular species; this is up to the creativity of the researcher.

Very often with Galliformes species that are relatively unstudied the first assessments of populations are usually based on surveys of occurrence records. These come from a variety of sources and often vary widely in quality (e.g. some might come from rapid assessment surveys whereas others might come from birder records). These data also provide no information on non-occurrence. The result is often very biased coverage. From these data little inference on populations is possible. However, these types of analyses can give us a foot in the door for designing better studies. An example of this is the bearded wood-partridge *Dendrortyx barbatus* in Mexico. In 1995, the species was considered Critically Endangered because recent site records had only come from one or two locations in the vicinity of Veracruz (Howell and Webb, 1992; Carroll *et al.*, 1994; McGowan *et al.*, 1995). However, more recent surveys using play-back to detect populations in remnant forests has produced a total of 14 populations, including some in rather expansive and protected forests (Eitniear *et al.*, 2000).

The next level of analysis is the use of presence/absence (not detected) studies. These are commonly applied in conservation assessments of rare species. These are a substantial improvement over the previous technique, especially if based on a legitimate spatial sampling framework. This technique may be capable of limited inference about absence (rather than simply missed), but this requires estimates of detection (β). This level of analysis is not utilized nearly as much as it should be. Very often researchers report detections, but fail to report lack of detections in surveyed areas. When they do they rarely provide any estimates of the level of survey needed to obtain some detection rate when the birds are present—that is they give no indication or estimate of how likely they were to miss populations in habitats they surveyed and failed to detect the target species.

The two previous examples are the level population analysis that could provide a rough assessment of conservation status. However, they are not an end-point and the latest criteria used by the IUCN to establish conservation status generally requires more quantitative data (Hilton-Taylor, 2000). The following techniques which should be the core of our population analysis methodology are outlined in Appendix A.

Population indices or simple counts (Appendix A, number IV). These can include call indices and playback studies, or point counts. It is most important that these are combined with a legitimate spatial sampling framework (e.g. random or stratified). May be useful for comparative (time, space) inference if strong assumptions about equal detection rates are met. However these assumptions are hardly ever examined! In the few intensively studied Galliformes where these assumptions have been examined we find that often indices often provide a poor assessment of populations and changes in those populations. For example, call-counts of northern bobwhite quail during the breeding season have been used extensively as a population index in the U.S.A; however, Preno and Labisky (1971) and DeMaso *et al.* (1992) found that the technique performed poorly in predicting populations. Others have found a positive relationship between breeding season call-counts and subsequent harvest by hunters (Curtis *et al.*, 1989). Similarly, counts of calling male common pheasants have been used as an index to breeding populations. However, Lachland and Bray (1976) and Hill and Robertson (1988) both demonstrated that numbers of territorial males (calling males) can remain rather stable despite wide fluctuations in hen populations. The numbers of hens with each territorial male in this harem polygynous species can vary from nearly 1:1 to 7 or 8:1.

We argue that much more emphasis be placed on incorporating the latter into study design. In many cases this can be done with little extra effort. We will discuss use of double sampling or use of other techniques such as radio telemetry for this purpose later.

Quadrat or plot sampling techniques (Appendix A, number I). Quadrat techniques, which are based on the generalized techniques of the animals being observable, have been successfully applied to a number of common species. Complete counts of a study area have been used by Potts (1986) to develop a census of gray partridge *Perdix perdix* for >30 years in southern England. Complete counts on standardized sample areas has been employed for the ring-necked pheasant in the United Kingdom (Hill and Robertson, 1988) and bobwhite quail in the U.S.A. (Wellendorf, 1999). Again, a legitimate spatial sampling scheme is necessary. These methods can be strengthened by development of detection rate estimates. For example, the use of radio-tagged birds to develop estimates of calling rates (providing an estimate of detection rate β) for the quadrat sampling of autumn populations of the northern bobwhite in the U.S.A. (Wellendorf *et al.*, 2001).

Distance sampling (Appendix A, number I; Buckland *et al.*, 1993, see Appendix B). When properly designed this family of methods can provide direct estimates of population densities as well as provide estimates of detection. Minimally, at the least this method can resolve the issues of homogeneity of detection needed for indices. Ideally, properly designed distance sampling projects can provide unbiased estimates of density/abundance that do not require strong assumptions (exception is usual assumption of 100% detection at the line or point). This method has performed well for bobwhite quail (Guthery, 1988), mountain quail *Oreortyx pictus* (Brennan and Block, 1986) and gray partridge (Ratti *et al.*, 1983). Among tropical species, Sande (2001) employed point-distance techniques to establish population estimates for Nahan's francolins *Francolinus nahani*. In the latter example, Sande (2001) suspected that detection distances could be biased because he used playback and he believed that if the birds did not respond immediately that they would approach the observer then call. This would result in an overestimate of the population. Although some researchers have found that line transect can work well for northern bobwhite quail, others found it to perform poorly (Kuvlesky *et al.*, 1989) under different sets of conditions (e.g. in areas with very low population densities).

Mark-resighting/recapture/removal (Appendix A, numbers II and III; White, 2000, see Appendix B). If properly designed these provide a direct estimate of detection. At the least can resolve the issues of homogeneity of detection needed for indices. Ideally can provide unbiased estimates of density/abundance that do not require strong assumptions. Multiple recapture/resightings allow robust estimation of detection (so do not require assumptions that all animals are equally catchable, or sightable). Comparisons of mark-recapture and capture-removal have been done for bobwhite quail by O'Brien *et al.* (1985) and they suggested that mark-recapture provided biased (and low) estimates of populations due to heterogeneity in trapping and "trap happy" responses. In this case removal through harvest (III) was combined with marking techniques (II). Kuvlesky *et al.* (1989) found that mark-recapture techniques tended to underestimate populations of bobwhites at low population densities. Change-in-ratio estimators were used by Church and Porter (1990) to estimate mortality of gray partridge during winter. This can also be extended to population estimation.

There are obviously many variations on each of the techniques outlined very briefly here. For example, in distance sampling this can include line transect and/or point counts.

Double sampling approaches

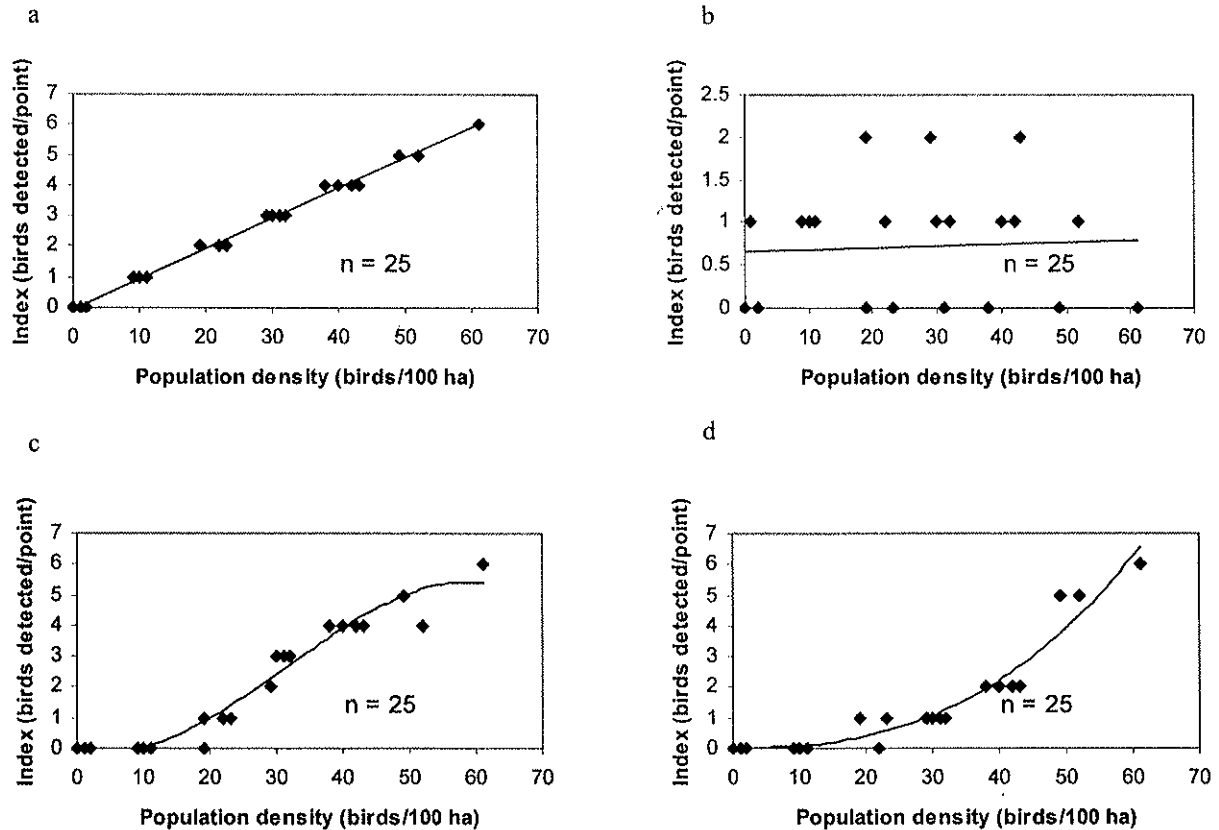
As we look at the continuum of techniques available to estimate populations of Galliformes, more intensive techniques, such as mark-recapture often can provide more reliable and robust estimates of abundance, but are often expensive and time consuming to undertake. Within the logistical and financial constraints most Galliformes biologists face these may not be practical for the entire study sample. Conversely, less intensive techniques, such as indices based on call counts may be less reliable, but are usually cheaper, faster, and can be used to cover a larger area.

Double sampling provides the opportunity for us to use more intensive sub-sampling. The general idea is that intensive and more quantitative methods are used on a sub-sample of the study area. The less intensive method is then used for all the samples collected throughout the study area. Since some samples will be collected using both techniques, relationships between the two methods can be developed. This relationship is then used to extend inference (quantitative population estimates) from the sub-sample to the entire sample.

To illustrate this point let us take a sample of 100 randomly located points in the study area and conduct a playback survey at each point. At 25 of the points we also use a distance-based method (e.g., point sampling with distance to the detected birds measured) to obtain unbiased estimates of density. We can then establish the predictive relationship between the two techniques. This relationship might take any number of forms, but ideally we would like to see some linear relationship with a rather simple slope function. For example, in Figure 1a we see that as our estimate from the intensive method increases, the value derived from the index method increases in a linear fashion. We might also get a relationship that suggests our index is not useful in detecting population variation (Figure 1b). We might also get relationships that are non-linear which might make estimates of density more complicated to interpret. For example, in Figure 1c, our index has difficulty detecting density differences at both low densities and

high densities, whereas the relationship, outlined in Figure 1d, suggests that the index has little ability to detect differences in populations at low densities and may only be useful with higher density populations.

Figure 1. Hypothetical relationships between a quantitative population estimate on the x-axis and an index on the y-axis. Figure 1a shows a positive and linear relationship, 1b suggests no relationship, and 1c and d suggest positive relationships that are not linear.



Other techniques which are currently being employed by Galliformes biologists can also be used to improve the quality (or developing better values for α and β). The most obvious is the use of radio-telemetry. A good example from this volume is the use of radio-tagged bobwhite quail by Wellendorf *et al.* (2001) to determine detection rates (β) of calling birds.

CONCLUSIONS AND RECOMMENDATIONS

The Galliformes are a diverse group of species inhabiting a wide range of ecosystems and exhibiting a wide range of behaviours that affect the quality and value of population parameter estimates. However, as in other species, there are a large number of practical and logistical constraints with these species. The most important starting point is the objective of the research. In many cases we are attempting to provide information to make conservation assessments on these species and provide information for practical management. The better the information the better we can do both of these things. The important consideration here is that some of the basic population work that is minimally necessary to make conservation recommendations can be made better using some of the techniques outlined here.

We must combine our practical knowledge of the birds' biology and behaviour along with our quantitative tools (sampling design, models) to make the best use of limited time and resources. Methods that provide unbiased estimates, and estimates of reliability (variance, CI) will be more reliable and defensible than ad hoc approaches. Finally, we must move beyond simple estimation of abundance to estimates of demographics and development of predictive relationships. Abundance estimation is just the first step. Fortunately, many sampling methods (e.g., mark-recapture) can be extended to allow explicit estimation of survival, movements, reproduction, and other important parameters.

In the past conservation assessment on species for which we had little data in threatened habitats we often left the job of understanding the population dynamics of these species undone. It is now quite apparent based on some important projects that are now being completed (e.g. Eric Sande's Ph.D. thesis project on Nahan's francolin) that

we can by careful planning and just a bit more investment in resources make much better and defensible statements on the conservation status of our species.

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