



BTO Research Report No. 377

**Investigation of methods for
producing joint CBC-BBS trends**

David G. Noble, Stuart E. Newson & Andrew C. Joys

March 2004

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Part 1. Options and problems associated with the production of joint CBC/BBS weighted indices

EXECUTIVE SUMMARY

1. In the production of joint CBC/BBS indices, inclusion of weightings in the SAS GENMOD analyses for the BBS data (to account for differences in survey coverage among regions) requires that some weighting for the CBC is also used.
2. Although the coverage of the CBC is mainly restricted to Southern Britain and is not randomly based, regional weighting has not been previously used in the production of trends based solely on the CBC. Given that the CBC ended in 2000 anyway, we did not want to expend effort on introducing regional weighting in the CBC at this stage that would retrospectively change all previously reported changes. This means that we needed to assign an arbitrary and equal weighting across all CBC sites.
3. Standard BBS and CBC analyses (on their own) correct for over-dispersion in the data using scaling (pscale or dscale commands), so it makes sense to continue to do this. In the presence of scaling, an increase in the absolute weighting values does not influence the estimated parameters. However, CBC or BBS weights should be adjusted so that they are comparable (i.e. either adjust up CBC weights, giving all CBC sites the mean BBS weight across sites/years, or adjust down the BBS to have a mean weight of 1 and give CBC sites a weight of one). Both methods give the same estimates and standard errors, so the choice of these is analytically irrelevant. We decided to keep the BBS weightings the same as in previous BBS analyses and scale up the CBC weights.
4. A problem, however, is that by scaling, one is assuming that over-dispersion is the same in both CBC and BBS surveys. The results here suggest that this assumption is basically true for non-flocking species, with the over-dispersion likely to be relatively similar between surveys. However for flocking species, where the over-dispersion is likely to differ between surveys, the standard errors of the resulting joint estimates may not represent the combined situation particularly well. This is especially apparent in the Wood Pigeon when joint CBC/BBS trends are presented for the period 1965 to 2000, with BBS trends from 1994 to 2000. Ideally each survey should be scaled separately, although there is no obvious way to do this in SAS and further work would be needed to examine this problem further.

INTRODUCTION

The Common Birds Census (CBC) was introduced in 1961, at the request of the then Nature Conservancy, to monitor national trends of widespread and abundant breeding bird species in the UK. These data have been fundamental in highlighting declining trends in a number of species and have underpinned many recent conservation initiatives, including the Birds of Conservation Concern, the government's populations of wild birds indicators, the UK Biodiversity Action Plan and the State of the UK's Breeding Birds. However, the CBC has a number of limitations as a national monitoring scheme. It involves the mapping of bird territories from observations during seven to ten visits per year, making it relatively time-consuming and expensive for both observers and BTO staff. Secondly, because observers select their own CBC plots, mainly in farmland or woodland, there is unrepresentative habitat coverage and a bias towards the southern and eastern areas of the UK where observer densities are greatest (Gregory *et al.* 1995). Whilst the CBC plots are probably not representative of the UK as a whole, farmland CBC plots at least have been found to be representative of most of lowland farmland in England south of the river Humber and east of the River Severn (Fuller *et al.* 1985), within a square of roughly easting 3000 and northing 5000 of the National Grid, referred hereafter as Southern Britain (shown in Figure 1.1).

To address the limitations of the CBC methodology, the BTO in collaboration with the Royal Society for the Protection of Birds (RSPB) and Joint Nature Conservancy Council (JNCC) introduced the Breeding Bird Survey (BBS) in 1994, which uses the line transect method for recording birds. BBS survey squares are randomly selected from a list of all 1 km squares in the National Grid that comprise the UK, excluding coastal squares with less than 50% land. Use of volunteers is maximised through a stratified random sampling design. Initially, the number of squares allocated to each of the BTO's 83 regions (roughly counties or groups of counties) was a fixed proportion of the number of potential volunteers in the region, estimated using BTO membership information. For regions with relatively few potential volunteers, a minimum level of coverage was set. Within each region, squares are selected randomly, and allocated to volunteers through a network of voluntary regional organisers (Organisers receive a list of target squares for their region, and to maintain the random design of the survey, are asked to allocate them to volunteers in the order generated. Because the stratified sampling design results in unequal representation of regions across the UK, annual counts are weighted by the inverse of the proportion of the area of each region that is surveyed that year.

Because the BBS requires fewer visits to each site, and through its active promotion as a national monitoring scheme, a much greater and, importantly, random coverage of the UK was achieved. In 2000, 2248 BBS squares were surveyed, compared to 212 CBC plots, which vary in area from about 5 to 100 ha. The long-term aim is to replace the CBC with the BBS following a period of overlap, during which trends could be compared and calibrated. Freeman *et al.* 2003, compared species trends calculated from the CBC and BBS surveys for 74 species for which annual indices are routinely calculated by both surveys during the period of overlap (1994 to 2000) to examine the potential for producing combined CBC/BBS indices. This showed that the majority of species CBC and BBS trends were similar within an area of Southern Britain (defined as a square with easting 3000 and northing 5000), although at the UK level trends were comparable for only around half the species examined. In this study we examine the options and problems associated with the production of joint and weighted CBC/BBS indices.

METHODS

In the past annual BBS and CBC population indices have been calculated in SAS (SAS 1996) using a log-linear regression model with Poisson error terms. Counts are modelled as a function of site and year effects using the SAS GENMOD procedure. The year effect is used as an annual index of total numbers, whilst the site effect describes how species abundance at sites differ from one another. The first index in a run of years is set to an arbitrary value 1 and other indices are measured relative to this. The GENMOD procedure uses the maximum likelihood method to fit the model and corrects for over-dispersion in the data using the `pscale` and `dscale` options. Whilst these have no effect on the estimates of parameters, they can have important effects on estimated standard errors.

Because the stratified sampling design of the BBS results in unequal representation of regions across the UK, annual counts are routinely weighted by the inverse of the proportion of the area of each of 83 regions surveyed in each year. The CBC is more restricted in its range than the BBS, with most sites located in Southern Britain (Fuller *et al.* 1985 as a square bounded by easting 3000 and northing 5000) and this survey has not used weightings in the past.

Freeman *et al.* 2003 examining the potential for combining data from CBC and BBS surveys to produce long-term combined indices, demonstrated that for the majority of species routinely monitored by both surveys, CBC and BBS trends were not significantly different within the above area of Southern Britain defined above. However, BBS trends for the entire UK were not comparable with CBC trends within Southern Britain for around half of the species examined. This suggested that combined CBC/BBS indices could be produced for the majority of species in Southern Britain, but Southern Britain data were not representative of trends within the UK for around half of the species examined. Discussions following these findings led to the decision to produce combined indices for England rather than an arbitrary area of Southern Britain, for greater political meaning. There is an approximately 90% overlap between the sites in England and sites covered by Southern Britain, and trends for the two areas were very similar (Newson, unpublished).

Earlier analyses by Freeman *et al.* 2003 produced combined CBC/BBS indices by multiplying the likelihoods of the two surveys and maximising the joint likelihood. These combined indices used unweighted data, noting that the problem of weighting in combined indices would need to be addressed. The problem is that we want to continue to weight the BBS in the same way as in previous years, but using GENMOD would mean that CBC data would also have to be weighted. However, we want to weight the CBC in such a way that when CBC only trends and associated standard errors are produced using these weightings, they are not different from previously unweighted CBC only trends and standard errors. One option would be to start weighting CBC data by region, although because of the limited geographic spread and smaller sample, it would be necessary to weight at a larger geographic scale (e.g. government office region) than the BBS. However, CBC-only indices and standard errors generated using this method would be different from previous estimates. Therefore, it was considered preferable to use a single CBC weighting across sites. One problem with this is that the choice of weighting is likely to be important, because as the weighting increases, the standard error of the resulting estimates are likely to decline, although correcting for over-dispersion using `pscale` or `dscale` commands, which are routinely used in the production of CBC and BBS only indices corrects for this.

The aim of the following work is to examine how best to produce weighted joint CBC/BBS indices. For this we need to examine the importance of scaling (using the `pscale` and `dscale` commands to correct for over-dispersion) and weighting, initially examining their influences on the production of single survey indices and associated standard errors and later using these findings to help in decisions relating to the production of weighted combined CBC/BBS indices. We use data from three example species, Willow Tit, Nuthatch and Wood Pigeon in this report to examine various scenarios. These species are chosen to

cover a flocking species, Wood Pigeon for which the BBS data is likely to be over-dispersed and Willow Tit and Nuthatch, as species which mainly occur in small numbers (one's and two's) and for which data are likely to be less dispersed (see Table 1.1 for dispersion coefficient values for these and other species routinely monitored by both CBC and BBS surveys).

RESULTS

Single survey indices: influence of weighting

To examine the effect of weighting and scaling (dscale command) on the resulting standard errors and estimates we run two sets of analyses. The first analysis examines the effect of using increasing weight (1, 10, 100 and 1000) in the absence of scaling, and second analyses using scaling to correct for over-dispersion. We examine the results for two example species, Willow Tit and Nuthatch.

The results presented in Table 1.2a and 1.2b for Willow Tit and Nuthatch in the absence of scaling demonstrate that as the weighting increases, the standard error of the resulting estimates decreases. However, if we use scaling to correct for over-dispersion, increasing the weight has no effect on the resulting standard errors or estimates (see Tables 1.3a and 1.3b). In other words, if we use scaling, the actual weighting chosen (obviously if the same across sites) is not important in a single survey analysis at least.

Combined CBC/BBS indices: how best to weight in a combined situation

As we show above, the choice of weighting is not important as long as we use scaling to correct for over-dispersion. However, when we have data from two surveys, it is likely that we need to adjust the BBS weights down or CBC weights up, so that the weightings are comparable. If the choice of weighting is not important if we correct for over-dispersion, we would expect the same results in a joint analysis by adjusting down the BBS to have a mean weight of 1 and CBC sites a weight of 1 as you would achieve by adjusting up the CBC, so that CBC sites have a mean equal to the mean BBS weight and using normal BBS weights.

To test the assumption that we need to adjust one or other surveys and that the choice of adjusting one survey up or another down is not important, we run three combined CBC/BBS analyses. In the first we, i) weight CBC sites by 1 and use normal BBS weighting as in standard BBS analyses, ii) adjust down the BBS so that it has a mean weight of 1 and give CBC sites a weight of 1, and iii) adjust up the CBC, so that it has a mean equal to the mean BBS weight and use normal BBS weights.

The results shown in Table 1.4, confirm that if we include scaling, the results are the same whether we adjust up the CBC or adjust down the BBS. However, it would not make sense to use a mean CBC weight of 1 and conventional BBS weightings, because in this case, one would be saying that individual BBS sites are more important than CBC sites and would individually contribute more to the results.

However using scaling introduces further complications. Using the pscale and dscale commands in combined CBC/BBS analyses, it would assume that over-dispersion is the same at CBC and BBS sites and use a single scaling value. Because of the greater quantity of BBS data, this scaling is likely to be most similar to BBS only scaling. To examine the extent which estimates from each survey independently are likely to be affected by this single scaling value, we compare results using i) BBS data only, ii) CBC data only, iii) BBS data only, but with scaling based on data from both surveys, and iv) CBC data only, but with scaling based on data from both surveys. We also run two joint CBC/BBS analyses to examine how the joint results compare with the above results, in one analysis we adjust down the BBS to have a mean weight of one and second to adjust up the CBC to have a mean equal to the mean BBS weight across years. We use as examples Willow Tit and Wood Pigeon. The Wood Pigeon is chosen because as a flocking species there is likely to be a large difference in over-dispersion between the two surveys therefore it is likely to show the greatest difference in the results.

The results shown in Table 1.5a and b confirm that because of the greater quantity of BBS data, the scaling based on data from both surveys is closer to the BBS only scaling i.e. provides a better correction for over-dispersion in the BBS data. Therefore, whilst standard errors or estimates using

BBS only data and BBS only data using scaling based on both surveys are a closer match than CBC only data and CBC only data using scaling based on both surveys. As expected this difference is greatest for the Wood Pigeon. Combined CBC/BBS analyses, produced results that are closer to the BBS only trends, because of the larger amount of BBS data used in the analyses.

The above analyses have looked at what happens during the period of overlap between the CBC and BBS from 1994 to 2000. To examine what happens when we extend the CBC back to 1965, we run three analyses using i) CBC data only, ii) CBC data only, but with scaling based on data from both surveys, and iii) a joint CBC/BBS trend. The results presented in Table 1.6 show that for a non-flocking species such as Willow Tit where the over-dispersion is likely to be fairly similar between the CBC and BBS surveys, using scaling based on both surveys produces standard errors of the estimate that are pretty similar. However, for a flocking species the Wood Pigeon, over-dispersion is very different between the two surveys, which means that standard errors of estimates based on a single scaling from both surveys, results in CBC standard errors that are considerably different from those resulting from scaling based on CBC data only.

DISCUSSION

The key point is that for GENMOD you have to use some weighting for the CBC if you use weighting for the BBS. Although one would like to say 'weight the BBS, but not the CBC', this is not possible in SAS. Therefore some weighting for the CBC would need to be used in a combined CBC/BBS analyses.

Because the coverage of the CBC is mainly restricted to Southern Britain, regional weighting has not been used in the past in CBC only trends to control for variation in observer coverage. For this reason, we do not want at this stage to introduce regional weighting in the CBC, which means we should assign an arbitrary and equal weighting across CBC sites.

In standard BBS and CBC only analyses we correct for over-dispersion in the data using scaling (pscale or dscale commands), so it makes sense to continue to do this. Also in the presence of scaling, an increase in the absolute weighting values doesn't matter. However, we should obviously adjust CBC or BBS weights so that they are comparable (i.e. either adjust up CBC weights, giving all CBC sites the mean BBS weight across sites/years, or adjust down the BBS to have a mean weight of 1 and give CBC sites a weight of one) – both methods give the same estimates and standard errors, so the choice of these is irrelevant.

However, one problem with this scaling method is that by scaling, one is assuming that over-dispersion is the same in both CBC and BBS surveys. The results here suggest that this is not too bad for non-flocking species, where the over-dispersion is likely to be relatively similar between surveys, although for flocking species, where the over-dispersion is likely to be most different between surveys, the standard errors of the resulting joint estimates may not represent the combined situation particularly well. This is especially apparent in the Wood Pigeon examined here when combined CBC/BBS trends are presented for the period 1965 to 2000, with BBS running the trend from 1994 to 2000. Ideally one would scale each survey separately, although there is no obvious way to do this in SAS and further work would need to examine this problem further.

Table 1.1 Estimates of dispersion after modelling CBC and BBS data, as measured by the deviance divided by degrees of freedom. If the dispersion estimate is greater than 1 the data may be overdispersed or underdispersed if the dispersion estimate is less than 1.

Species	CBC deviance/df (1965-2000)	BBS deviance/df (1994-2000)
Little Grebe	0.8744	1.2819
Mute Swan	0.6179	2.5755
Shelduck	1.1347	2.6696
Mallard	0.8796	2.3988
Tufted Duck	1.1499	2.9955
Sparrowhawk	0.5936	0.8896
Buzzard	0.4758	1.0737
Kestrel	0.5968	0.9305
Red-legged Partridge	0.7037	1.6547
Grey Partridge	0.7811	1.6634
Pheasant	0.9279	1.4696
Moorhen	0.7487	1.0985
Coot	1.2095	1.8801
Lapwing	1.2119	4.2325
Curlew	0.6200	1.8078
Woodcock	0.6924	0.7754
Stock Dove	0.8355	2.4044
Woodpigeon	1.3328	7.2473
Turtle Dove	0.9363	1.4185
Collared Dove	0.9222	1.5922
Cuckoo	0.6280	1.0074
Little Owl	0.6584	0.8568
Tawny Owl	0.6338	0.8457
Green Woodpecker	0.6034	0.9335
Great Spotted Woodpecker	0.5546	0.9891
Lesser Spotted Woodpecker	0.5870	0.8729
Skylark	0.9992	1.4619
Swallow	0.9107	2.7251
House Martin	2.4993	4.0919
Carrion Crow	0.5785	4.0890
Jackdaw	1.1098	4.8579
Magpie	0.5408	1.4140
Jay	0.5180	1.2010
Great Tit	0.7261	1.4445
Blue Tit	0.7615	1.8754
Coal Tit	0.8965	1.3500
Marsh Tit	0.7315	1.2652
Willow Tit	1.1202	1.2680
Long-tailed Tit	0.7450	2.4939
Nuthatch	0.6968	1.1130
Treecreeper	0.7004	1.0591
Wren	1.3238	1.3359
Robin	1.0253	1.2373
Redstart	0.7982	1.1561
Blackbird	0.7974	1.3383
Song Thrush	0.8431	1.2636
Mistle Thrush	0.6380	1.2652
Reed Warbler	1.4481	1.3988
Sedge Warbler	1.1734	1.3577

Blackcap	0.8114	1.0675
Garden Warbler	0.9694	1.0643
Whitethroat	1.1202	1.2684
Lesser Whitethroat	0.8210	1.0425
Willow Warbler	1.1889	1.2757
Chiffchaff	0.9069	1.1370
Goldcrest	1.0367	1.2446
Spotted Flycatcher	0.8036	1.0492
Dunnock	0.9949	1.2455
Meadow Pipit	1.0437	2.1853
Tree Pipit	0.8936	1.2696
Pied Wagtail	0.6482	1.2090
Grey Wagtail	0.6138	1.0867
Yellow Wagtail	0.8853	1.5413
Starling	1.5232	14.6031
House Sparrow	1.3087	3.4898
Tree Sparrow	1.3610	2.2705
Greenfinch	1.0123	2.2974
Goldfinch	0.9248	2.3809
Linnet	1.2336	3.4405
Redpoll	0.9629	2.8852
Bullfinch	0.7190	1.3507
Chaffinch	0.8416	1.4431
Corn Bunting	0.9930	1.4365
Yellowhammer	0.9903	1.2526
Reed Bunting	0.9188	1.2114

Table 1.2a. Effect of increasing the weight in a CBC only analyses, using the example Willow Tit in the absence of scaling.

Weight	Year	DF	Estimate	SE	LCL	UCL	Chi-sq	Pr > Chi-sq
Weight=1	2000	1	-0.7135	0.3753	-1.4491	0.0222	3.61	0.0573
	1999	1	-0.6609	0.3428	-1.3328	0.0111	3.72	0.0539
	1998	1	-0.2646	0.2931	-0.839	0.3098	0.82	0.3666
	1997	1	-0.485	0.3053	-1.0833	0.1134	2.52	0.1121
	1996	1	0.1303	0.2645	-0.3881	0.6486	0.24	0.6223
	1995	1	0.1856	0.2534	-0.3111	0.6824	0.54	0.4639
	1994	0	0	0	0	0	.	.
Weight=10	2000	1	-0.7135	0.1187	-0.9461	-0.4809	36.13	<.0001
	1999	1	-0.6609	0.1084	-0.8733	-0.4484	37.16	<.0001
	1998	1	-0.2646	0.0927	-0.4462	-0.083	8.15	0.0043
	1997	1	-0.485	0.0965	-0.6742	-0.2958	25.24	<.0001
	1996	1	0.1303	0.0836	-0.0336	0.2942	2.43	0.1193
	1995	1	0.1856	0.0801	0.0285	0.3427	5.36	0.0206
	1994	0	0	0	0	0	.	.
Weight=100	2000	1	-0.7135	0.0375	-0.7871	-0.6399	361.34	<.0001
	1999	1	-0.6609	0.0343	-0.728	-0.5937	371.6	<.0001
	1998	1	-0.2646	0.0293	-0.322	-0.2072	81.51	<.0001
	1997	1	-0.485	0.0305	-0.5448	-0.4252	252.38	<.0001
	1996	1	0.1303	0.0264	0.0784	0.1821	24.27	<.0001
	1995	1	0.1856	0.0253	0.1359	0.2353	53.64	<.0001
	1994	0	0	0	0	0	.	.
Weight=1000	2000	1	-0.7135	0.0119	-0.7367	-0.6902	3613.43	<.0001
	1999	1	-0.6609	0.0108	-0.6821	-0.6396	3715.98	<.0001
	1998	1	-0.2646	0.0093	-0.2828	-0.2464	815.15	<.0001
	1997	1	-0.485	0.0097	-0.5039	-0.4661	2523.84	<.0001
	1996	1	0.1303	0.0084	0.1139	0.1467	242.67	<.0001
	1995	1	0.1856	0.008	0.1699	0.2013	536.43	<.0001
	1994	0	0	0	0	0	.	.

Table 1.2b. Effect of increasing the weight in a CBC only analyses, using the example Nuthatch in the absence of scaling.

Weight	Year	DF	Estimate	SE	LCL	UCL	Chi-sq	Pr > Chi-sq
Weight=1	2000	1	0.1788	0.121	-0.0583	0.4159	2.19	0.1393
	1999	1	0.1811	0.1142	-0.0426	0.4048	2.52	0.1126
	1998	1	0.2443	0.111	0.0267	0.4619	4.84	0.0278
	1997	1	0.1641	0.1113	-0.054	0.3822	2.17	0.1403
	1996	1	0.2466	0.1078	0.0354	0.4579	5.24	0.0221
	1995	1	-0.0024	0.1102	-0.2185	0.2136	0	0.9824
	1994	0	0	0	0	0	.	.
Weight=10	2000	1	0.1788	0.0383	0.1039	0.2538	21.85	<.0001
	1999	1	0.1811	0.0361	0.1104	0.2519	25.17	<.0001
	1998	1	0.2443	0.0351	0.1755	0.3131	48.42	<.0001
	1997	1	0.1641	0.0352	0.0951	0.2331	21.75	<.0001
	1996	1	0.2466	0.0341	0.1798	0.3134	52.37	<.0001
	1995	1	-0.0024	0.0349	-0.0708	0.0659	0	0.9445
	1994	0	0	0	0	0	.	.
Weight=100	2000	1	0.1788	0.0121	0.1551	0.2025	218.52	<.0001
	1999	1	0.1811	0.0114	0.1587	0.2035	251.7	<.0001
	1998	1	0.2443	0.0111	0.2226	0.2661	484.25	<.0001
	1997	1	0.1641	0.0111	0.1423	0.1859	217.48	<.0001
	1996	1	0.2466	0.0108	0.2255	0.2678	523.66	<.0001
	1995	1	-0.0024	0.011	-0.024	0.0192	0.05	0.8257
	1994	0	0	0	0	0	.	.
Weight=1000	2000	1	0.1788	0.0038	0.1713	0.1863	2185.21	<.0001
	1999	1	0.1811	0.0036	0.174	0.1882	2516.99	<.0001
	1998	1	0.2443	0.0035	0.2374	0.2512	4842.45	<.0001
	1997	1	0.1641	0.0035	0.1572	0.171	2174.82	<.0001
	1996	1	0.2466	0.0034	0.24	0.2533	5236.64	<.0001
	1995	1	-0.0024	0.0035	-0.0093	0.0044	0.49	0.4861
	1994	0	0	0	0	0	.	.

Table 1.3a. Effect of increasing the weight in a CBC only analyses with scaling (pscale dscale commands) using the example Willow Tit.

Weight	Year	DF	Estimate	SE	LCL	UCL	Chi-sq	Pr > Chi-sq
No weight	2000	1	-0.7135	0.3187	-1.3381	-0.0888	5.01	0.0252
	1999	1	-0.6609	0.2911	-1.2314	-0.0903	5.15	0.0232
	1998	1	-0.2646	0.2488	-0.7523	0.2231	1.13	0.2877
	1997	1	-0.485	0.2592	-0.9930	0.0231	3.50	0.0614
	1996	1	0.1303	0.2246	-0.3099	0.5604	0.34	0.5618
	1995	1	0.1856	0.2152	-0.2362	0.6074	0.74	0.3884
	1994	0	0	0	0	0	.	.
Weight=1	2000	1	-0.7135	0.3187	-1.3381	-0.0888	5.01	0.0252
	1999	1	-0.6609	0.2911	-1.2314	-0.0903	5.15	0.0232
	1998	1	-0.2646	0.2488	-0.7523	0.2231	1.13	0.2877
	1997	1	-0.485	0.2592	-0.9930	0.0231	3.50	0.0614
	1996	1	0.1303	0.2246	-0.3099	0.5604	0.34	0.5618
	1995	1	0.1856	0.2152	-0.2362	0.6074	0.74	0.3884
	1994	0	0	0	0	0	.	.
Weight=10	2000	1	-0.7135	0.3187	-1.3381	-0.0888	5.01	0.0252
	1999	1	-0.6609	0.2911	-1.2314	-0.0903	5.15	0.0232
	1998	1	-0.2646	0.2488	-0.7523	0.2231	1.13	0.2877
	1997	1	-0.485	0.2592	-0.9930	0.0231	3.50	0.0614
	1996	1	0.1303	0.2246	-0.3099	0.5604	0.34	0.5618
	1995	1	0.1856	0.2152	-0.2362	0.6074	0.74	0.3884
	1994	0	0	0	0	0	.	.
Weight=100	2000	1	-0.7135	0.3187	-1.3381	-0.0888	5.01	0.0252
	1999	1	-0.6609	0.2911	-1.2314	-0.0903	5.15	0.0232
	1998	1	-0.2646	0.2488	-0.7523	0.2231	1.13	0.2877
	1997	1	-0.485	0.2592	-0.9930	0.0231	3.50	0.0614
	1996	1	0.1303	0.2246	-0.3099	0.5604	0.34	0.5618
	1995	1	0.1856	0.2152	-0.2362	0.6074	0.74	0.3884
	1994	0	0	0	0	0	.	.
Weight=1000	2000	1	-0.7135	0.3187	-1.3381	-0.0888	5.01	0.0252
	1999	1	-0.6609	0.2911	-1.2314	-0.0903	5.15	0.0232
	1998	1	-0.2646	0.2488	-0.7523	0.2231	1.13	0.2877
	1997	1	-0.485	0.2592	-0.9930	0.0231	3.50	0.0614
	1996	1	0.1303	0.2246	-0.3099	0.5604	0.34	0.5618
	1995	1	0.1856	0.2152	-0.2362	0.6074	0.74	0.3884
	1994	0	0	0	0	0	.	.

Table 1.3b. Effect of increasing the weight in a CBC only analyses with scaling (pscale dscale commands) using the example Nuthatch.

Weight	Year	DF	Estimate	SE	LCL	UCL	Chi-sq	Pr > Chi-sq
No weight	2000	1	0.1788	0.0909	0.0007	0.3570	3.87	0.0491
	1999	1	0.1811	0.0858	0.1030	0.3492	4.46	0.0347
	1998	1	0.2443	0.0834	0.0808	0.4078	8.58	0.0034
	1997	1	0.1641	0.0836	0.0002	0.3280	3.85	0.0497
	1996	1	0.2466	0.0810	0.0879	0.4054	9.28	0.0023
	1995	1	-0.0024	0.0828	-0.1648	0.1599	0.00	0.9766
	1994	0	0	0	0	0	.	.
Weight=1	2000	1	0.1788	0.0909	0.0007	0.3570	3.87	0.0491
	1999	1	0.1811	0.0858	0.1030	0.3492	4.46	0.0347
	1998	1	0.2443	0.0834	0.0808	0.4078	8.58	0.0034
	1997	1	0.1641	0.0836	0.0002	0.3280	3.85	0.0497
	1996	1	0.2466	0.0810	0.0879	0.4054	9.28	0.0023
	1995	1	-0.0024	0.0828	-0.1648	0.1599	0.00	0.9766
	1994	0	0	0	0	0	.	.
Weight=10	2000	1	0.1788	0.0909	0.0007	0.3570	3.87	0.0491
	1999	1	0.1811	0.0858	0.1030	0.3492	4.46	0.0347
	1998	1	0.2443	0.0834	0.0808	0.4078	8.58	0.0034
	1997	1	0.1641	0.0836	0.0002	0.3280	3.85	0.0497
	1996	1	0.2466	0.0810	0.0879	0.4054	9.28	0.0023
	1995	1	-0.0024	0.0828	-0.1648	0.1599	0.00	0.9766
	1994	0	0	0	0	0	.	.
Weight=100	2000	1	0.1788	0.0909	0.0007	0.3570	3.87	0.0491
	1999	1	0.1811	0.0858	0.1030	0.3492	4.46	0.0347
	1998	1	0.2443	0.0834	0.0808	0.4078	8.58	0.0034
	1997	1	0.1641	0.0836	0.0002	0.3280	3.85	0.0497
	1996	1	0.2466	0.0810	0.0879	0.4054	9.28	0.0023
	1995	1	-0.0024	0.0828	-0.1648	0.1599	0.00	0.9766
	1994	0	0	0	0	0	.	.
Weight=1000	2000	1	0.1788	0.0909	0.0007	0.3570	3.87	0.0491
	1999	1	0.1811	0.0858	0.1030	0.3492	4.46	0.0347
	1998	1	0.2443	0.0834	0.0808	0.4078	8.58	0.0034
	1997	1	0.1641	0.0836	0.0002	0.3280	3.85	0.0497
	1996	1	0.2466	0.0810	0.0879	0.4054	9.28	0.0023
	1995	1	-0.0024	0.0828	-0.1648	0.1599	0.00	0.9766
	1994	0	0	0	0	0	.	.

Table 1.4a. Comparing the results from three possible weighing options for combined CBC/BBS indices - example Willow Tit.

i) Weight CBC by 1 keeping BBS as same as normal (with pscale dscale commands)						
Year	df	estimate	stderr	lcl	ucl	Chi-sq
2000	1	-0.6674	0.1626	-0.9861	-0.3488	16.85
1999	1	-0.5286	0.1563	-0.8350	-0.2222	11.43
1998	1	-0.4066	0.1527	-0.7058	-0.1073	7.09
1997	1	-0.4067	0.1502	-0.7012	-0.1123	7.33
1996	1	-0.3072	0.1457	-0.5929	-0.0216	4.44
1995	1	-0.3054	0.1413	-0.5823	-0.0285	4.67
1994	0	0.0000	0.0000	0.0000	0.0000	.
Scale	0	10.2422	0.0000	10.2422	10.2422	

ii) Scale down BBS so it has a mean of 1 and give CBC mean of 1 (with pscale dscale commands)						
Year	df	estimate	stderr	lcl	ucl	Chi-sq
2000	1	-0.6726	0.1572	-0.9806	-0.3646	18.32
1999	1	-0.5514	0.1499	-0.8451	-0.2577	13.54
1998	1	-0.3836	0.1431	-0.6640	-0.1032	7.19
1997	1	-0.4296	0.1424	-0.7087	-0.1505	9.10
1996	1	-0.2041	0.1342	-0.4672	0.0589	2.31
1995	1	-0.1908	0.1297	-0.4450	0.0634	2.16
1994	0	0.0000	0.0000	0.0000	0.0000	.
Scale	0	1.0594	0.0000	1.0594	1.0594	

iii) Scale up the CBC so it has a mean equal to the mean BBS weight and use normal BBS weights (with pscale dscale commands)						
Year	df	estimate	stderr	lcl	ucl	Chi-sq
2000	1	-0.6726	0.1572	-0.9806	-0.3646	18.32
1999	1	-0.5514	0.1499	-0.8451	-0.2577	13.54
1998	1	-0.3836	0.1431	-0.6640	-0.1032	7.19
1997	1	-0.4296	0.1424	-0.7087	-0.1505	9.10
1996	1	-0.2041	0.1342	-0.4672	0.0589	2.31
1995	1	-0.1908	0.1297	-0.4450	0.0634	2.16
1994	0	0.0000	0.0000	0.0000	0.0000	.
Scale	0	10.8038	0.0000	10.8038	10.8038	

Table 1.4b. Comparing the results from three possible weighing options for combined CBC/BBS indices - example Nuthatch.

i) Weight CBC by 1 keeping BBS as same as normal (with pscale dscale commands)						
Year	df	estimate	stderr	lcl	ucl	Chi-sq
2000	1	0.0796	0.0714	-0.0604	0.2195	1.24
1999	1	0.1012	0.0709	-0.0377	0.2401	2.04
1998	1	0.1539	0.0700	0.0167	0.2911	4.83
1997	1	0.2327	0.0681	0.0992	0.3662	11.68
1996	1	0.2676	0.0683	0.1337	0.4015	15.34
1995	1	0.0491	0.0702	-0.0885	0.1868	0.49
1994	0	0.0000	0.0000	0.0000	0.0000	.
Scale	0	8.6857	0.0000	8.6857	8.6857	

ii) Scale down BBS so it has a mean of 1 and give CBC mean of 1 (with pscale dscale commands)						
Year	df	estimate	stderr	lcl	ucl	Chi-sq
2000	1	0.1061	0.0631	-0.0177	0.2298	2.82
1999	1	0.1252	0.0618	0.0041	0.2463	4.10
1998	1	0.1818	0.0607	0.0627	0.3008	8.96
1997	1	0.2114	0.0596	0.0945	0.3283	12.56
1996	1	0.2599	0.0592	0.1438	0.3759	19.27
1995	1	0.0325	0.0608	-0.0866	0.1516	0.29
1994	0	0.0000	0.0000	0.0000	0.0000	.
Scale	0	0.9710	0.0000	0.9710	0.9710	

iii) Scale up the CBC so it has a mean equal to the mean BBS weight and use normal BBS weights (with pscale dscale commands)						
Year	df	estimate	stderr	lcl	ucl	Chi-sq
2000	1	0.1061	0.0631	-0.0177	0.2298	2.82
1999	1	0.1252	0.0618	0.0041	0.2463	4.10
1998	1	0.1818	0.0607	0.0627	0.3008	8.96
1997	1	0.2114	0.0596	0.0945	0.3283	12.56
1996	1	0.2599	0.0592	0.1438	0.3759	19.27
1995	1	0.0325	0.0608	-0.0866	0.1516	0.29
1994	0	0.0000	0.0000	0.0000	0.0000	.
Scale	0	9.1088	0.0000	9.1088	9.1088	

Table 1.5a. Extent to which standard errors associated with estimates from a single survey are likely to be affecting by using a single scaling value based on CBC and BBS surveys as in a joint analyses using the example Willow Tit. In the following analyses we scale up the CBC to have use the mean BBS weight.

a) BBS only

Criterion	DF	Value	Value/DF
Deviance	1001	124277.2598	124.1531
Scaled Deviance	1001	1001.0000	1.0000
Pearson Chi-Square	1001	151850.6556	151.6990
Scaled Pearson X2	1001	1223.0919	1.2219
Log Likelihood		-633.1543	

Year	df	estimate	stderr	lcl	ucl	Chi-sq
2000	1	-0.6674	0.1770	-1.0144	-0.3204	14.21
1999	1	-0.5283	0.1702	-0.8620	-0.1947	9.63
1998	1	-0.4068	0.1663	-0.7328	-0.0808	5.98
1997	1	-0.4064	0.1636	-0.7271	-0.0858	6.17
1996	1	-0.3086	0.1588	-0.6198	0.0027	3.78
1995	1	-0.3069	0.1540	-0.6086	-0.0051	3.97
1994	0	0.0000	0.0000	0.0000	0.0000	.
Scale	0	11.1424	0.0000	11.1424	11.1424	

b) CBC only

Criterion	DF	Value	Value/DF
Deviance	179	13422.4576	74.9858
Scaled Deviance	179	179.0000	1.0000
Pearson Chi-Square	179	13601.7037	75.9872
Scaled Pearson X2	179	181.3904	1.0134
Log Likelihood		-186.3316	

Year	df	estimate	stderr	lcl	ucl	Chi-sq
2000	1	-0.7135	0.3187	-1.3381	-0.0888	5.01
1999	1	-0.6609	0.2911	-1.2314	-0.0903	5.15
1998	1	-0.2646	0.2488	-0.7523	0.2231	1.13
1997	1	-0.4850	0.2592	-0.9930	0.0231	3.50
1996	1	0.1303	0.2246	-0.3099	0.5704	0.34
1995	1	0.1856	0.2152	-0.2362	0.6074	0.74
1994	0	0.0000	0.0000	0.0000	0.0000	.
Scale	0	8.6594	0.0000	8.6594	8.6594	

c) BBS trend (from joint model)

Criterion	DF	Value	Value/DF
Deviance	1180	137699.7174	116.6947
Scaled Deviance	1180	1180.0000	1.0000
Pearson Chi-Square	1180	165452.3627	140.2139
Scaled Pearson X2	1180	1417.8227	1.2015
Log Likelihood		-793.3549	

Year	df	estimate	stderr	lcl	ucl	Chi-sq
2000	1	-0.6674	0.1716	-1.0038	-0.3310	15.12
1999	1	-0.5283	0.1651	-0.8518	-0.2048	10.25
1998	1	-0.4068	0.1613	-0.7229	-0.0908	6.36
1997	1	-0.4064	0.1586	-0.7173	-0.0956	6.57
1996	1	-0.3086	0.1540	-0.6103	-0.0068	4.02
1995	1	-0.3069	0.1493	-0.5994	-0.0143	4.23
1994	0	0.0000	0.0000	0.0000	0.0000	.
Scale	0	10.8025	0.0000	10.8025	10.8025	

d) CBC trend (from joint model)

	Criterion	DF	Value	Value/DF		
	Deviance	1180	137699.7174	116.6947		
	Scaled Deviance	1180	1180.0000	1.0000		
	Pearson Chi-Square	1180	165452.3627	140.2139		
	Scaled Pearson X2	1180	1417.8227	1.2015		
	Log Likelihood		-793.3549			
2000	1	-0.7135	0.3976	-1.4927	0.0658	3.22
1999	1	-0.6609	0.3631	-1.3726	0.0509	3.31
1998	1	-0.2646	0.3104	-0.8730	0.3438	0.73
1997	1	-0.4850	0.3234	-1.1188	0.1488	2.25
1996	1	0.1303	0.2801	-0.4188	0.6793	0.22
1995	1	0.1856	0.2685	-0.3406	0.7118	0.48
1994	0	0.0000	0.0000	0.0000	0.0000	.
Scale	0	10.8025	0.0000	10.8025	10.8025	

d) Combined CBC/BBS analyses

	Criterion	DF	Value	Value/DF		
	Deviance	1186	138431.9047	116.7217		
	Scaled Deviance	1186	1186.0000	1.0000		
	Pearson Chi-Square	1186	167256.2343	141.0255		
	Scaled Pearson X2	1186	1432.9492	1.2082		
	Log Likelihood		-796.3079			
2000	1	-0.6726	0.1572	-0.9806	-0.3646	18.32
1999	1	-0.5514	0.1499	-0.8451	-0.2577	13.54
1998	1	-0.3836	0.1431	-0.6640	-0.1032	7.19
1997	1	-0.4296	0.1424	-0.7087	-0.1505	9.10
1996	1	-0.2041	0.1342	-0.4672	0.0589	2.31
1995	1	-0.1908	0.1297	-0.4450	0.0634	2.16
1994	0	0.0000	0.0000	0.0000	0.0000	.
Scale	0	10.8038	0.0000	10.8038	10.8038	

Table 1.5b. Extent to which standard errors associated with estimates from a single survey are likely to be affected by using a single scaling value based on CBC and BBS surveys as in a joint analyses using the example Wood Pigeon. In the following analyses we scale up the CBC to have use the mean BBS weight.

a) BBS only

Criterion		DF	Value		Value/DF	
Deviance		8400	4939822.0608		588.0741	
Scaled Deviance		8400	8400.0000		1.0000	
Pearson Chi-Square		8400	5558547.7558		661.7319	
Scaled Pearson X2		8400	9452.1221		1.1253	
Log Likelihood			74947.7950			
2000	1	0.0532	0.0217	0.0106	0.0957	6.00
1999	1	0.0095	0.0218	-0.0333	0.0522	0.19
1998	1	0.0052	0.0219	-0.0376	0.0481	0.06
1997	1	-0.0184	0.0217	-0.0609	0.0241	0.72
1996	1	-0.0891	0.0219	-0.1319	-0.0462	16.60
1995	1	-0.1504	0.0220	-0.1936	-0.1072	46.55
1994	0	0.0000	0.0000	0.0000	0.0000	.
Scale	0	24.2502	0.0000	24.2502	24.2502	

b) CBC only

Criterion		DF	Value		Value/DF	
Deviance		769	64489.0289		83.8609	
Scaled Deviance		769	769.0000		1.0000	
Pearson Chi-Square		769	62464.2354		81.2279	
Scaled Pearson X2		769	744.8553		0.9686	
Log Likelihood			14348.3256			
2000	1	0.1589	0.0448	0.0711	0.2468	12.57
1999	1	0.1660	0.0409	0.0858	0.2462	16.45
1998	1	0.1352	0.0402	0.0565	0.2139	11.33
1997	1	0.0784	0.0395	0.0011	0.1558	3.95
1996	1	0.1111	0.0389	0.0348	0.1874	8.15
1995	1	-0.0065	0.0385	-0.0819	0.0688	0.03
1994	0	0.0000	0.0000	0.0000	0.0000	.
Scale	0	9.1576	0.0000	9.1576	9.1576	

c) BBS trend (from joint model)

Criterion		DF	Value		Value/DF	
Deviance		9169	5004311.0897		545.7859	
Scaled Deviance		9169	9169.0000		1.0000	
Pearson Chi-Square		9169	5621011.9913		613.0453	
Scaled Pearson X2		9169	10298.9319		1.1232	
Log Likelihood			82959.4821			
2000	1	0.0532	0.0209	0.0122	0.0941	6.46
1999	1	0.0095	0.0210	-0.0317	0.0507	0.20
1998	1	0.0052	0.0211	-0.0360	0.0465	0.06
1997	1	-0.0184	0.0209	-0.0593	0.0225	0.78
1996	1	-0.0891	0.0211	-0.1304	-0.0478	17.88
1995	1	-0.1504	0.0212	-0.1921	-0.1088	50.16
1994	0	0.0000	0.0000	0.0000	0.0000	.
Scale	0	23.3621	0.0000	23.3621	23.3621	

d) CBC trend (from joint model)

	Criterion		DF		Value	Value/DF
	Deviance		9175		5006824.6191	545.7030
	Scaled Deviance		9175		9175.0000	1.0000
	Pearson Chi-Square		9175		5626265.6864	613.2170
	Scaled Pearson X2		9175		10310.1250	1.1237
	Log Likelihood				82969.7914	
2000	1	0.0577	0.0206	0.0174	0.0980	7.89
1999	1	0.0159	0.0206	-0.0245	0.0563	0.60
1998	1	0.0106	0.0206	-0.0298	0.0510	0.26
1997	1	-0.0145	0.0204	-0.0546	0.0255	0.51
1996	1	-0.0804	0.0206	-0.1208	-0.0400	15.24
1995	1	-0.1441	0.0208	-0.1848	-0.1035	48.24
1994	0	0.0000	0.0000	0.0000	0.0000	.
Scale	0	23.3621	0.0000	23.3621	23.3621	

e) Combined CBC/BBS analyses

	Criterion		DF		Value	Value/DF
	Deviance		9175		5006824.6191	545.7030
	Scaled Deviance		9175		9175.0000	1.0000
	Pearson Chi-Square		9175		5626265.6864	613.2170
	Scaled Pearson X2		9175		10310.1250	1.1237
	Log Likelihood				82969.7914	
year	1	0.0577	0.0206	0.0174	0.0980	7.89
year	1	0.0159	0.0206	-0.0245	0.0563	0.60
year	1	0.0106	0.0206	-0.0298	0.0510	0.26
year	1	-0.0145	0.0204	-0.0546	0.0255	0.51
year	1	-0.0804	0.0206	-0.1208	-0.0400	15.24
year	1	-0.1441	0.0208	-0.1848	-0.1035	48.24
year	0	0.0000	0.0000	0.0000	0.0000	.
Scale	0	23.3603	0.0000	23.3603	23.3603	

Table 1.6a. Wood Pigeon indices run from 1965 (set to an value of 1) with scaling (pscale dscale) commands and the CBC adjust up to have a weight equal to the mean BBS weight for a) CBC only trend b) CBC only trend in joint model c) Combined CBC/BBS trend.

a) CBC only

Criterion	DF	Value	Value/DF
Deviance	2576	319299.5920	123.9517
Scaled Deviance	2576	2576.0000	1.0000
Pearson Chi-Square	2576	318352.6462	123.5841
Scaled Pearson X2	2576	2568.3604	0.9970
Log Likelihood		23412.6394	

Year	df	estimate	stderr	lcl	ucl	Chi-sq
2000	1	0.5003	0.1684	0.1702	0.8305	8.82
1999	1	0.5121	0.1671	0.1846	0.8395	9.39
1998	1	0.4884	0.1668	0.1614	0.8154	8.57
1997	1	0.4324	0.1667	0.1056	0.7591	6.73
1996	1	0.4636	0.1666	0.1370	0.7902	7.74
1995	1	0.3495	0.1667	0.0228	0.6762	4.40
1994	1	0.3619	0.1665	0.0357	0.6882	4.73
1993	1	0.3152	0.1667	-0.0116	0.6420	3.57
1992	1	0.3715	0.1667	0.0448	0.6982	4.97
1991	1	0.3534	0.1671	0.0259	0.6808	4.47
1990	1	0.3524	0.1672	0.0248	0.6800	4.45
1980	1	0.3080	0.1677	-0.0207	0.6367	3.37
1988	1	0.3066	0.1678	-0.0223	0.6355	3.34
1987	1	0.1924	0.1678	-0.1365	0.5213	1.31
1986	1	0.0619	0.1690	-0.2692	0.3931	0.13
1985	1	0.1591	0.1689	-0.1718	0.4901	0.89
1984	1	0.1159	0.1691	-0.2156	0.4474	0.47
1983	1	0.0626	0.1691	-0.2687	0.3940	0.14
1982	1	0.0275	0.1695	-0.3048	0.3597	0.03
1981	1	-0.0188	0.1684	-0.3489	0.3112	0.01
1980	1	-0.0607	0.1693	-0.3925	0.2711	0.13
1979	1	-0.0138	0.1650	-0.3371	0.3096	0.01
1978	1	-0.1289	0.1691	-0.4604	0.2025	0.58
1977	1	-0.2675	0.1660	-0.5928	0.0578	2.60
1976	1	-0.3073	0.1719	-0.6442	0.0296	3.20
1975	1	-0.5633	0.1798	-0.9157	-0.2110	9.82
1974	1	-0.6074	0.1624	-0.9257	-0.2891	13.99
1973	1	-0.4050	0.1844	-0.7664	-0.0436	4.82
1972	1	-0.2680	0.1808	-0.6223	0.0864	2.20
1971	1	-0.0225	0.1792	-0.3738	0.3287	0.02
1970	1	-0.1111	0.2035	-0.5100	0.2877	0.30
1969	1	0.0808	0.1921	-0.2958	0.4573	0.18
1968	1	0.0700	0.1875	-0.2975	0.4376	0.14
1967	1	-0.1493	0.1550	-0.4530	0.1544	0.93
1966	1	-0.2076	0.1383	-0.4788	0.0635	2.25
1965	0	0.0000	0.0000	0.0000	0.0000	.
Scale	0	11.1334	0.0000	11.1334	11.1334	

b) CBC trend (from joint model)

	Criterion		DF		Value	Value/DF
	Deviance		11E3		5259121.6529	479.1474
	Scaled Deviance		11E3		10976.0000	1.0000
	Pearson Chi-Square		11E3		5876900.6612	535.4319
	Scaled Pearson X2		11E3		12265.3298	1.1175
	Log Likelihood				98042.6736	
2000	1	0.5003	0.3312	-0.1487	1.1494	2.28
1999	1	0.5121	0.3285	-0.1317	1.1558	2.43
1998	1	0.4884	0.3280	-0.1545	1.1314	2.22
1997	1	0.4324	0.3278	-0.2101	1.0748	1.74
1996	1	0.4636	0.3276	-0.1785	1.1058	2.00
1995	1	0.3495	0.3277	-0.2928	0.9918	1.14
1994	1	0.3619	0.3273	-0.2795	1.0034	1.22
1993	1	0.3152	0.3278	-0.3273	0.9578	0.92
1992	1	0.3715	0.3277	-0.2708	1.0138	1.28
1991	1	0.3534	0.3285	-0.2904	0.9971	1.16
1990	1	0.3524	0.3286	-0.2917	0.9966	1.15
1989	1	0.3080	0.3298	-0.3383	0.9543	0.87
1988	1	0.3066	0.3300	-0.3401	0.9533	0.86
1987	1	0.1924	0.3299	-0.4542	0.8390	0.34
1986	1	0.0619	0.3322	-0.5892	0.7130	0.03
1985	1	0.1591	0.3320	-0.4916	0.8099	0.23
1984	1	0.1159	0.3325	-0.5358	0.7676	0.12
1983	1	0.0626	0.3324	-0.5888	0.7141	0.04
1982	1	0.0275	0.3333	-0.6258	0.6807	0.01
1981	1	-0.0188	0.3311	-0.6678	0.6301	0.00
1980	1	-0.0607	0.3328	-0.7130	0.5916	0.03
1979	1	-0.0138	0.3244	-0.6495	0.6219	0.00
1978	1	-0.1289	0.3325	-0.7806	0.5228	0.15
1977	1	-0.2675	0.3263	-0.9070	0.3720	0.67
1976	1	-0.3073	0.3380	-0.9697	0.3551	0.83
1975	1	-0.5633	0.3535	-1.2562	0.1295	2.54
1974	1	-0.6074	0.3193	-1.2332	0.0185	3.62
1973	1	-0.4050	0.3625	-1.1155	0.3055	1.25
1972	1	-0.2680	0.3554	-0.9646	0.4287	0.57
1971	1	-0.0225	0.3524	-0.7131	0.6681	0.00
1970	1	-0.1111	0.4001	-0.8953	0.6730	0.08
1969	1	0.0808	0.3777	-0.6596	0.8211	0.05
1968	1	0.0700	0.3687	-0.6526	0.7926	0.04
1967	1	-0.1493	0.3047	-0.7464	0.4478	0.24
1966	1	-0.2076	0.2720	-0.7407	0.3255	0.58
1965	0	0.0000	0.0000	0.0000	0.0000	.
Scale	0	21.8894	0.0000	21.8894	21.8894	

c) Combined CBC/BBS indices

Criterion	DF	Value	Value/DF
Deviance	11E3	5261565.1490	479.1081
Scaled Deviance	11E3	10982.0000	1.0000
Pearson Chi-Square	11E3	5882502.8676	535.6495
Scaled Pearson X2	11E3	12278.0284	1.1180
Log Likelihood		98048.1620	

Year	df	estimate	stderr	lcl	ucl	Chi-sq
2000	1	0.5176	0.3227	-0.1148	1.1500	2.57
1999	1	0.4759	0.3226	-0.1565	1.1082	2.18
1998	1	0.4708	0.3226	-0.1615	1.1032	2.13
1997	1	0.4457	0.3226	-0.1866	1.0781	1.91
1996	1	0.3798	0.3226	-0.2526	1.0122	1.39
1995	1	0.3161	0.3226	-0.3163	0.9485	0.96
1994	1	0.4600	0.3226	-0.1722	1.0923	2.03
1993	1	0.3166	0.3278	-0.3259	0.9591	0.93
1992	1	0.3733	0.3277	-0.2689	1.0156	1.30
1991	1	0.3555	0.3284	-0.2882	0.9992	1.17
1990	1	0.3544	0.3286	-0.2897	0.9984	1.16
1989	1	0.3085	0.3297	-0.3377	0.9547	0.88
1988	1	0.3074	0.3299	-0.3392	0.9541	0.87
1987	1	0.1929	0.3299	-0.4536	0.8394	0.34
1986	1	0.0626	0.3322	-0.5884	0.7136	0.04
1985	1	0.1598	0.3320	-0.4909	0.8104	0.23
1984	1	0.1163	0.3325	-0.5354	0.7679	0.12
1983	1	0.0631	0.3323	-0.5883	0.7145	0.04
1982	1	0.0280	0.3333	-0.6253	0.6812	0.01
1981	1	-0.0188	0.3311	-0.6677	0.6301	0.00
1980	1	-0.0601	0.3328	-0.7124	0.5922	0.03
1979	1	-0.0133	0.3243	-0.6490	0.6224	0.00
1978	1	-0.1287	0.3325	-0.7804	0.5229	0.15
1977	1	-0.2675	0.3263	-0.9069	0.3720	0.67
1976	1	-0.3073	0.3379	-0.9697	0.3550	0.83
1975	1	-0.5634	0.3535	-1.2562	0.1294	2.54
1974	1	-0.6074	0.3193	-1.2332	0.0184	3.62
1973	1	-0.4050	0.3625	-1.1155	0.3055	1.25
1972	1	-0.2681	0.3554	-0.9647	0.4286	0.57
1971	1	-0.0227	0.3523	-0.7133	0.6679	0.00
1970	1	-0.1112	0.4001	-0.8953	0.6730	0.08
1969	1	0.0808	0.3777	-0.6595	0.8211	0.05
1968	1	0.0700	0.3687	-0.6525	0.7926	0.04
1967	1	-0.1494	0.3046	-0.7465	0.4477	0.24
1966	1	-0.2076	0.2720	-0.7407	0.3254	0.58
1965	0	0.0000	0.0000	0.0000	0.0000	.
Scale	0	21.8885	0.0000	21.8885	21.8885	

Table 1.6b. Willow Tit indices run from 1965 (set to an value of 1) with scaling (pscale dscale) commands and the CBC adjust up to have a weight equal to the mean BBS weight for a) CBC only trend b) CBC only trend in joint model c) Combined CBC/BBS trend d) Combined CBC/BBS trends as above, but adjusting BBS down to have mean weight of one and CBC a weight of one.

a) CBC only

Criterion	DF	Value	Value/DF
Deviance	1918	143264.8472	74.6949
Scaled Deviance	1918	1918.0000	1.0000
Pearson Chi-Square	1918	162202.9272	84.5688
Scaled Pearson X2	1918	2171.5391	1.1322
Log Likelihood		-1753.7772	

Year	df	estimate	stderr	lcl	ucl	Chi-sq
2000	1	-1.1157	0.3679	-1.8367	-0.3947	9.20
1999	1	-1.0759	0.3462	-1.7544	-0.3973	9.66
1998	1	-0.6819	0.3129	-1.2952	-0.0686	4.75
1997	1	-0.9060	0.3217	-1.5364	-0.2756	7.93
1996	1	-0.2963	0.2945	-0.8736	0.2810	1.01
1995	1	-0.2840	0.2903	-0.8529	0.2849	0.96
1994	1	-0.4463	0.2960	-1.0265	0.1340	2.27
1993	1	-0.6358	0.3085	-1.2403	-0.0312	4.25
1992	1	-0.2078	0.2867	-0.7698	0.3542	0.53
1991	1	0.0224	0.2802	-0.5269	0.5716	0.01
1990	1	-0.1025	0.2801	-0.6515	0.4465	0.13
1989	1	0.1540	0.2715	-0.3781	0.6861	0.32
1988	1	0.1917	0.2715	-0.3406	0.7239	0.50
1987	1	0.1359	0.2731	-0.3994	0.6711	0.25
1986	1	0.0307	0.2757	-0.5097	0.5711	0.01
1985	1	0.1243	0.2732	-0.4110	0.6597	0.21
1984	1	0.1570	0.2687	-0.3696	0.6837	0.34
1983	1	0.0837	0.2695	-0.4446	0.6120	0.10
1982	1	0.1737	0.2664	-0.3484	0.6958	0.43
1981	1	0.0827	0.2635	-0.4338	0.5991	0.10
1980	1	0.3958	0.2569	-0.1078	0.8993	2.37
1979	1	0.2008	0.2594	-0.3076	0.7092	0.60
1978	1	0.3335	0.2565	-0.1693	0.8363	1.69
1977	1	0.4006	0.2570	-0.1032	0.9043	2.43
1976	1	0.5419	0.2551	0.0419	1.0419	4.51
1975	1	0.7150	0.2521	0.2209	1.2091	8.04
1974	1	0.6821	0.2543	0.1837	1.1804	7.20
1973	1	0.7573	0.2525	0.2625	1.2521	9.00
1972	1	0.6102	0.2505	0.1193	1.1011	5.94
1971	1	0.7626	0.2462	0.2801	1.2450	9.60
1970	1	0.5153	0.2479	0.0294	1.0013	4.32
1969	1	0.6562	0.2474	0.1713	1.1411	7.03
1968	1	0.5990	0.2449	0.1190	1.0790	5.98
1967	1	0.2406	0.2488	-0.2470	0.7282	0.94
1966	1	-0.1116	0.2499	-0.6014	0.3782	0.20
1965	0	0.0000	0.0000	0.0000	0.0000	.
Scale	0	8.6426	0.0000	8.6426	8.6426	

b) CBC trend (from joint model)

	Criterion		DF		Value	Value/DF
	Deviance		2919		267542.1071	91.6554
	Scaled Deviance		2919		2919.0000	1.0000
	Pearson Chi-Square		2919		314053.5830	107.5894
	Scaled Pearson X2		2919		3426.4603	1.1738
	Log Likelihood				-2286.8954	
year	1	-1.1157	0.4075	-1.9144	-0.3171	7.50
2000	1	-1.0759	0.3835	-1.8275	-0.3242	7.87
1999	1	-0.6819	0.3466	-1.3612	-0.0026	3.87
1998	1	-0.9060	0.3563	-1.6043	-0.2076	6.47
1997	1	-0.2963	0.3263	-0.9358	0.3432	0.82
1996	1	-0.2840	0.3215	-0.9142	0.3462	0.78
1995	1	-0.4463	0.3279	-1.0890	0.1965	1.85
1994	1	-0.6358	0.3417	-1.3055	0.0340	3.46
1993	1	-0.2078	0.3176	-0.8303	0.4147	0.43
1992	1	0.0224	0.3104	-0.5860	0.6308	0.01
1991	1	-0.1025	0.3103	-0.7107	0.5056	0.11
1990	1	0.1540	0.3007	-0.4354	0.7434	0.26
1989	1	0.1917	0.3008	-0.3979	0.7812	0.41
1988	1	0.1359	0.3025	-0.4570	0.7288	0.20
1987	1	0.0307	0.3054	-0.5679	0.6293	0.01
1986	1	0.1243	0.3026	-0.4687	0.7174	0.17
1985	1	0.1570	0.2977	-0.4264	0.7404	0.28
1984	1	0.0837	0.2986	-0.5015	0.6689	0.08
1983	1	0.1737	0.2951	-0.4047	0.7521	0.35
1982	1	0.0827	0.2919	-0.4894	0.6548	0.08
1981	1	0.3958	0.2846	-0.1620	0.9535	1.93
1980	1	0.2008	0.2873	-0.3624	0.7639	0.49
1978	1	0.3335	0.2842	-0.2235	0.8904	1.38
1977	1	0.4006	0.2847	-0.1574	0.9586	1.98
1976	1	0.5419	0.2826	-0.0119	1.0958	3.68
1975	1	0.7150	0.2793	0.1676	1.2623	6.55
1974	1	0.6821	0.2816	0.1300	1.2341	5.86
1973	1	0.7573	0.2797	0.2092	1.3054	7.33
1972	1	0.6102	0.2774	0.0664	1.1540	4.84
1971	1	0.7626	0.2727	0.2281	1.2970	7.82
1970	1	0.5153	0.2747	-0.0230	1.0536	3.52
1969	1	0.6562	0.2741	0.1190	1.1933	5.73
1968	1	0.5990	0.2713	0.0673	1.1307	4.88
1967	1	0.2406	0.2756	-0.2996	0.7808	0.76
1966	1	-0.1116	0.2768	-0.6542	0.4310	0.16
1965	0	0.0000	0.0000	0.0000	0.0000	.
Scale	0	9.5737	0.0000	9.5737	9.5737	

c) Combined CBC/BBS indices

Criterion	DF	Value	Value/DF
Deviance	2925	268213.2817	91.6968
Scaled Deviance	2925	2925.0000	1.0000
Pearson Chi-Square	2925	315853.4398	107.9841
Scaled Pearson X2	2925	3444.5398	1.1776
Log Likelihood		-2289.5214	

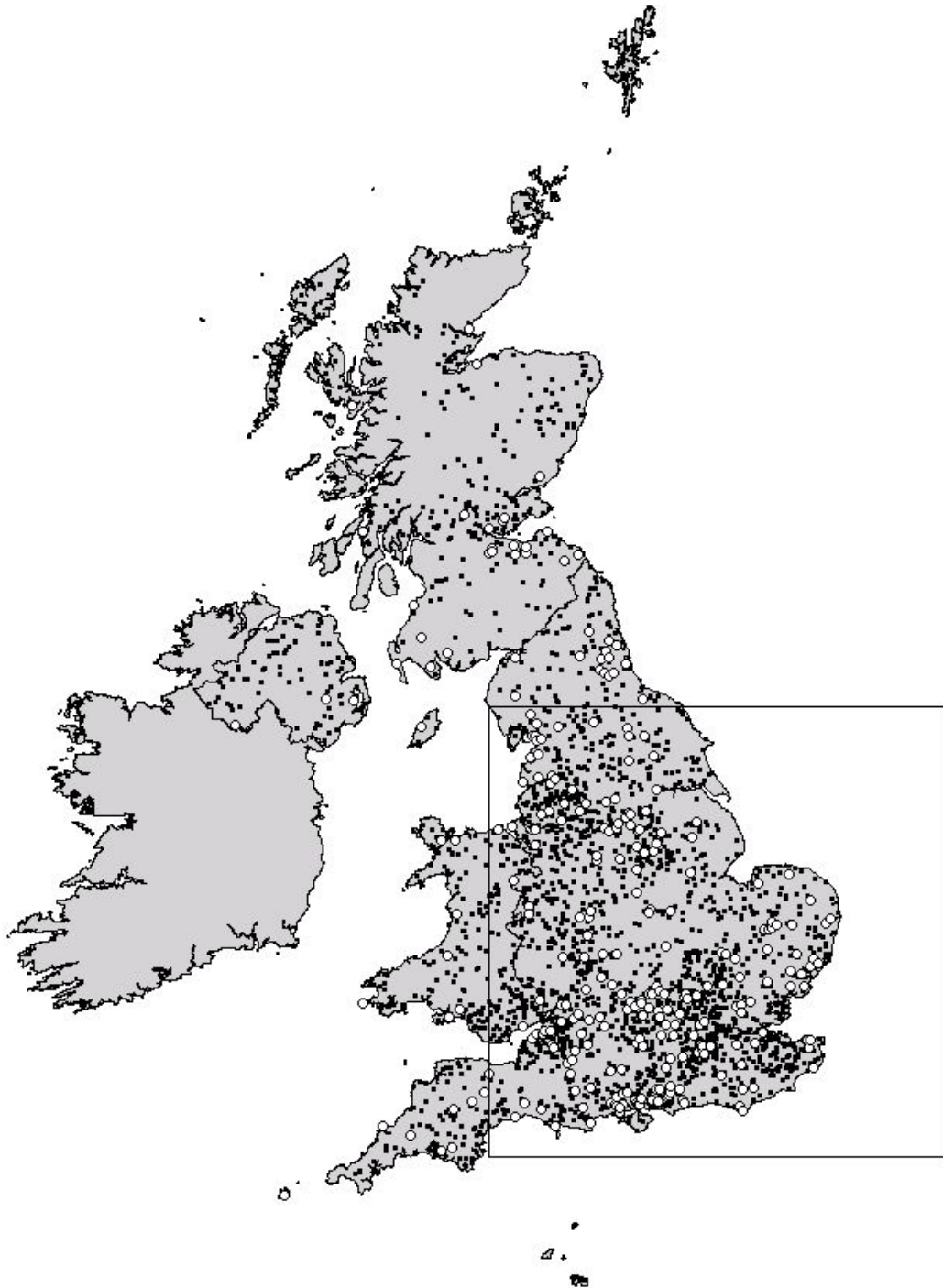
year	df	estimate	stderr	lcl	ucl	Chi-sq
2000	1	-0.9734	0.3085	-1.5780	-0.3687	9.96
1999	1	-0.8535	0.3054	-1.4521	-0.2550	7.81
1998	1	-0.6858	0.3028	-1.2793	-0.0923	5.13
1997	1	-0.7327	0.3029	-1.3264	-0.1390	5.85
1996	1	-0.5090	0.3005	-1.0979	0.0800	2.87
1995	1	-0.5047	0.2991	-1.0910	0.0816	2.85
1994	1	-0.3104	0.2971	-0.8927	0.2718	1.09
1993	1	-0.6382	0.3418	-1.3080	0.0317	3.49
1992	1	-0.2078	0.3177	-0.8304	0.4148	0.43
1991	1	0.0216	0.3105	-0.5869	0.6302	0.00
1990	1	-0.1031	0.3103	-0.7114	0.5052	0.11
1989	1	0.1534	0.3008	-0.4361	0.7429	0.26
1988	1	0.1910	0.3009	-0.3987	0.7807	0.40
1987	1	0.1352	0.3026	-0.4578	0.7283	0.20
1986	1	0.0301	0.3055	-0.5686	0.6288	0.01
1985	1	0.1237	0.3027	-0.4695	0.7169	0.17
1984	1	0.1564	0.2977	-0.4271	0.7399	0.28
1983	1	0.0835	0.2987	-0.5018	0.6689	0.08
1982	1	0.1736	0.2952	-0.4049	0.7521	0.35
1981	1	0.0826	0.2920	-0.4896	0.6549	0.08
1980	1	0.3957	0.2847	-0.1622	0.9536	1.93
1979	1	0.2008	0.2874	-0.3625	0.7640	0.49
1978	1	0.3335	0.2842	-0.2236	0.8906	1.38
1977	1	0.4006	0.2848	-0.1575	0.9587	1.98
1976	1	0.5420	0.2826	-0.0120	1.0959	3.68
1975	1	0.7150	0.2793	0.1676	1.2625	6.55
1974	1	0.6821	0.2817	0.1300	1.2343	5.86
1973	1	0.7573	0.2797	0.2091	1.3056	7.33
1972	1	0.6102	0.2775	0.0663	1.1541	4.83
1971	1	0.7625	0.2727	0.2280	1.2971	7.82
1970	1	0.5153	0.2747	-0.0231	1.0537	3.52
1969	1	0.6562	0.2741	0.1189	1.1935	5.73
1968	1	0.5990	0.2713	0.0672	1.1308	4.87
1967	1	0.2406	0.2757	-0.2997	0.7809	0.76
1966	1	-0.1116	0.2769	-0.6543	0.4311	0.16
1965	0	0.0000	0.0000	0.0000	0.0000	.
Scale	0	9.5758	0.0000	9.5758	9.5758	

d) Combined CBC/BBS indices as above, but adjusting BBS down to have mean weight of one and CBC a weight of one

Criterion	DF	Value	Value/DF
Deviance	2925	2578.9739	0.8817
Scaled Deviance	2925	2925.0000	1.0000
Pearson Chi-Square	2925	3037.0523	1.0383
Scaled Pearson X2	2925	3444.5398	1.1776
Log Likelihood		-2289.5214	

year	df	estimate	stderr	lcl	ucl	Chi-sq
2000	1	-0.9734	0.3085	-1.5780	-0.3687	9.96
1999	1	-0.8535	0.3054	-1.4521	-0.2550	7.81
1998	1	-0.6858	0.3028	-1.2793	-0.0923	5.13
1997	1	-0.7327	0.3029	-1.3264	-0.1390	5.85
1996	1	-0.5090	0.3005	-1.0979	0.0800	2.87
1995	1	-0.5047	0.2991	-1.0910	0.0816	2.85
1994	1	-0.3104	0.2971	-0.8927	0.2718	1.09
1993	1	-0.6382	0.3418	-1.3080	0.0317	3.49
1992	1	-0.2078	0.3177	-0.8304	0.4148	0.43
1991	1	0.0216	0.3105	-0.5869	0.6302	0.00
1990	1	-0.1031	0.3103	-0.7114	0.5052	0.11
1989	1	0.1534	0.3008	-0.4361	0.7429	0.26
1988	1	0.1910	0.3009	-0.3987	0.7807	0.40
1987	1	0.1352	0.3026	-0.4578	0.7283	0.20
1986	1	0.0301	0.3055	-0.5686	0.6288	0.01
1985	1	0.1237	0.3027	-0.4695	0.7169	0.17
1984	1	0.1564	0.2977	-0.4271	0.7399	0.28
1983	1	0.0835	0.2987	-0.5018	0.6689	0.08
1982	1	0.1736	0.2952	-0.4049	0.7521	0.35
1981	1	0.0826	0.2920	-0.4896	0.6549	0.08
1980	1	0.3957	0.2847	-0.1622	0.9536	1.93
1979	1	0.2008	0.2874	-0.3625	0.7640	0.49
1978	1	0.3335	0.2842	-0.2236	0.8906	1.38
1977	1	0.4006	0.2848	-0.1575	0.9587	1.98
1976	1	0.5420	0.2826	-0.0120	1.0959	3.68
1975	1	0.7150	0.2793	0.1676	1.2625	6.55
1974	1	0.6821	0.2817	0.1300	1.2343	5.86
1973	1	0.7573	0.2797	0.2091	1.3056	7.33
1972	1	0.6102	0.2775	0.0663	1.1541	4.83
1971	1	0.7625	0.2727	0.2280	1.2971	7.82
1970	1	0.5153	0.2747	-0.0231	1.0537	3.52
1969	1	0.6562	0.2741	0.1189	1.1935	5.73
1968	1	0.5990	0.2713	0.0672	1.1308	4.87
1967	1	0.2406	0.2757	-0.2997	0.7809	0.76
1966	1	-0.1116	0.2769	-0.6543	0.4311	0.16
1965	0	0.0000	0.0000	0.0000	0.0000	.
Scale	0	0.9390	0.0000	0.9390	0.9390	

Figure 1.1. Map of the UK showing the boundary of Southern Britain used in the analyses presented in this report and the location of BBS squares (■) and CBC plots (○) in 2000. The boundary of Southern Britain is defined by an easting of 3000 and northing of 5000 of the National Grid (after Fuller *et al.* 1985).



Part 2. Joint population modelling of the CBC and the BBS: exploration of software packages and the time constraints of using GAM's versus GLM's

EXECUTIVE SUMMARY

1. A previous report by Freeman *et al.* (2002) compared the trends from the long-running CBC (from early 1960's to 2000) with the more recent BBS (since 1994) and showed that for the majority of species there were *comparable trends* within Southern Britain during the period of overlap 1994-2000. This suggested that it would be possible to combine the BBS and the CBC to produce a joint trend from the early 1960's up until present for these species. This could be extended to include the entire UK for approximately half of the species as their trends during the 1990's from the BBS data were comparable within and outside of Southern Britain.
2. In this report we explore the practicalities of producing and modelling joint population trends from 1966 to 2002 for those species identified by Freeman *et al.* 2002. This is in respect to the computing time required and the methodology to be used for producing the smoothed trends. Two main approaches were used to produce smoothed population trends; the first involved the use of GAM's which combines the smoothing and modelling of the trend and the second involves generating annual indices from a GLM, followed by smoothing of these indices to produce a trend.
3. The statistical software packages SAS and R and the specialised package for running GAM's called GAIM, written by Hastie & Tibshirani, (1990) were compared for their suitability for producing the joint trends using a GAM approach. In addition, CPU time and the trends produced were compared with post hoc smoothed trends from a GLM. Initial analyses involved BBS data alone for assessing the suitability and options available for the GAM in the three packages. For the joint modelling of the BBS and the CBC data, 20 species were used in the pilot study. These included 18 of the 20 farmland bird indicators; Goldfinch, Greenfinch, Jackdaw, Corn Bunting, Kestrel, Lapwing, Grey Partridge, Reed Bunting, Starling, Stock Dove, Turtle Dove, Wood Pigeon, Tree Sparrow, Whitethroat, Linnet, Skylark, Yellowhammer and Yellow Wagtail. The two additional species were Blackbird and Wren, both of which have large sample sizes. The farmland bird indicator species represented a suitable selection of species as they differ in overall population trends, sample size and other characteristics.
4. As SAS GAM had no option for the inclusion of weights, only R and GAIM were suitable for the modelling and of all three packages tested, GAIM required less CPU time for the actual modelling step. There were slight differences in the population trends produced between the three packages and these were partly attributed to their different smoothing algorithms used in the GAM. With the GAM formulated as an annual site by year model (comparable to a GLM) there were more marked differences between the trends from the GAM run in GAIM and the equivalent GLM (run in either SAS or R). In contrast to the results from GAIM, the trends from a GAM run in R were almost identical to the GLM run in SAS.
5. Modelling the trends using a GLM approach and smoothing the annual indices offered considerable savings in computing time compared to using GAM's. This was exacerbated by using bootstraps to generate confidence intervals around the trends. There also appeared to be problems associated with using GAIM for the widespread and common species as it reached the limits of its memory requirements (this may be dependent on hardware specifications). SAS was used for the GLM and post hoc smoothing as it required less computing time compared to the modelling in R. Not surprisingly the majority of the computing time was associated with the GLM. There was minimal difference between the confidence intervals

generated from 199 iterations compared to 99 iterations. As bootstrapping required substantial amounts of time it was recommended that 119 iterations would be sufficient to generate confidence intervals. In contrast to using 99 iterations, this would allow 85 or 95% confidence intervals to be calculated.

INTRODUCTION

The continued production of long-term population trends and the identification of birds undergoing defined population declines necessary for the publication of ALERT's and highlighting of 'birds of conservation concern', requires a rigorous and robust protocol for the combining of the two main terrestrial surveys organised by the BTO: CBC and BBS. It is thus necessary to assess if the population trends from the two partly overlapping surveys can be combined and used in a joint analysis.

Comparison of the CBC and the BBS schemes

There are a number of differences in the methodology and survey coverage of the two schemes. The two main differences between the CBC and the BBS are; firstly, the CBC is biased towards the south east of England, whilst BBS is more widespread. The second is that whereas squares are chosen by the observer with the CBC, in the BBS they are randomly selected within stratified regions. The CBC despite being a valuable survey method and in particular allowing an assessment of bird to habitat relationships has a number of limitations, which led to the development of the BBS and the eventual replacement by the BBS in 2000. Its main weaknesses are: (1) that it is very time consuming for observers; (2) is mainly focused on farmland and woodland habitats; (3) is biased towards the southern and eastern areas of England. It has been shown that CBC plots are representative only of lowland farmland in England south of the River Humber and east of the River Severn (Fuller *et al.* 1995). This is often referred to as Southern Britain and corresponds with a square of easting 3000 and northing 5000 of the National Grid. Southern Britain thus represents a convenient area to compare the BBS and the CBC trends.

Previous analyses involving combined CBC and BBS indices

Freeman *et al.* (2002) compared the trends from the long-running CBC (from early 1960's to 2000) with the more recent BBS (since 1994) data for consistency in population trends during the period of overlap 1994-2000. If long-term trends are to be produced for a number of species it is important to know if the two surveys show similar population trends during the period of overlap. If for example there is a difference between the two surveys during the period of overlap, then it is inadvisable to combine the BBS and the CBC to produce a joint trend from the early 1960's up until present. Their analysis showed that for 75 species that are routinely monitored by both surveys, 68 of these showed *comparable trends* within Southern Britain and for which joint CBC/BBS indices could be produced. A comparison of BBS trends within and outside of Southern Britain revealed that for 52 % of the 75 species considered, trends within Southern Britain are *not* representative of trends outside of this region. Thus CBC data for these species should not be used to produce trends for the whole of the UK.

To enable fair comparison between the two surveys, both the CBC and the BBS data were analysed using a log-linear Poisson regression model fitted in SAS (SAS, 1996). Counts are modelled as a function of site and year affects to produce yearly indices relative to a base point. Inclusion of site effect allows for species abundance to vary from site to site. Current modelling of the BBS data alone uses the same method, along with inclusion of a weighting term. This weighting is to take into account the difference in observer coverage across the UK. Weights are assigned as an inverse to the degree of coverage i.e. regions that receive a high degree of coverage are given a low weighting in the analysis. As analysis of CBC data has never involved the use of weighting, for comparative purposes, no weighting was used for the analysis of BBS and the CBC data for the period of overlap (Freeman *et al.* 2002). For further details on the issue of weighting, see (Newson *et al.* in prep).

Potential use of GAM's for modelling population trends

Generalized Additive Models (GAM's) are generalized linear models in which the linear predictors are constructed as sums of low dimensional smooth functions of covariates. This effectively means that nonlinear trends can be modelled and unlike GLM's, the distribution of the data determines the shape of the curve as opposed to the parametric assumptions surrounding the model. GAM's are extremely flexible models for fitting smooth curves to data. They have received a lot of attention in the ecological literature and they often achieve results superior to GLM's, at least in terms of goodness-of-fit on ecological data.

Smoothing in general is about identifying the trends or patterns in the data from the systematic effects or random variation in the data. This is often referred to as identifying the 'signal' from the noise. Smoothing is one technique that can be used to identify this trend and remove the effects of noise in the data. There are a variety of smoothing methods and the type of smoothing available differs between software packages. For the finer details of the range of smoothing techniques available and differences between them, a thorough discussion of this is provided by Hastie & Tibshirani (1990). The degree of smoothing determines the complexity of the model and is determined by the effective degrees of freedom. The degrees of freedom determines the degree of smoothing and ranges from the maximum amount of smoothing with 1 df to the least amount of smoothing with $t - 1$, where t is the number of time points in the data set (Fewster *et al.* 2000). A model with 1 df is equivalent to a straight line, where as one with $t-1$ degrees of freedom is equivalent to the annual year by year model. Thus as the degrees of freedom increases from 1, the smooth function gains complexity, allowing more turning points and gradient changes.

Determining the degrees of freedom of the smooth function depends largely on the objectives of the analysis, length of the time series available and the pattern of the data. For example, identification of long-term trends will be favoured by a low df, where as annual estimates will need maximum df. With respect to smoothing in general, a model that is too smooth will not closely match the data to which it has been fitted and will tend to do no better on missing data. Conversely, a model that is over flexible will fit every bump and wiggle of the data, including the noise component, and will thus tend to do rather poorly at predicting missing data. Models of intermediate complexity will do better.

Choice of the number of df is an important stage of the modelling process and several automatic selection procedures exist. However, using automatic selection procedures for the purposes of modelling long term population trends is not recommended and earlier work modelling CBC data has suggested that df should be approximately 0.3 times the length of the time series considered (Fewster *et al.* 2000). These are the df that will be used in this report and are also those used in the wider countryside report.

In the context of modelling long term population trends they have the potential advantage of improving the precision of the trends and providing smoothing of the trends (Freeman *et al.* 2002). Up to present GAM's have been fitted to CBC data using both the modified FORTRAN program GAIM (Hastie & Tibshirani, 1990) and S-Plus (Fewster *et al.* 2000). GAM's are becoming readily available in general statistical packages and may offer advantages in ease of use compared to some of the more specialised GAM programs available. Where they may differ is in the area of computational efficiency, with particular respect to bootstrapping. Even minor differences in the timing of the procedures between software packages can lead to big differences where bootstrapping is required.

Aims

The aim of the report is to assess the practicalities of modelling the combined CBC and BBS data, with particular respect to demands on computing time. This is important as GAM's and bootstrapping to obtain more reliable confidence intervals can be very time consuming. Two main techniques were explored for the production of the population trends; the first involved the use of GAM's to enable a joint approach to modelling and smoothing of the population trend. The second involves two steps, the traditional log-linear annual site by year model (GLM), followed by smoothing of the annual indices from this model to produce the long-term smoothed population trend. The first approach involving smoothing of all data points will require more computing time, as opposed to the second approach where smoothing is restricted to the smaller number of annual indices. It is likely that the first approach will produce the most accurate population trend as it involves smoothing the data points as opposed to the annual indices. However, the long time series of the data suggest there should be little difference between the two approaches in terms of population trends, but considerable differences in computing time and resources.

The computational constraints of using GAM's for the joint analysis of CBC and BBS data was first assessed, in particular the use of bootstrapping to obtain confidence intervals. Different software packages were compared to assess ease of use and computational demands. The requirement to include weights was one of the criteria used to select appropriate software packages, in addition to being widely available to the BTO. The first step was to devise a program to actually run a GAM in all the software packages and explore the built-in functions available. To enable a comparison and check initial results, the GAM was first formulated in the framework of an annual log-linear Poisson regression with year and site effects (allows comparison with GLM results).

METHODS

Three available statistical packages capable of modelling long-term population trends (using both GLM's and GAM's) were used. Two of these are general statistical packages, the first being the commercially available SAS, and secondly, R. R is a dialect of the S language that was developed at the Bell laboratories by Rick Becker, John Chambers and Allan Wilks (Venables & Smith, 1992). It is also the basis of the widely known commercial statistical software package called S-Plus. Unlike S-Plus, R is freely available and despite this comes with a wealth of user manuals, resources, comprehensive help files and dedicated web site. It also includes a number of routines that can be classed as leading edge and specialised functions are available for download from the CRAN (Comprehensive R Archive Network) site, written and contributed by a variety of outside people. In addition, users can refer to the widely available documentation available for S/S-Plus, although some differences do exist between S/S-Plus and R. GAM's within R were done using the 'gam' function loaded using the 'mgcv' library. Details of the functions contained within the 'mgcv' library can be obtained from the R website or the following pdf file; (<http://www.stats.gla.ac.uk/~simon/mgcv/mgcv-manual.pdf>). R is available for Windows, UNIX and Linux systems. The third was a modified FORTRAN version of the stand-alone component of Hastie and Tibshirani's GAM software (1990). Details of how to use this can be found in the appendix.

Comparison of the GAM's (population trend) between the three statistical packages

The first step was to formulate the GAM so that it was equivalent to the GLM annual site by year Poisson model. This would allow the comparison of the results with the actual parameter estimates from a standard GLM to ensure the correct specification of the GAM model. This was achieved by specifying the df for the smoothing function for year of t-1 (where t is the length of the time series considered). As weights can not be included within SAS GAM's and the output from SAS did not routinely produce smoothed year indices, GAM's were only run with R and GAIM and these results were compared with the annual estimates from a GLM of the same data run using proc GENMOD in SAS. R and SAS were run using the windows versions, where as GAIM was run using the UNIX system. For the initial stages of model running and program development, BBS data alone (no CBC) was used for a selected group of species (from years 1994 to 2000). Initially, facilities for using R were only available for running them on the Windows operating system. The computational limits of the PC running the Windows model restricted the size of the species datasets (in terms of the number of site factors) to those species with small to moderate sample sizes for the testing of the GAM. Species chosen were Marsh Tit, Corn Bunting, Reed Warbler, Redstart, Wood Warbler and Whinchat. Secondly the population trends for the six species were re-calculated again with smoothing of the GAM set at three df, again using both R and GAIM.

In addition, the computing time (CPU) taken to perform the GAM analyses (no weights) were compared with the annual site by year model (GLM) for the six species using the UNIX system to ensure comparability (time includes actual modelling process only). It is likely that the timings will be slightly longer with weighting included in the models. For a few species, a comparison was made between the GAM and GLM in SAS (this was not pursued further as the GAM routine is unable to include weightings and so is unsuitable for our purposes). The program/s used in R were based on those used by Fewster *et al.* 2000 and freely available on her website.

As the preliminary analysis indicated that CPU time was considerably longer for running a GAM within R compared with the equivalent GAIM, comparison was restricted to using GAM using GAIM and a GLM in SAS. In addition, problems were encountered with R memory limits.

Comparison of CPU time and population trend between a GAM in GAIM and a GLM in SAS for 10 species using combined CBC and BBS data for England from 1966 to 2000

To enable comparison of the population trends from the GAM using smoothing and the annual indices from the GLM, the annual indices from the GLM were smoothed using an equivalent amount of smoothing (same df). The degrees of freedom for the smoothing was based on the protocol set out in the previous wider countryside reports and was based on $0.3 * \text{the length of the time series (no. of total years)}$. This gave a degrees of freedom of 11 for the smoothing. A SAS program was written using proc GENMOD for the GLM and proc TSPLINE for the smoothing of the annual indices. 199 bootstraps were used to generate confidence intervals as opposed to using the analytical confidence intervals that are provided by the software. To assess if it was possible to use a few number of iterations, a comparison was made between the smoothed bootstrapped 90% CI's for all 199 iterations and the first and last 99 iterations separately. For example if it is shown that there are close similarities in the smoothed CI's between the 199 and 99 iterations, then it may be possible to use only 99 iterations. This would make considerable savings on the computing time, especially for the larger sample sizes.

The 10 species consisted of Corn Bunting, Kestrel, Lapwing, Grey Partridge, Reed Bunting, Stock Dove, Turtle Dove, Tree Sparrow, Yellowhammer and Yellow Wagtail. These were selected from a larger selection of 20 species on the basis of their smaller sample sizes compared to the other 10 species due to the lengthy time required to run the analyses. These 20 selected species consisted of the 18 farmland bird indicator species and two additional species (Wren and Blackbird). The farmland bird indicator species were considered a suitable selection of species as they are all routinely covered by both the two schemes and contain a wide ranging suite of species. They differ in overall population trends, sample size and level of dispersion relative to the Poisson distribution (measure of the variance to the mean). The Wren was included as it has a fluctuating population and the Blackbird has a very large sample size (Wren also has a large sample size in terms of site effects). There are both species which have seen population declines and increases across the period.

Due to an error detected in the original program for generating the combined datasets, the CBC data for all the species were run using incorrect weights, this means that the population trends may differ slightly from the actual trends using the correct weights. This does not however invalidate the comparison between the GAIM and the SAS GLM as the same datasets were used for both.

Modelling of the joint CBC and BBS data from 1996 to 2002 for England using GLM in SAS with smoothing of the annual indices for 20 species

A weighted GLM in SAS with post hoc smoothing of the indices were run using the data from 1996 to 2002 for England for the 20 selected species. 119 bootstraps were used to generate confidence intervals as opposed to using the analytical confidence intervals that are provided by the software. There was an important addition to the program to cope with the problem caused by the missing data for 2001 as a result of the foot and mouth disease. There are two main ways of dealing with the 2001 excluded data in the programs: (1) Exclude 2001 completely so that there is NO 2001 variable and then re-number the years consecutively so that there is no year missing (this can be confusing for other programmers and requires the conversion of the years back into the correct years at the end of the program); (2) Keep in 2001 variable but with missing counts for it so that the years as they stand are correct and so this avoids the problems caused by any need to consecutively renumber the years again. As the SAS GLM used year as a class variable, having no class for 2001 would cause no problem with the analysis. However, due to the nature of the programming techniques and the desire to maintain a program that could be used from year to year with very little changes, the program kept in a variable for year 2001, but effectively removed year 2001 for the analysis stage. How does GAIM handle this problem?

RESULTS

Comparison of the options for GAM's between the three statistical packages

The options for GAM's and the type of smoothing employed by the three packages varies (Table 2.1). For details regarding the smoothing techniques, consult Hastie & Tibshirani, (1990). It is possible that minimal differences existing between the trends from the three different packages may be attributed to the differences of the smoothing algorithms. One of the main disadvantages of using SAS is its inability to include weights in the modelling process, this precludes its use for the joint modelling of the CBC and the BBS data, but for some preliminary analyses it was used to enable a comparison with the other GAM's with respect to CPU requirements/computing timing and the population trends.

Comparison of the population trends and CPU time between a GAM formulated as an annual site by year model (GLM)

Table 2.2 illustrates the differences in CPU time between the GAM formulated as an annual site by year model (effectively a GLM, run in R and GAIM) and a formal GLM run in SAS. Not surprisingly the fastest model was a GLM, but the timing differed appreciably between the individual GAM's run in the different software packages. The GAM run in GAIM is about three to four times quicker than R and both are quicker than the GAM run in SAS. In addition with modelling of some species with larger sample sizes than those contained in Table 2.2, the package R (specifically the 'mgcv' library for GAM's) was unable to compute the GAM and error messages indicated that the memory limit was reached. It was possible that the large number of site factors in BBS data was responsible for the high computational demands placed by the GAM and the R package (preliminary analysis of CBC data alone for species which occur on a small number of sites suggested that it was possible to analyse successfully a longer run of years than the seven years used for the BBS, as shown by the Nuthatch.

Figure 2.1 illustrates that the population trend modelled using the three software packages is similar between the two GAM's run in R and GAIM and the GLM run in SAS. However it can be seen that the trend from the GAM run in R is more similar to the trend from the GLM run in SAS, as opposed to the trend obtained from the GAM run in GAIM. Despite the short time series of the BBS data, the GAM's were formulated to incorporate a degree of smoothing ($df=3$) and a comparison was made between R and GAIM to assess how the population trend varied between the two (Figure 2.2). It appears that similarity is greatest between the two software packages the more linear the trend becomes. Differences appear to be highest when the species undergoes marked fluctuations from year to year. Again this difference may be due to the difference in the smoothing algorithm used by the two software packages. However, it is possible that any differences between the two may be exacerbated by the short time series available from the BBS.

Comparison of CPU time and population trend between a GAM in GAIM and a GLM in SAS for 10 species using combined CBC and BBS data for England from 1966 to 2000

To enable comparison of the population trends from the GAM using smoothing and the annual indices from the GLM, the annual indices from the GLM were smoothed using an equivalent amount of smoothing (same df). The degrees of freedom for the smoothing was based on the protocol set out in the previous wider countryside reports and was based on $0.3 * \text{the length of the time series (no. of total years)}$. This gave a degree of freedom of 11 for the smoothing. The 20 selected species consisted of the 18 farmland bird indicator species (originally 20 species, but Rook and Barn Owl were excluded due to the absence of data) and two additional species (Wren and Blackbird). The farmland bird indicators were a suitable selection of species as they differed in overall population trends, sample size and level of dispersion relative to the Poisson distribution (measure of the variance to the mean). Table 2.3a summarises the characteristics of the data for these species. Fourteen out of the

eighteen species have declined, the others; Stock Dove, Woodpigeon, Greenfinch and Goldfinch have increased. Lapwing, Woodpigeon, Starling, Linnet and Tree Sparrow have higher values of over dispersion relative to the other species, not surprising for species that tend to flock or be colonial. A number of species are actually under-dispersed. The Wren and Blackbird were also included, the former because it has a fluctuating population and the latter as it has a very large sample size. Selection of these species should ensure that the assessment of the GAM and GLM is robust in respect to the wide-ranging characteristics of the species data. It was especially important to ensure that the software could cope adequately with the large sample size of Blackbird.

Table 2.3b details the differences in the CPU times between GLM and GAIM run on the UNIX system. Note the timings for the SAS GLM does not include the smoothing step and only includes the actual running of the GLM. However, it is the GLM that is the time consuming step and the smoothing is very quick relative to the GLM. It is expected that the CPU times should reflect the time required by the processor and should not be affected by other jobs in progress on the UNIX system. Not surprisingly the GAM run in GAIM took considerably longer to complete than the GLM. The array size had to be adjusted to run GAM in GAIM for species with larger samples than for Corn Bunting (shown in Table 2.3b) and the actual times are no longer available. However, the important point is that they were orders of magnitude longer than for the GLM and we did not pursue this option further. Figure 2.3a illustrates the curvilinear relationship of sample size (number of sites in model) with CPU time for the 11 species for data 1966 to 2000 using SAS GLM with 199 bootstraps. As sample size increases so does CPU time.

To assess how similar the population trends are between the GAM in GAIM and the smoothed indices from the GLM in SAS, they are plotted together in Figure 2.3b. It can be seen from Figure 2.3b, that there is a difference between the smoothed trend from the GAM in GAIM and the GLM in SAS. This discrepancy varies with species and seems to be greatest for those species which show a strong fluctuating trend. Some of the differences in the trends between the smoothed trend of the GLM in SAS and the GAM in GAIM may be related to the error messages given in GAIM ('underflow warning'). To see if the differences were associated with the GAM or the GLM, the same data was used to run an identical GLM in R and then the indices from this were smoothed using the same method as those for the SAS GLM. This was done for a few species only and are illustrated in Figure 2.3c. There is very little difference between the GLM's run in either R or SAS, in fact the two lines are nearly identical that it is impossible to distinguish between the two in Figure 2.3c. Thus, the difference seems to be with the GAM in GAIM.

Figure 2.3d illustrates the unsmoothed GLM population trends for the 11 species, including the unsmoothed bootstrapped confidence limits and the unsmoothed analytical confidence limits. These 11 species were selected from the original 20 species which were chosen for a pilot study of the joint modelling. Figure 2.3e illustrates the smoothed GLM trend for the 20 species and a comparison of the smoothed CI's from the analytical model and the bootstrap procedure. It can be seen that for the majority of the species the bootstrapped CI's are wider than the CI's calculated from the model SE. The similarity between the two CI's varies between species and for some these differences are large. This suggests that it is advisable to use the CI's generated from the bootstrap procedure.

For ten species (generally those that had the smaller sample sizes out of the 20 species) a comparison was made between the smoothed bootstrap 90% CI for all 199 iterations with only the first or last set of 99 iterations (Fig. 2.3f). Figure d shows there is little difference in the smoothed bootstrap 90% CI between the 99 iterations with the full 199 iterations, this being the case for when making the comparison using the first and last 99 iterations with the full 199 iterations. The problem with using 99 iterations is that one can only give CI for 90 or 80% as you cannot extract the lower and upper values for 85 or 95% (this gives rise to a real value which cannot be extracted from the bootstraps). The advantage of using 99 iterations is that it will approximately half the computing time needed to obtain the CI's for each species. This may make some considerable savings for the species with the larger sample size. For a small increase in the number of iterations, one may obtain 85 or 95% confidence intervals with 119 iterations.

CONCLUSIONS

Joint modelling of the bird population trends for 1966 to 2002 in England uses year indices produced from a GLM with post hoc smoothing to give a smooth population trend. This was modelled using SAS software. Post hoc smoothing of annual indices was chosen as modelling using GAM's proved to be too time consuming considering the large size of the dataset and the computing facilities available at present. The large demand place on processor time and memory requirements is probably a result of the large number of site effects which are included in the model. For some of the common and widespread species, the total number of site effects included in the model exceeds 3000 (considering the area of England only). This is the case for Blackbird and Wren. For those species for which joint CBC and BBS trends can be produced reliably for the UK as a whole, this sample size is likely to increase further.

SAS had advantages over the R statistical package for the modelling of the bird population trends as it required less computing time for an equivalent GLM on the same data. The downside in respect to modelling using GAM's was its inability to include weights. Using the GAM in R for the same dataset resulted in the memory limits of R being exceeded, which is likely to be specific to the hardware used for the modelling. More worryingly was the error messages associated with the 'mgcv' library which is the library used in R for GAM's. This is unlikely to be resolved by improved hardware specifications. Similar problems associated with memory limits were experienced in using GAIM for GAM's; although it is unclear whether this would be resolved with different hardware specifications.

Regardless of whether GAM's were run using the GAIM or R package; for those species for which memory and computing requirements were sufficient, GAM's required considerably more computing time compared to an equivalent GLM. This was the main reason why post hoc smoothing of the annual indices from a GLM were chosen as the method for production of the smoothed population trends as opposed to the combined smoothing and modelling involved with a GAM.

Table 2.1 Comparison of the options available for running GAM's in the three software packages

Details	Software package		
	SAS	R	GAIM
Weighting allowed	No	Yes	Yes
Choice of smoothing	Yes Loess	Yes Penalized regression splines	Yes Cubic spline smoother
Choice of distribution	Spline Yes	Thin-plate spline Yes	Local linear smoother Yes

Table 2.2 Comparison of CPU time of GAM's between R, GAIM, SAS and GLM in SAS on the UNIX system. Data used was UK BBS data from 1994 to 2000. No weights are used in the analysis and times are for the GAM or GLM computation only. The GAM's were formulated to be equivalent to a GLM (df of 6). Note that SAS GLM was based on the GLM only and no smoothing was used after.

Species	GAM	GAM	GAM	GLM
	GAIM	R	SAS	SAS
Corn Bunting	0m 44.52s	3m 9s	14m 41.61s	0m 3.10s
Reed Warbler	0m 8.94s	0.56m	1m 15.15s	0m 0.67s
Redstart	0m 7.46s	0.46m		0m 0.53s
Whinchat	0m 2.97s	0.23m	0m 28.61s	0m 0.28s
Marsh Tit	0m 59.59s	4m 54s		0m 3.88s

Table 2.3a Data characteristics of the 20 selected species used in the GAM and smoothed GLM index population trends for 1966 to 2000

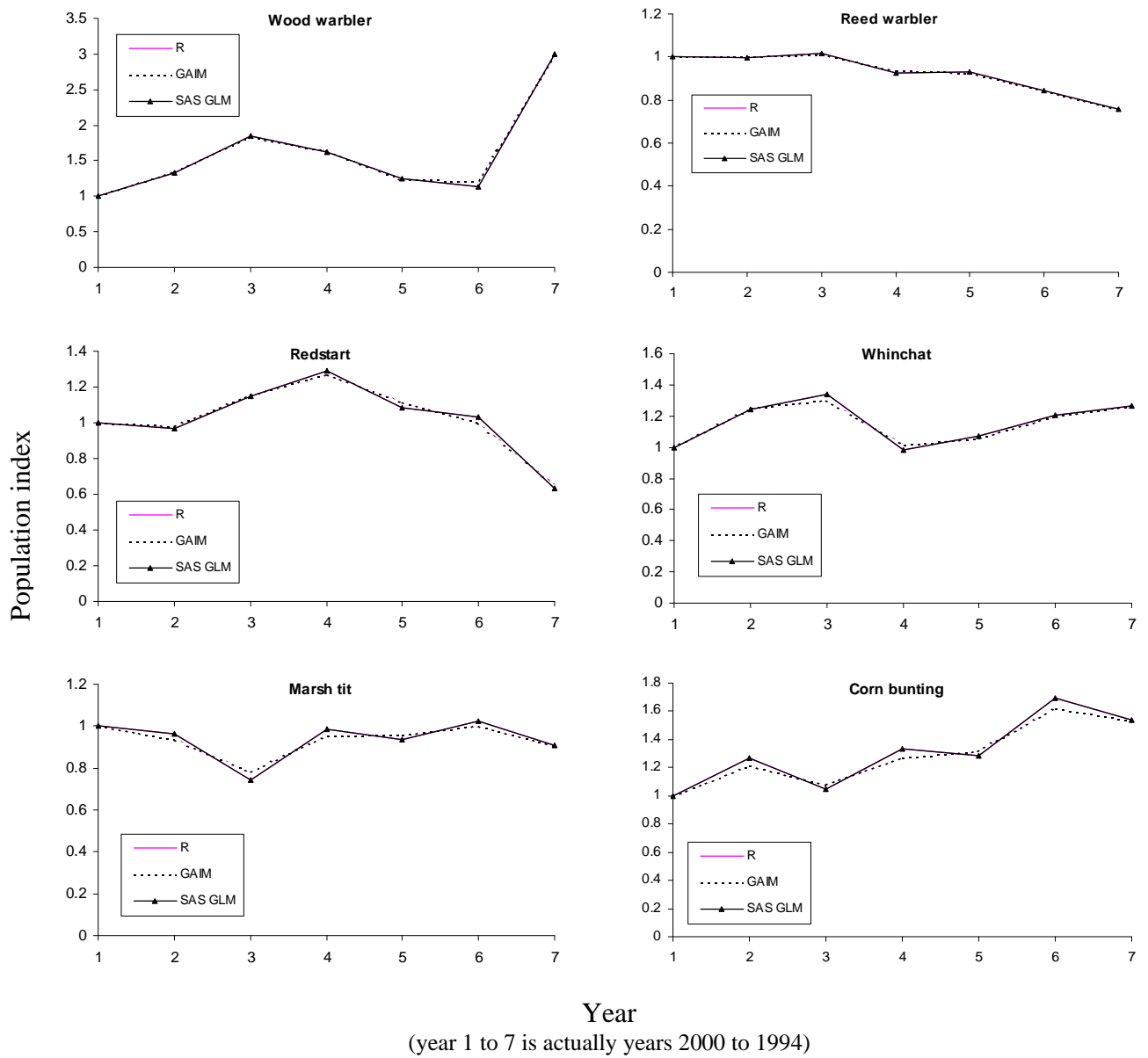
Species	Rank order (high to low dispersion) of all 75 species		Yearly mean No. of plots		Population change (%)		Total no. of plots		
	CBC deviance/df (1965-2000)	BBS deviance/df (1994-2000)	CBC	BBS	CBC (1968-1999)	BBS (1994-2000)			
Kestrel	0.60	0.93	68	70	80	439	-4	-15	2033
Grey Partridge	0.78	1.66	48	24	59	193	-85	-26	530
Lapwing	1.21	4.23	9	4	53	426	-34	5	1446
Stock Dove	0.84	2.40	42	15	75	538	183	8	1757
Woodpigeon	1.33	7.25	5	2	98	1456	90	5	2512
Turtle Dove	0.94	1.42	28	33	59	189	-70	-23	968
Skylark	1.00	1.46	22	29	120	1075	-54	-19	2347
Jackdaw	1.11	4.86	17	3	79	924	79	27	2089
Wren	1.32	1.34	6	40	220	1375	67	11	3031
Blackbird	0.80	1.34	47	39	225	1438	-25	10	3043
Whitethroat	1.12	1.27	16	44	118	844	-55	25	2319
Yellow Wagtail	0.89	1.54	37	27	27	154	-48	-4	2161
Starling	1.52	14.60	2	1	125	1213	-75	-21	2568
Tree Sparrow	1.36	2.27	4	19	59	114	-96	3	771
Greenfinch	1.01	2.30	21	18	142	1088	11	34	2632
Goldfinch	0.92	2.38	30	17	96	844	18	0	2384
Linnet	1.23	3.44	8	8	123	829	-58	-19	2323
Corn Bunting	0.99	1.44	24	32	24	139	-87	-38	547
Yellowhammer	0.99	1.25	25	49	132	871	-53	-13	2161
Reed Bunting	0.92	1.21	32	53	84	250	-48	-23	1158

Table 2.3b Timings are for UNIX system for the 11 species for SAS GLM and GAIM comparison (CPU times)

Species	SAS GLM (199 bootstraps)	GAIM GAM (1 run)	Sample size
		199 * 12m 2.1s	
Corn Bunting	52m 31.35s	(> 40h)	547
Yellow Wagtail	1h 25m 59.89s	N/A	645
Tree Sparrow	2h 7m 28.74s	N/A	771
Lapwing	22h 13m 57.14s	N/A	1446
Grey Partridge	50m 9.47s	N/A	530
Turtle Dove	4h 3m 26.59s	N/A	968
Kestrel	65h 15m 0.89s	N/A	2033
Reed Bunting	9h 19m 15.51s	N/A	1158
Stock Dove	41h 16m 20.03s	N/A	1757
Yellowhammer	78h 27m 14.75s	N/A	2161
Jackdaw	71h 52m 15.33s	N/A	2089
Blackbird	1h 5m 24.12s (for 1 run only)		

For comparison the timings for corn bunting were run for a GLM using R with the same criteria as SAS, the time for 1 GLM bootstrap was 7.86 minutes. This is considerably longer than the SAS GLM when considering 1 run only (<1m).

Figure 2.1 Comparison of the BBS population trend obtained from three different statistical packages; R, GAIM and SAS for six species from 1994 to 2000. The trend from R and GAIM was modelled using a GAM constrained to be an annual year by year model and is compared with a normal annual year by year model using a GLM in SAS.



Indices are scaled relative to year 1. For the GAM's, the df was set to be t-1, where t is the time length. In this instance there are seven years and so df was six.

Figure 2.2 Comparison of the BBS population trend between R and GAIM for six species from 1994 to 2000 using a GAM with smoothing set at three df.

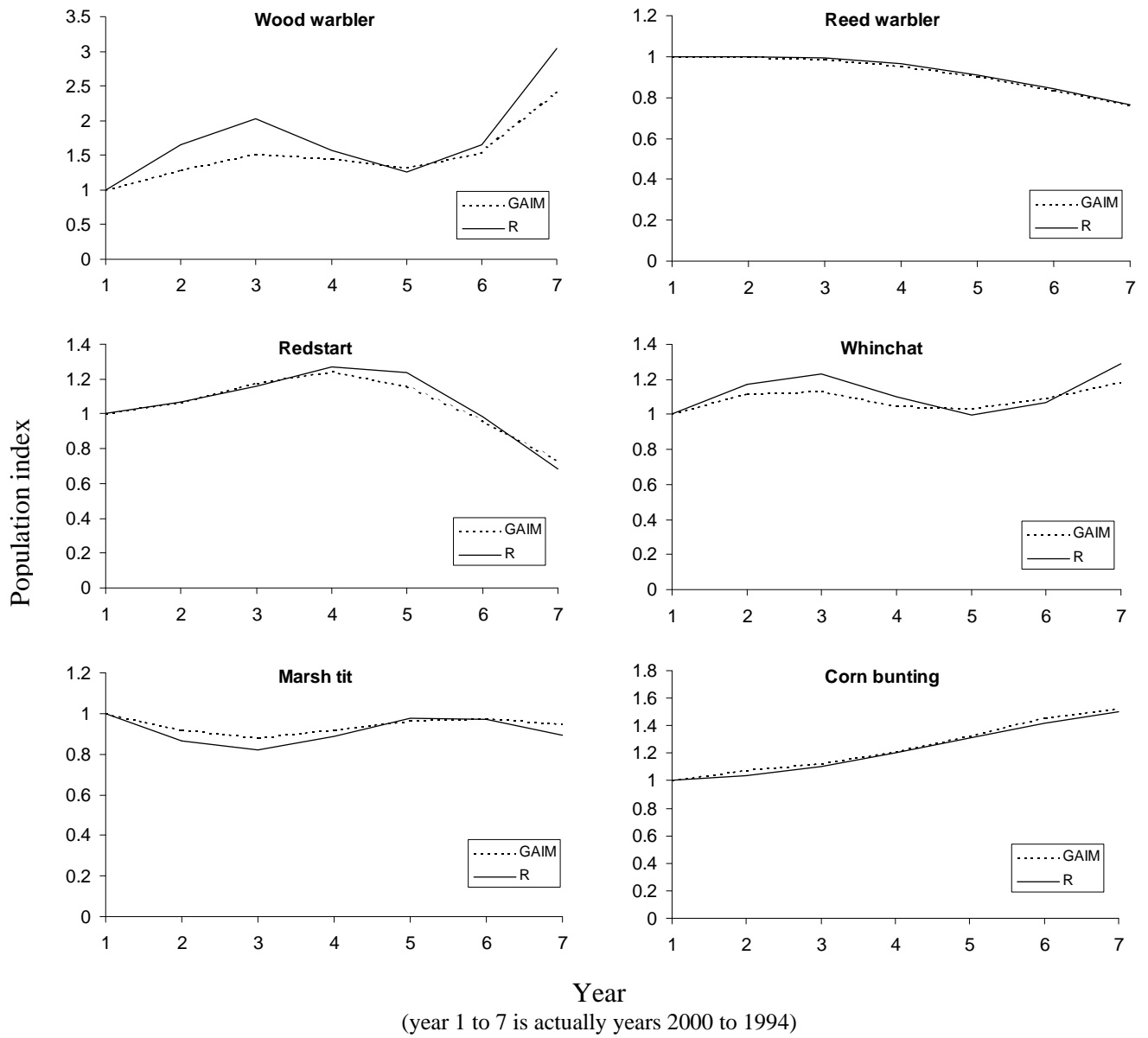


Figure 2.3a Illustrates the relationship of sample size (no. sites in model) with CPU time for the 11 species for data 1966 to 2000 using SAS GLM with 199 bootstraps (species with the smaller sample size)

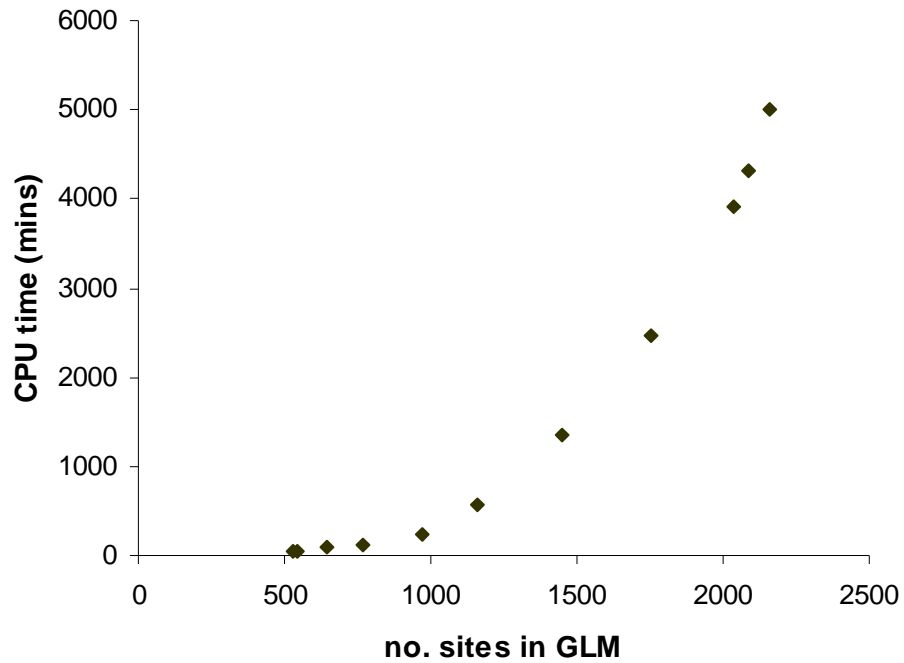


Figure 2.3b Comparison of the trend between the GAM in GAIM and the GLM run in SAS for the 10 species with equivalent degrees of smoothing (incorrect weights)

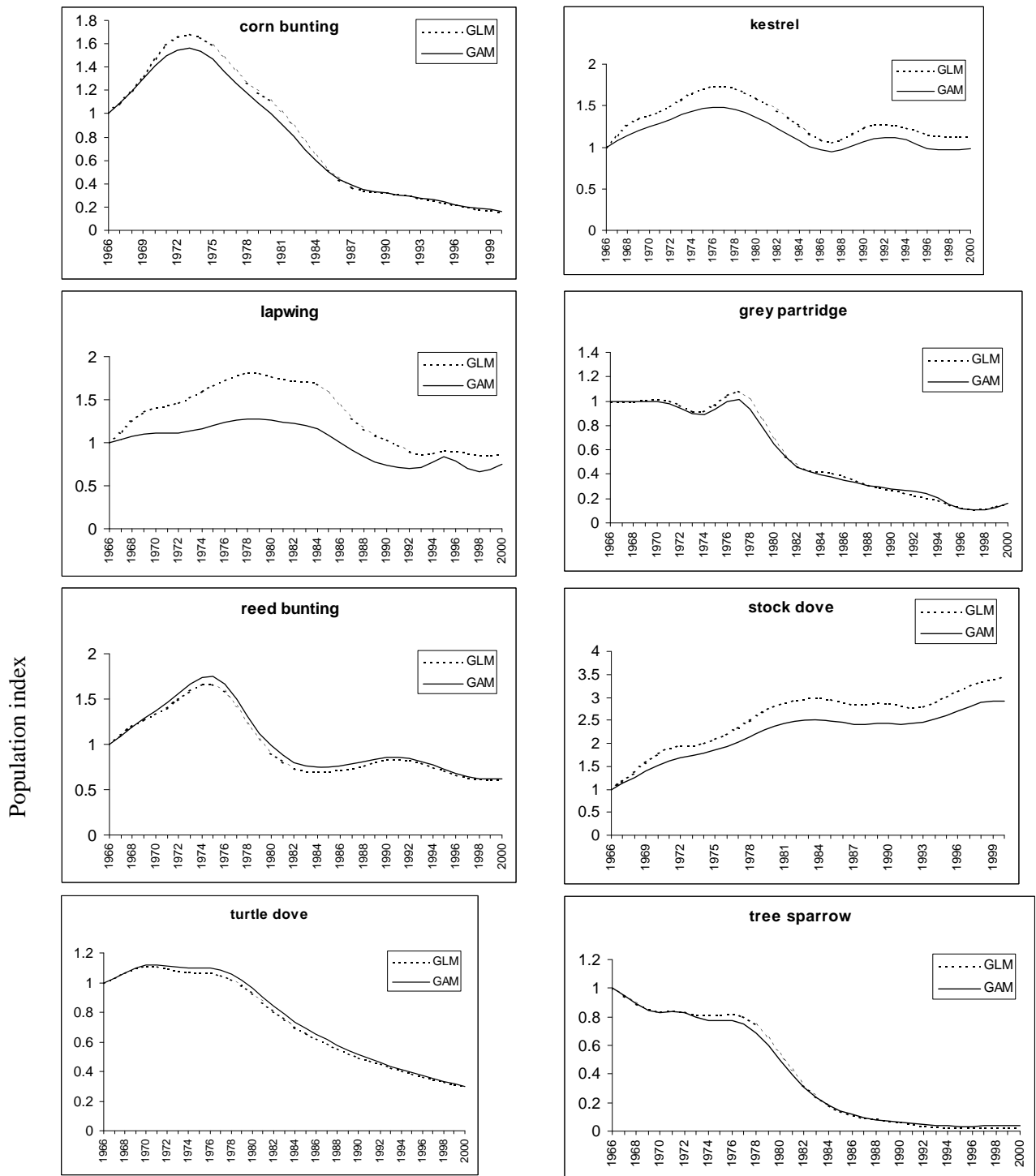


Figure 2.3b Continued

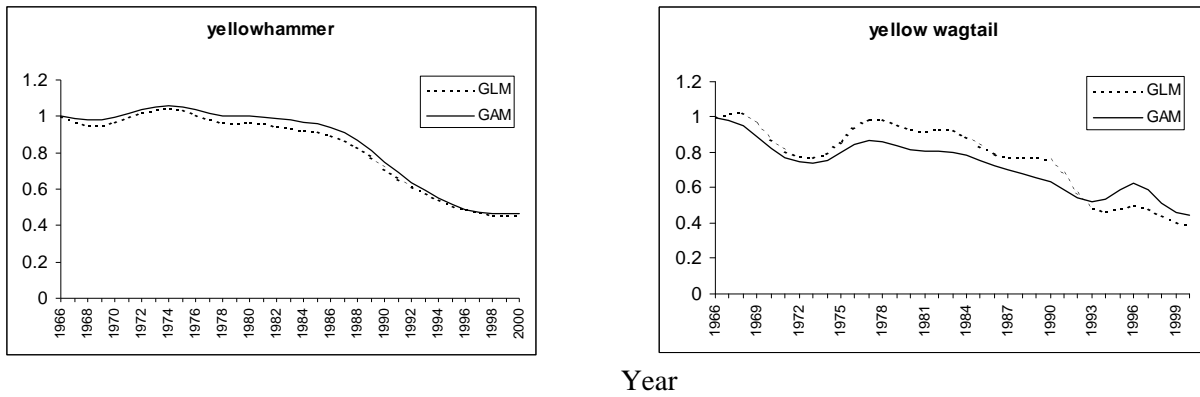


Figure 2.3c Comparison of the trend between the GAM in GAIM and the GLM run in SAS and R with equivalent degrees of smoothing for the 10 species (incorrect weights)

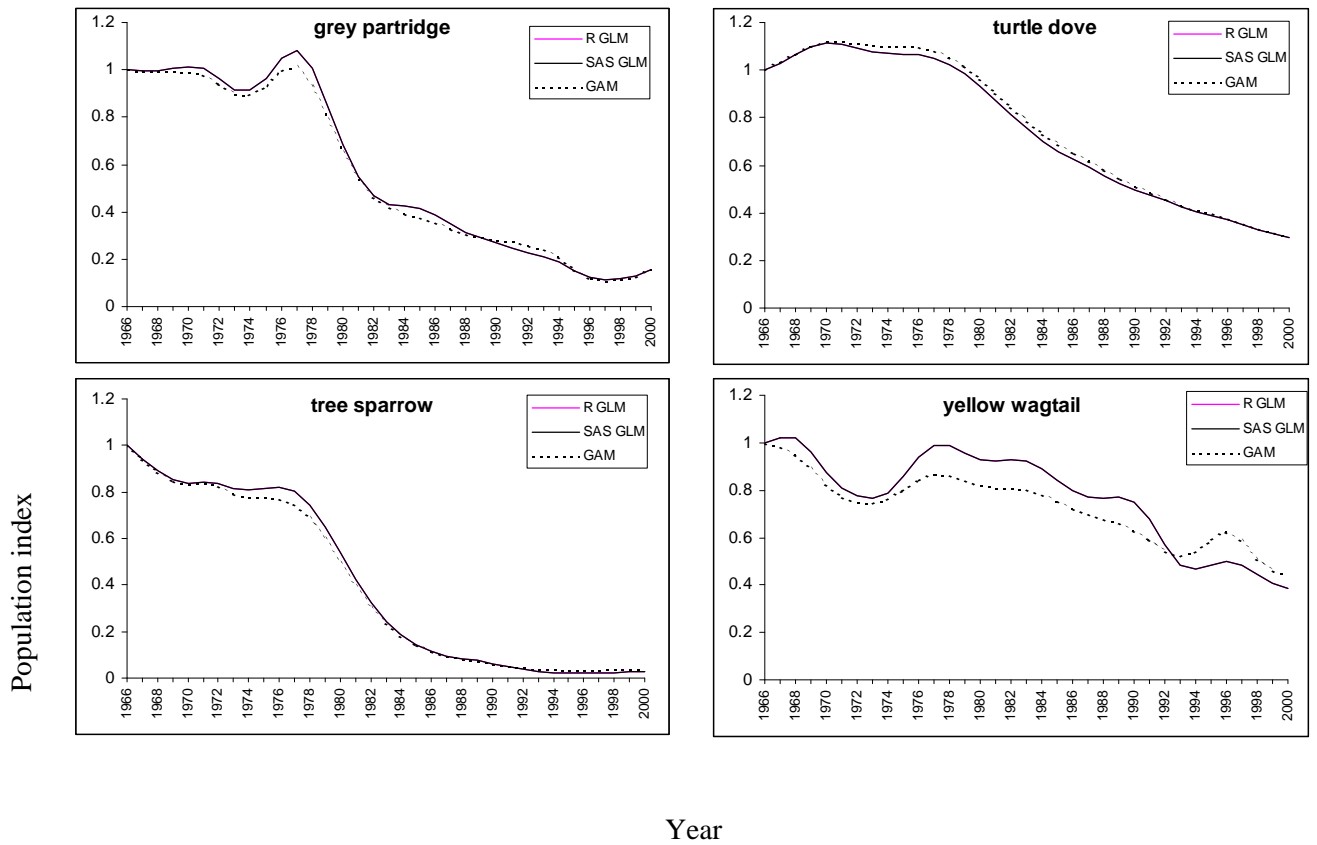


Figure 2.3d Unsmoothed trend from the GLM analysis and comparison between the unsmoothed CI's from the bootstrap procedure and the unsmoothed analytical model estimates

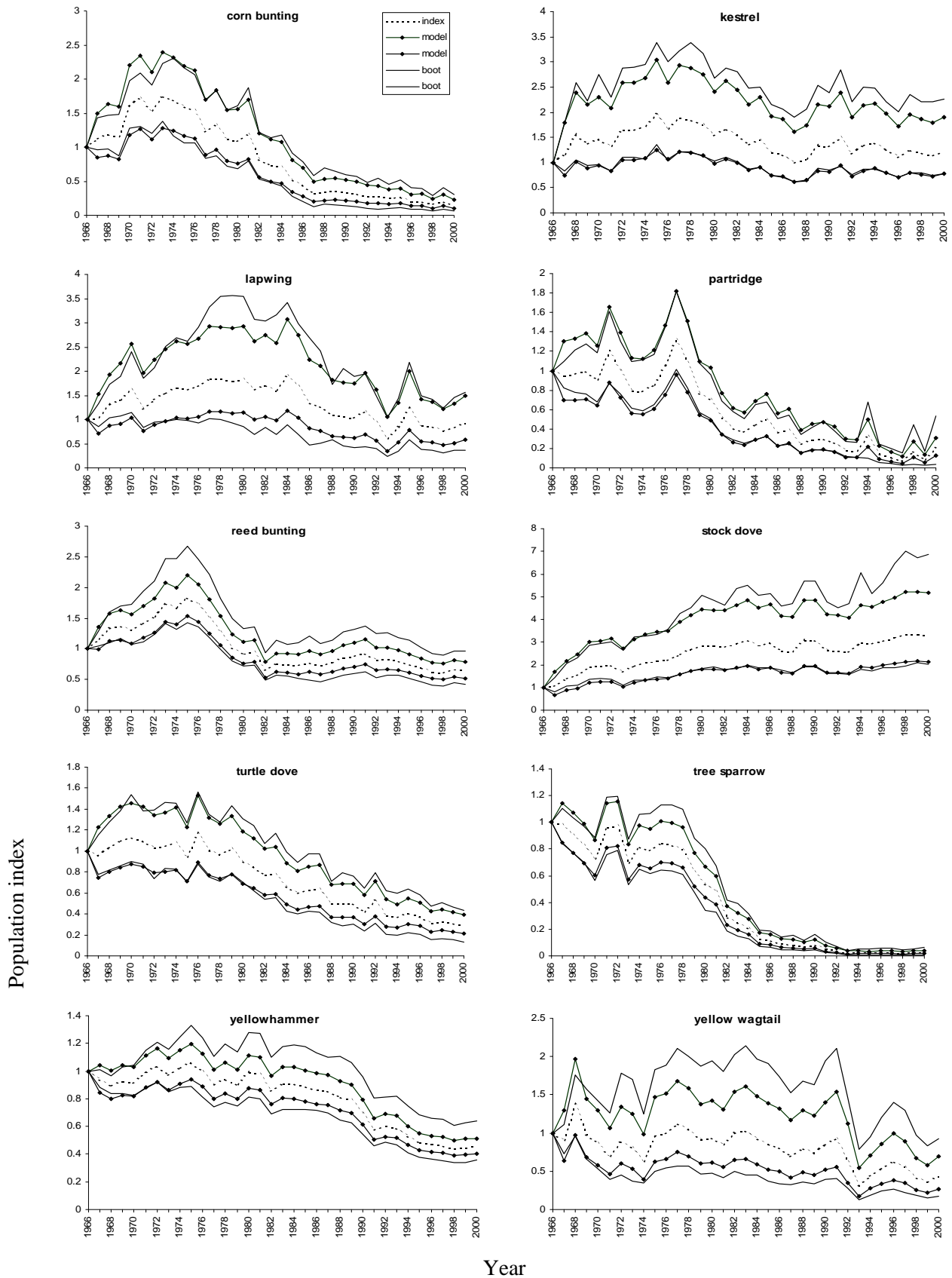
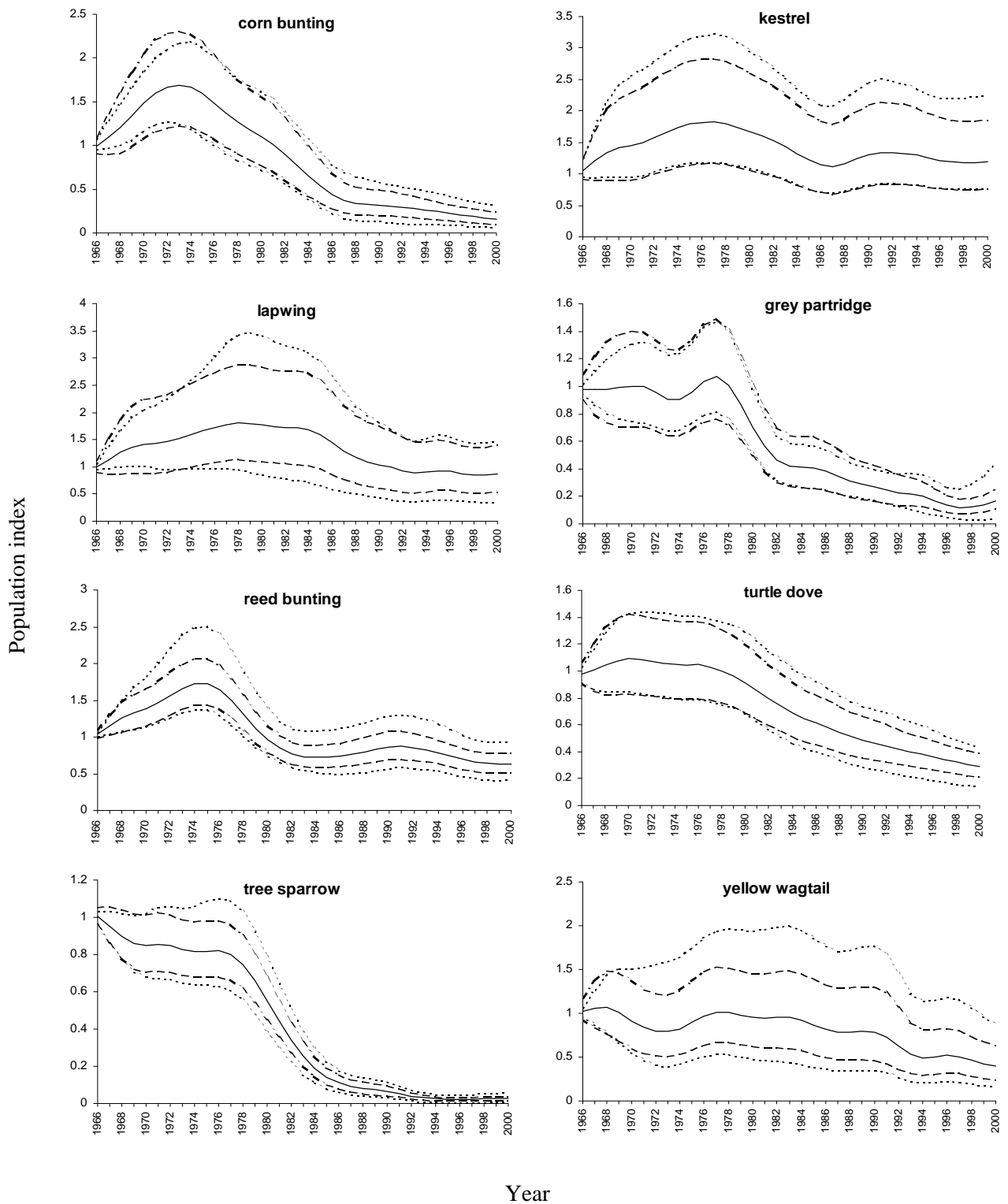


Figure 2.3e Smoothed trend from the GLM analysis and comparison between the smoothed CI's from the bootstrap procedure and the smoothed analytical model estimates (smoothing using 11 degrees of freedom)



Notes : Solid black line is smoothed trend; large dashed line is smoothed upper and lower 95% analytical model CI's and dotted line is smoothed upper and lower 95% CI's from the 199 bootstraps.

Figure 2.3e continued

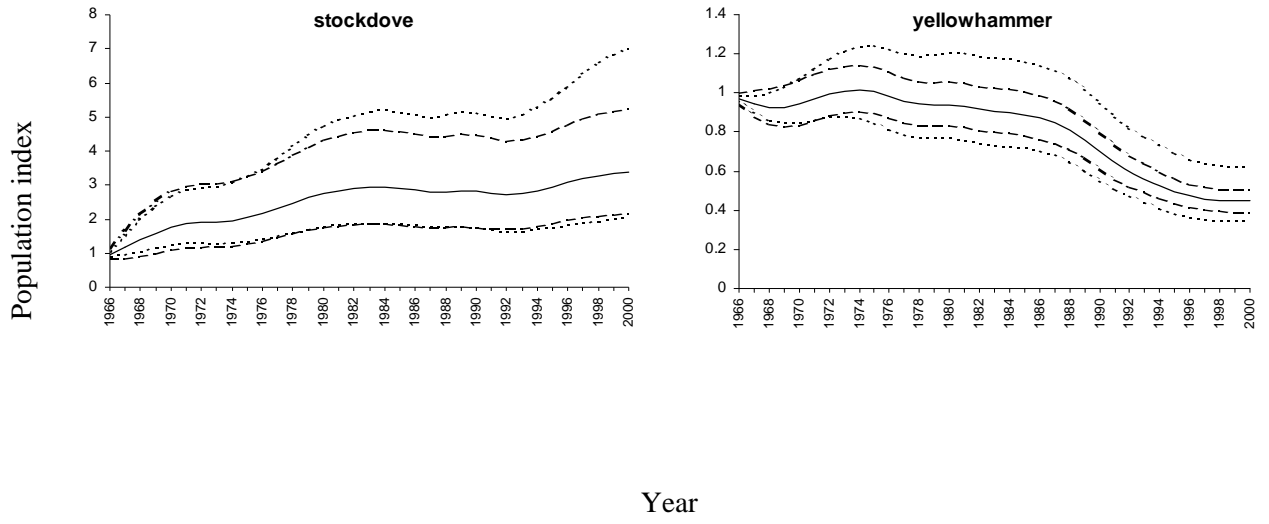


Figure 2.3f Smoothed index and comparison of the 90% smoothed CI for all 199 iterations with the first 99 iterations (a) and with the last 99 iterations (b)

a) Smoothed index and comparison between 90% CI for all 199 iterations and the **first** 99 iterations

b) Smoothed index and comparison between 90% CI for all 199 iterations and the **last** 99 iterations

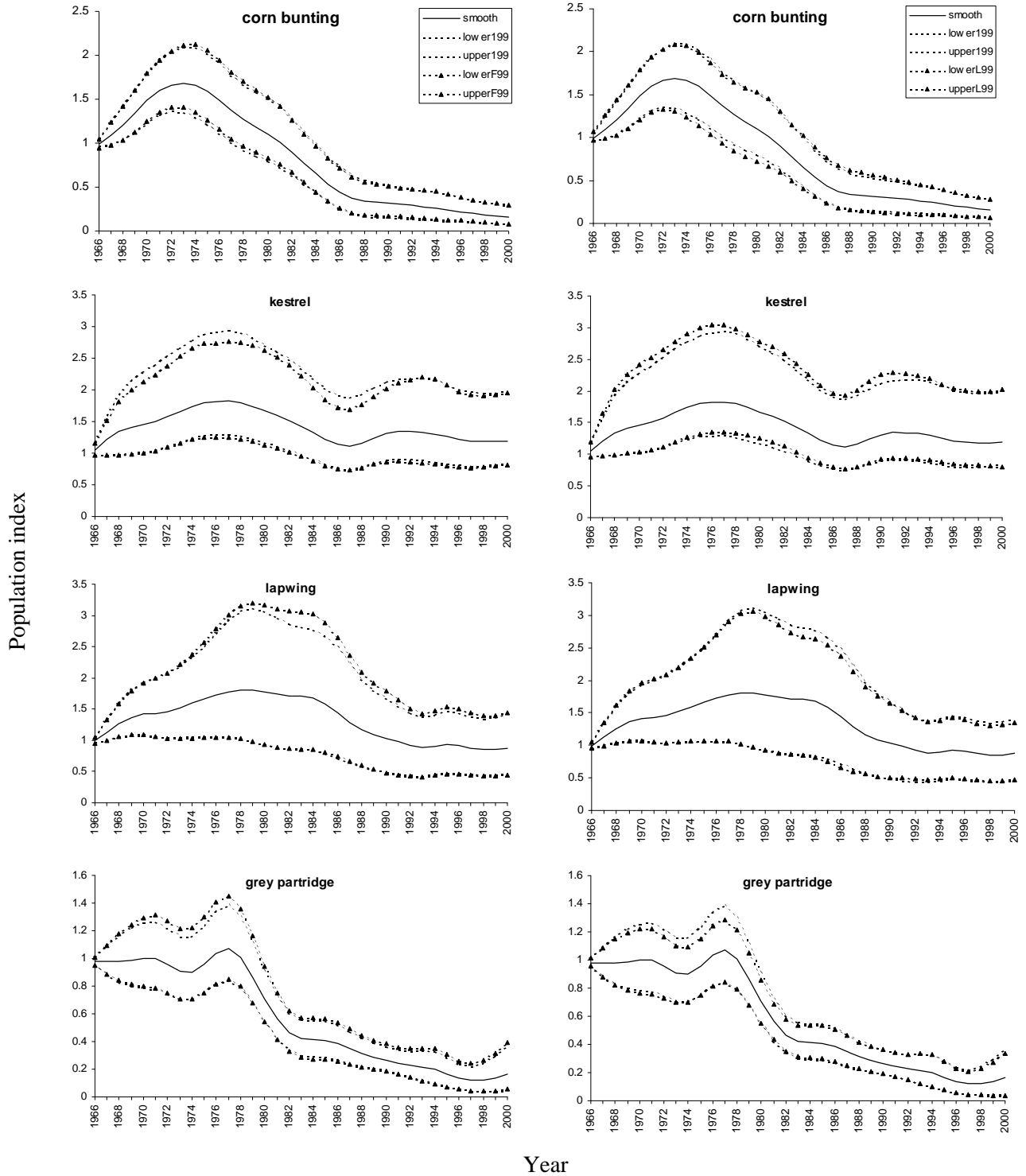


Figure 2.3f continued

a) Smoothed index and comparison between 90% CI for all 199 iterations and the **first** 99 iterations

b) Smoothed index and comparison between 90% CI for all 199 iterations and the **last** 99 iterations

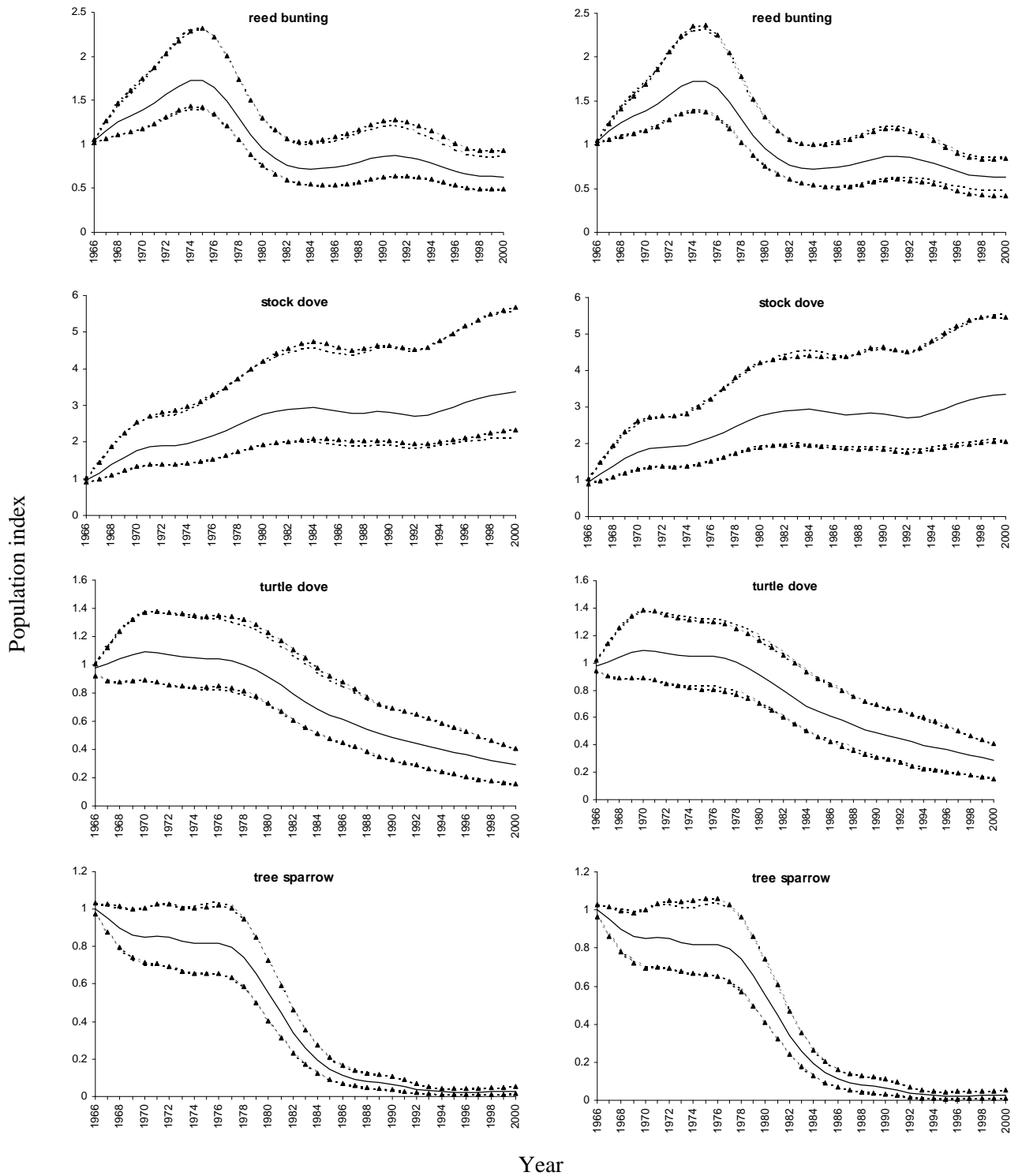
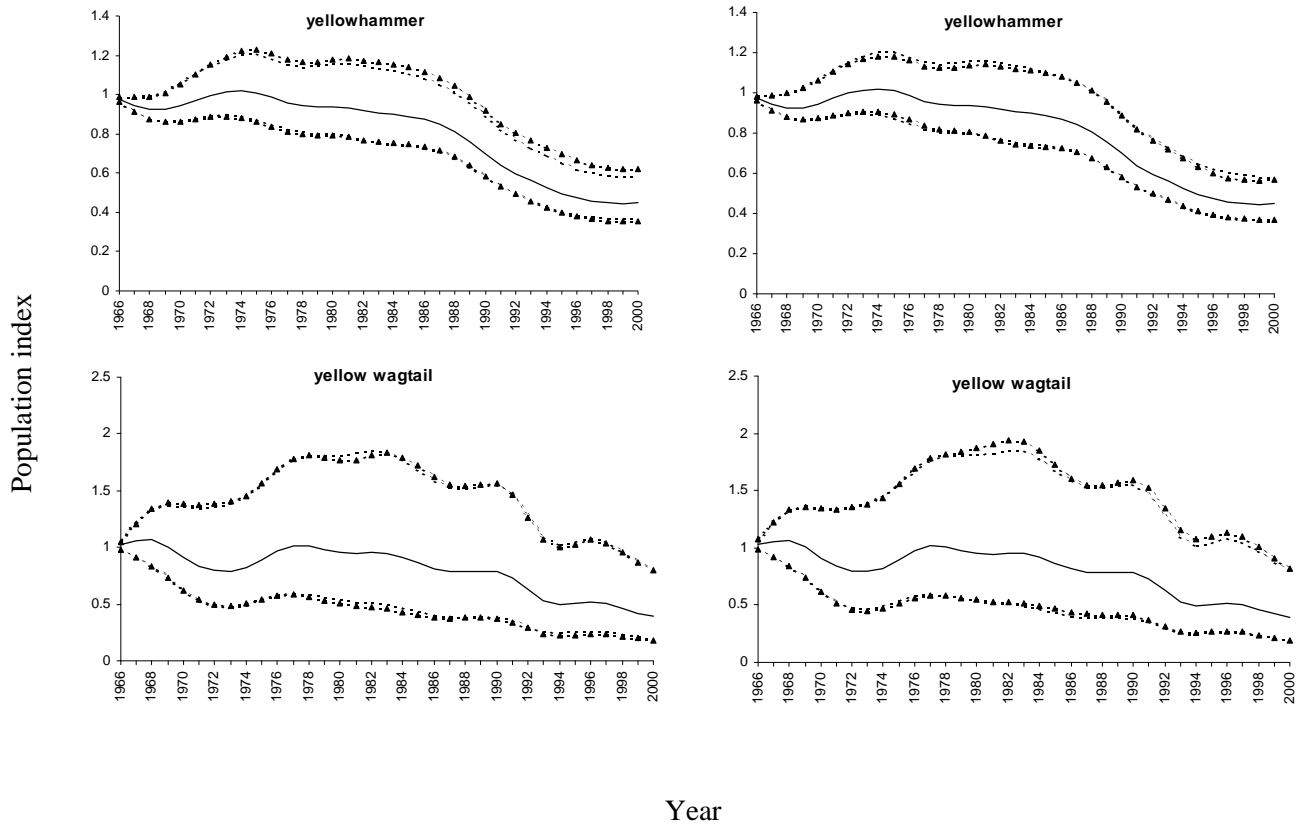


Figure 2.3f continued

a) Smoothed index and comparison between 90% CI for all 199 iterations and the **first** 99 iterations

b) Smoothed index and comparison between 90% CI for all 199 iterations and the **last** 99 iterations



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APPENDIX 1.

Instructions for operating Gamfit to enable comparison of the smoothed year estimates between software packages

The below instructions are not deemed to be complete and further details should be obtained from the available documentation. It is continually being updated and developed by Trevor Hastie and Rob Tibshirani, (see <http://elib.zib.de/netlib/a/gaim> for up to date information). It is designed to allow assessment of the smoothed year estimates from the GAM. Gamfit can be run from calling “gaim” at the appropriate command line and requires two main files, the data file and a file detailing the degree of smoothing, number of data points, formulae etc. The data file must end with the suffix ‘.dat’, so for example a file containing data for robin could be called ‘robin.dat’. The columns of the data file should be separated by ‘white spaces’. The output from Gamfit is a file called "output.fit" as well as graph files for each predictor.

The second file must be called ‘input.mod’ and unless data files are identical in terms of the number of sites, years and variables etc between species, this must be altered for each run of gaim using a different data file. An example of an input.mod file is given below.

```
'DATA: ', 'cornb'  
'P: ', 3  
'N: ', -1  
'FORMAT: ', 'free'  
'MISSING-CODE: ', 99999  
'INTERCEPT: ', 'yes'  
'VARIABLE NAME      MODE      DF '  
'site', 'factor', 344  
'year', 'predictor', 4  
'count', 'response', 0  
'FAMILY: ', 'poiss'  
'LINK: ', 'logar'  
'THRESHOLDS: ', .001, .001  
'MAX ITERS: ', 20, 15  
'NYEARS: ', 6
```

In the above example, we are using a GAM, using a smooth function of year with 4 df, site effects and intercept. There are 345 site effects (gaim requires that specify total number of site effects minus one). The ‘NYEARS’ relates to bootstrapping and is an additional option added to the original gaim program. Further details of all the code in the input.mod file can be sought from the following description of Gamfit obtained from the documentation from the Biostatistics Software Resources Page (slightly modified to clarify issues) (see <http://www.biostat.ucsf.edu/docs/gaim.html>).

All fields must be in quotes. The first line gives the name of the file containing the data. The data should be 1 line per observation, all numeric. The next two lines give the number of variables (P) and number of observations (N). For the latter, you can put -1 if you want the program to figure out the number of observations or a number $k < N$ if you want to use only the first k observations. The FORMAT line indicates the FORTRAN format for reading the data. THE MISSING gives the (numeric) missing code. GAIM does not throw out incomplete observations but deals with them as described in HT.

THE INTERCEPT line indicates whether you want an intercept (yes) or not (no).

THE lines following the VARIABLE line specify the type of each variable and the degrees of freedom associated with it. The possibilities are response, predictor, factor, weight, censoring. Response, weight and censoring variables must have $df=0$. For a predictor, $df=0$ means the variable is

excluded; $df=1$ means a linear fit, and $df>1$ means a nonparametric fit with the desired degrees of freedom df . A factor is a categorical variable; its df must be one less than the number of distinct values.

The FAMILY line indicate the error model: gauss, binom, poiss, gamma or cox. The LINK line is the link function: ident, inver, logit, logar or cox. The THRESHOLDS line specify the convergence thresholds for the outer and inner loops of the local scoring procedure. THE MAX ITERS are the maximum number of iterations for each of these loops.

The '.FIT' file contains at the top, the fit summary; the analysis of deviance table, which includes the slope and standard error of the linear part of the fit, plus "nl-pval" a nonlinear pvalue that tests whether a function estimate is nonlinear (small p-value is evidence for nonlinearity). After that is information for plotting the results. The graph files end in .gra and contain the following variables for each predictor:

x , $s(x)$, $s(x)-1.96*se$, $s(x)+1.96*se$, partial residual.

The file "plot.gaim.s" contains an S function for reading in and plotting a variable. E.g. plot-gaim("age.gra").

The smoothed trends for the years can be extracted from the 'output.fit' file by using the simple command of 'tail' and specifying the number of lines to extract (this should usually be the number of years in the model). This simply extracts the last number of lines from the file and puts these into another file. An example to extract the last seven lines of the file is given below.

```
Tail -7 output.fit > output.ind
```

The above extracts the last seven lines from 'output.fit' and puts into a file called 'output.ind' (this may be called any name).