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Exploration of a surplus production model in a Bayesian framework for Greenland Halibut in Disko Bay NAFO Division 1A Inshore

by

D. Maddock Parsons, Paul Regular and Rasmus Nygaard
Fisheries and Oceans Canada
Northwest Atlantic Fisheries Center
P.O. Box 5667 St. John's,
Canada, A1C 5X1
&
Greenland Institute of Natural Resources, P.O. Box 570, 3900 Nuuk, Greenland

Abstract

A surplus production model in a Bayesian framework was explored to model stock dynamics in Greenland halibut in NAFO Division 1A Inshore (Disko Bay stock). As a starting point, the model set up and priors for r and K that were used in the assessment of Yellowtail flounder in 2021 were applied to 5 input series (3 surveys and 2 cpue series) and a long catch history (1904-2021). The initial model run (Run1) showed higher autocorrelations and some problems with the Geweke convergence criteria. To address these issues, a second run with more iterations and thinning was conducted (Run2), and the diagnostics were improved. Further model runs are planned to explore input series and choice of priors for r and K.

Key words: Disko Bay, Greenland halibut, surplus production model, assessment

Surplus production model in a Bayesian Framework

For this exploration of an assessment model for Greenland halibut in Disko Bay NAFO Division Inshore 1A, the Schaefer (1954) form of a surplus production model was used:

$$P_t=[P_{t-1}+ r\cdot P_{t-1} (1 - P_{t-1})- C_{t-1}/K]\cdot \eta_t$$

Where:

P_{t-1} is exploitable biomass (as a proportion of carrying capacity) for year t-1

C_{t-1} is catch for year t-1

(Meyer and Millar, 1999a, 1999b).

K is carrying capacity (level of stock biomass at equilibrium prior to commencement of a fishery)

r is the intrinsic rate of population growth

η_t is a random variable describing stochasticity in the population dynamics (process error).

The model utilizes biomass proportional to an estimate of K in order to aid mixing of the Markov Chain Monte Carlo (MCMC) samples and to help minimize autocorrelation between each state and K (Meyer and Millar, 1999a, 1999b).

An observation equation is used to relate the unobserved biomass, Pt, to the research vessel survey indices:

$It = q \cdot Pt \cdot \varepsilon t$

Where:

q is the catchability parameter

Pt is an estimate of the biomass proportional to K at time t

εt is observation error

Input data are given in Table 1 (and appendix 1) and shown in Figure 1 scaled to each series mean. The model formulation is given in Appendix 2. The priors on r and initial population size were uninformative, with a uniform distribution ranging from 0.01 to 1 and 0.5 to 1, respectively. The prior for K was also intended to be uninformative, with a mean of 150 and very large CV (1000%) .

Priors used in the model were:

Initial population size	Pin~dunif(0.5, 1)	uniform(0.5 to 1)
Intrinsic rate of natural increase	r ~ dunif(0.01,1)	uniform (0.01 to 1)
Carrying capacity	K~dlnorm(2.703,0.2167)	lognormal (mean, precision)
Survey catchability	q ~dgamma(1,1)	gamma(shape, rate)
Process error	sigma ~ dunif(0,5) isigma2= $sigma^{-2}$	uniform(0 to 5)
Observation error	tau~dgamma(1,1)	gamma(shape, rate)

The initial model run (Run1) was configured to run 3 chains with 500,000 iterations, burn in was set to 50,000 and thin set to 10. Based on patterns in the sampler lag autocorrelation results in the initial run (Run1), an updated run (Run2) was conducted using 3 chains with a million iterations, burn in was set to 100 000 and thin set to 200.

Results

For the initial model run (Run1), the model fit and convergence diagnostics seemed good for all series, although a trend in residuals in seen in some of the indices (see Figures 8, Table 2 and Appendix 3). Posteriors for r and K were updated from their priors (Fig. 5). There were, however, some patterns in autocorrelation and issues with Geweke convergence seen for some of the estimates (see Appendix 3). In order to address these issues, a second run of the model was conducted, increasing the number of iterations to 1 000 000, with 100 000 burn in and thin set to 200 (Run2). This improved the diagnostics of the model, removing the problem with autocorrelation and also improving the Geweke convergence fits. The diagnostics for this updated model run are given in Appendix 4.

The production model (Run2) estimated that an *MSY* of 9 841 tons can be taken from a biomass of 36 710 tons at a fishing mortality of 0.28. Intrinsic rate of natural increase is estimated to be 0.57 and carrying capacity 67 410 tons (Table 4). The trends in relative biomass and fishing mortality estimates from the updated model run are given in Figure 5. At the beginning of 2022, the relative biomass B_t / B_{msy} is estimated to be 1.23 (80% CL = 0.90, 1.54). in 2021, the *F*-ratio is estimated to be 0.7 (80% CL = 0.42, 1.14).

The model diagnostics from this Bayesian formulation are given in Table 3 and results are given in Table 4. The estimates of r resulting from this model formulation seems higher than expected, and the posterior curve for r appears to hit the prior curve line (Fig. 6) which is not ideal.

Further work

A number of additional runs are planned to further investigate the use of this model formulation to provide advice for this stock. These will include refining the data series (removing the last year of Tskaervoy for example due to a change in gear in 2004), dropping cpue indices, refining the prior for r to be more informative (r~(-1.763,2.252) which is wider than used for 3LNO witch flounder; r~(-1.763,3.252);same as used for 3LNO witch flounder), and joining the Tskaervoy and Tcosmos surveys 1:1.

Summary

The exploration of the surplus production model in a Bayesian framework for use in this stock is very promising. Further work to refine model set up and parameters is ongoing.

Acknowledgments

The Bayesian surplus production models are based on programs originally developed by Jason Bailey.

Table 1. Input Indices used in the Bayesian surplus production model for Greenland halibut in NAFO Division 1A Inshore. Landings are given from 1990-2021 (series goes back to 1904, see Appendix 1 for complete catch series).

Year	Landings	Tskaervoy	Tcosmos	Gillnet	LogbookCPUE	FactoryCPUE
1990	3.82					
1991	5.37					
1992	6.58	4.99				
1993	5.37	2.51				
1994	5.20	3.60				
1995	7.40	5.79				
1996	7.84	8.59				
1997	8.60	6.46				
1998	10.67	11.87				
1999	10.59	8.06				
2000	7.57	9.54				
2001	7.07	10.16		18.08		
2002	11.72	9.07		9.44		
2003	11.57	16.56		12.94		
2004	12.86	28.23		14.86		
2005	12.45		22.58	16.32		
2006	12.11		20.25	8.89		
2007	10.38		13.14	7.12		
2008	7.70		16.42	14.80		
2009	6.32		19.90			
2010	8.46		17.56	14.01	43.65	
2011	8.49		23.98	25.10	39.14	
2012	7.76		16.17		41.77	
2013	9.07		15.10	12.53	39.13	47.39
2014	9.18		11.46	12.42	38.59	40.46
2015	8.67		13.18	10.11	31.81	35.79
2016	10.76		11.77	9.69	36.14	33.57
2017	6.41		12.04	9.14	23.08	23.99
2018	8.40		17.35	10.91	29.80	32.24
2019	8.76		11.60	16.44	27.83	28.73
2020	7.60		15.13	18.86	26.80	29.74
2021	9.03			27.40	30.22	36.21

Table 2. Convergence criteria and diagnostics for 2022 NAFO Division 1A Inshore Greenland Halibut in Bayesian surplus production model (initial; Run1). Grey cells denote chains in which the Geweke algorithm did not converge).

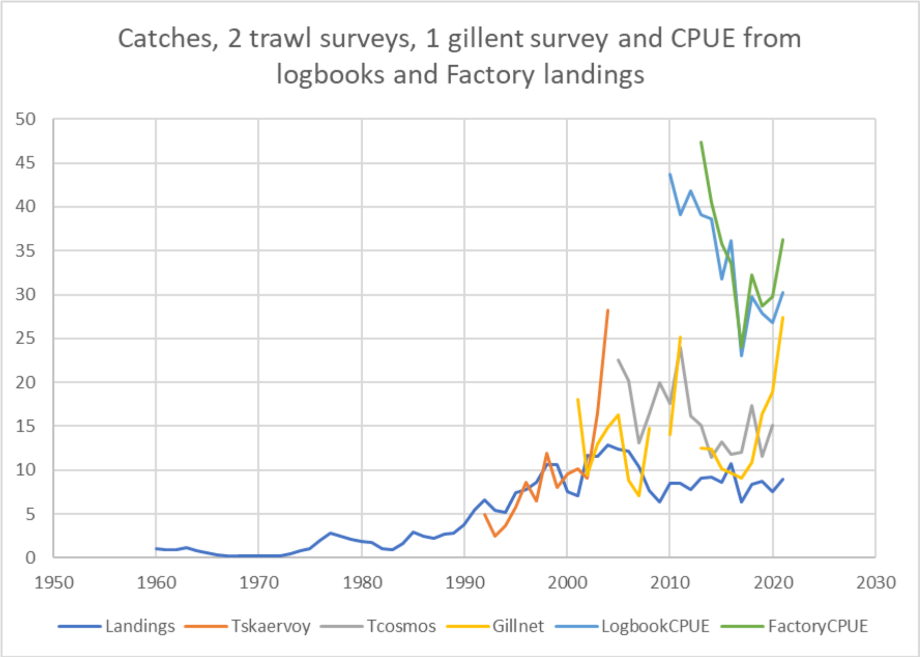
		Stats (miniter=1 maxiter=4500 sample=4500) Bin size for caculating Batch SE and (Lag 1) ACF=50 MC Error should be small compared to SD									Geweke convergence diag. fraction in 1st window 0.1 fraction in last window 0.5 (between -2 and 2 is good)		Brooks, Gelman, and Rubin Convergence diagnostics (near 1 is good)		
	Chain	Mean	SD	Naïve SE	MC Error	Batch SE	Batch ACF	0.025	0.5	0.975	z-score	p-score	Potential Scale Reduction Factors	Multivariate SRF	Corrected SRF
r	1	0.69	0.20	0.00	0.01	0.00	0.39	0.27	0.71	0.98	0.09652719	0.92310188	1.0012	1.00181	Estimate 0.975
	2	0.69	0.19	0.00	0.01	0.00	0.37	0.29	0.71	0.98	-0.8421962	0.3996781			x 1.001793 1.005084
	3	0.67	0.20	0.00	0.01	0.00	0.41	0.25	0.69	0.98	0.3996781	0.95712637			
K	1	70.16	27.97	0.13	1.25	0.80	0.51	40.64	62.95	147.40	-1.1554351	0.2479123	1.002464	1.003704	Estimate 0.975
	2	68.53	26.07	0.12	1.13	0.74	0.54	40.87	61.82	136.00	1.1255794	0.2603436			x 1.005503 1.012286
	3	72.22	29.45	0.14	1.77	0.85	0.54	41.15	64.45	152.90	0.3264909	0.744053			
sigma	1	0.149	0.050	0.000	0.001	0.001	0.071	0.076	0.141	0.272	-2.2759356	0.02284986	1.000054	1.000092	Estimate 0.975
	2	0.150	0.050	0.000	0.001	0.001	0.058	0.075	0.141	0.273	0.2585595	0.7959751			x 1.000112 1.000317
	3	0.149	0.051	0.000	0.001	0.001	0.117	0.074	0.141	0.272	-0.3425456	0.7319404			
logq.tskaervoy	1	0.186	0.075	0.000	0.003	0.002	0.473	0.069	0.176	0.362	0.5844446	0.5589212	1.000989	1.001494	Estimate 0.975
	2	0.189	0.075	0.000	0.002	0.002	0.463	0.071	0.180	0.364	-1.182073	0.2371767			x 1.001082 1.003797
	3	0.182	0.074	0.000	0.003	0.002	0.466	0.068	0.172	0.354	-0.1133245	0.9097733			
logq.tcosmos	1	0.403	0.159	0.001	0.007	0.004	0.508	0.144	0.384	0.762	0.9286731	0.3530585	1.001893	1.002849	Estimate 0.975
	2	0.412	0.156	0.001	0.006	0.004	0.492	0.156	0.397	0.761	-1.1374043	0.2553693			x 1.002163 1.007303
	3	0.395	0.157	0.001	0.008	0.004	0.496	0.144	0.377	0.741	-0.08051443	0.93582812			
logq.gillnet	1	0.337	0.132	0.001	0.006	0.004	0.510	0.120	0.323	0.631	0.9721957	0.3309532	1.001654	1.00249	Estimate 0.975
	2	0.344	0.129	0.001	0.005	0.003	0.496	0.131	0.332	0.628	-1.1679302	0.2428349			x 1.001958 1.006459
	3	0.330	0.130	0.001	0.007	0.003	0.495	0.121	0.316	0.620	-0.1095689	0.9127513			
logq.logbook	1	0.879	0.346	0.002	0.016	0.010	0.507	0.317	0.836	1.662	0.9742318	0.3299415	1.001966	1.002959	Estimate 0.975
	2	0.898	0.338	0.002	0.013	0.009	0.491	0.346	0.868	1.661	-1.1486535	0.2506989			x 1.002249 1.007584
	3	0.864	0.341	0.002	0.018	0.009	0.492	0.317	0.824	1.620	-0.05359758	0.95725579			
logq.factory	1	0.950	0.376	0.002	0.017	0.010	0.505	0.342	0.904	1.807	0.9540835	0.3400414	1.001997	1.003005	Estimate 0.975
	2	0.971	0.367	0.002	0.014	0.010	0.490	0.371	0.938	1.802	-1.1142976	0.2651516			x 1.002248 1.007666
	3	0.933	0.369	0.002	0.019	0.010	0.492	0.342	0.889	1.749	-0.07126474	0.94318705			

Table 3. Convergence criteria and diagnostics from a Bayesian surplus production model for Greenland Halibut in Disko Bay NAFO Division 1A Inshore (updated; Run2).

Updated 2022		Stats (miniter=1 maxiter=4500 sample=4500) Bin size for caculating Batch SE and (Lag 1) ACF=50 MC Error should be small compared to SD									Geweke convergence diag. fraction in 1st window 0.1 fraction in last window 0.5 (between -2 and 2 is good)		Brooks, Gelman, and Rubin Convergence diagnostics (near 1 is good)		
	Chain	Mean	SD	Naïve SE	MC Error	Batch SE	Batch ACF	0.025	0.5	0.975	z-score	p-score	Potential Scale Reduction Factors	Multivariate SRF	Corrected SRF
r	1	0.57	0.21	0.00	0.00	0.00	-0.02	0.19	0.57	0.96	-0.6844776	0.4936736	0.9998158	0.9998348	Estimate 0.975
	2	0.57	0.21	0.00	0.01	0.01	0.12	0.19	0.57	0.96	2.09963508	0.03576095			x 1.000036 1.000138
	3	0.57	0.21	0.00	0.01	0.01	0.10	0.18	0.56	0.96	-1.6392662	0.1011578			
K	1	81.82	35.56	0.53	1.27	1.22	0.02	42.25	73.47	170.23	0.654207	0.5129785	0.9998235	0.9998464	Estimate 0.975
	2	82.92	41.18	0.61	1.77	1.55	0.07	42.30	72.42	185.99	-1.5958595	0.1105202			x 1.002516 1.002641
	3	84.08	37.57	0.56	1.28	1.22	-0.08	42.44	74.57	181.95	1.3151795	0.1884496			
sigma	1	0.148	0.050	0.001	0.001	0.001	-0.189	0.069	0.141	0.262	0.2102924	0.8334394	0.9998622	0.9999045	Estimate 0.975
	2	0.148	0.049	0.001	0.001	0.001	0.153	0.070	0.142	0.266	0.7103516	0.4774862			x 1.000118 1.000345
	3	0.149	0.049	0.001	0.001	0.001	0.121	0.073	0.143	0.267	-0.5697975	0.5688151			
logq.tskaervoy	1	0.165	0.072	0.001	0.002	0.002	-0.050	0.060	0.153	0.334	-0.8667241	0.3860932	1.000137	1.000316	Estimate 0.975
	2	0.166	0.074	0.001	0.002	0.002	0.193	0.054	0.156	0.338	2.1446721	0.03197907			x 1.000343 1.001308
	3	0.163	0.074	0.001	0.002	0.002	0.054	0.055	0.152	0.339	-1.5371923	0.1242462			
logq.tcosmos	1	0.376	0.161	0.002	0.005	0.005	-0.006	0.134	0.355	0.749	-1.2439813	0.2135064	1.000461	1.000802	Estimate 0.975
	2	0.379	0.166	0.002	0.006	0.005	0.122	0.113	0.360	0.744	1.142775	0.253132			x 1.000474 1.002309
	3	0.368	0.164	0.002	0.006	0.005	0.011	0.118	0.344	0.750	-1.016158	0.3095541			
logq.gillnet	1	0.313	0.134	0.002	0.004	0.004	-0.003	0.109	0.296	0.615	-1.2379211	0.2157453	1.000418	1.000738	Estimate 0.975
	2	0.316	0.137	0.002	0.005	0.004	0.113	0.098	0.301	0.617	1.188341	0.2346991			x 1.000437 1.002157
	3	0.308	0.136	0.002	0.005	0.004	-0.017	0.099	0.289	0.621	-1.1587958	0.2465394			
logq.logbook	1	0.858	0.369	0.005	0.012	0.012	0.001	0.304	0.811	1.717	-1.3473467	0.1778686	1.000585	1.000989	Estimate 0.975
	2	0.865	0.377	0.006	0.014	0.012	0.123	0.261	0.822	1.697	1.1634391	0.2446514			x 1.000647 1.002816
	3	0.840	0.374	0.006	0.014	0.013	0.004	0.274	0.784	1.709	-1.1586655	0.2465926			
logq.factory	1	0.943	0.406	0.006	0.013	0.013	0.006	0.333	0.889	1.891	-1.3657272	0.1720246	1.000506	1.00087	Estimate 0.975
	2	0.952	0.418	0.006	0.015	0.014	0.112	0.282	0.903	1.889	1.1821363	0.2371516			x 1.000551 1.002507
	3	0.925	0.412	0.006	0.016	0.014	-0.004	0.297	0.864	1.885	-1.1495513	0.2503287			

Table 4. Assessment results for two surplus production model runs in a Bayesian framework of Disko Bay Greenland halibut in NAFO Division 1A Inshore.

	Initial Run (Run1) 500K iterations	Updated Run (Run2) 1M iterations
sigma	0.1409	0.142
K	63.04	73.41
r	0.704	0.5664
MSY	10.47	9.841
BMSY	31.52	36.71
Fmsy	0.352	0.2832
B/Bmsy	1.232	1.086
F/Fmsy	0.704	0.85885
deviance	380.6	403.5
Pin	0.7492	0.7549
q.Factory	0.911	0.8853
q.Gillnet	0.3238	0.2957
q.Logbook	0.843	0.805
q.Tcosmos	0.3864	0.3531
q.Tskaervoy	0.176	0.1538
tau.Factory	0.007398	0.007887
tau.Gillnet	0.1598	0.2004
tau.Logbook	0.008669	0.01038
tau.Tcosmos	0.05129	0.04839
tau.Tskaervoy	0.4408	0.4245



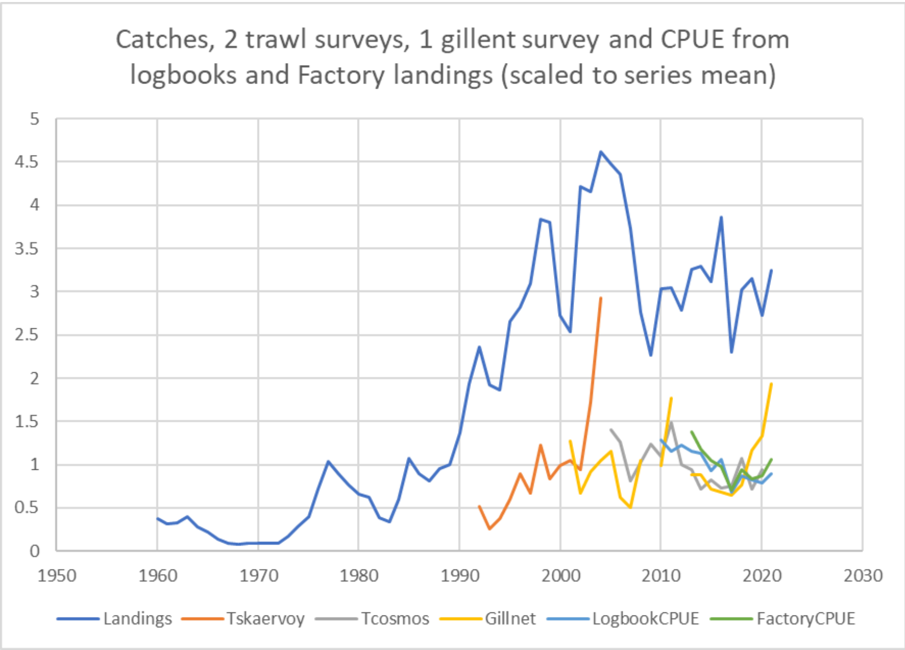


Figure 1. Catch and indices 1960-2021 (with indices scaled to the series mean in the right hand plot) input into the surplus production model in a Bayesian framework for the 2022 assessment of Greenland halibut in NAFO DIvision Inshore 1A. Catch series goes back to 1904 (see appendix A).

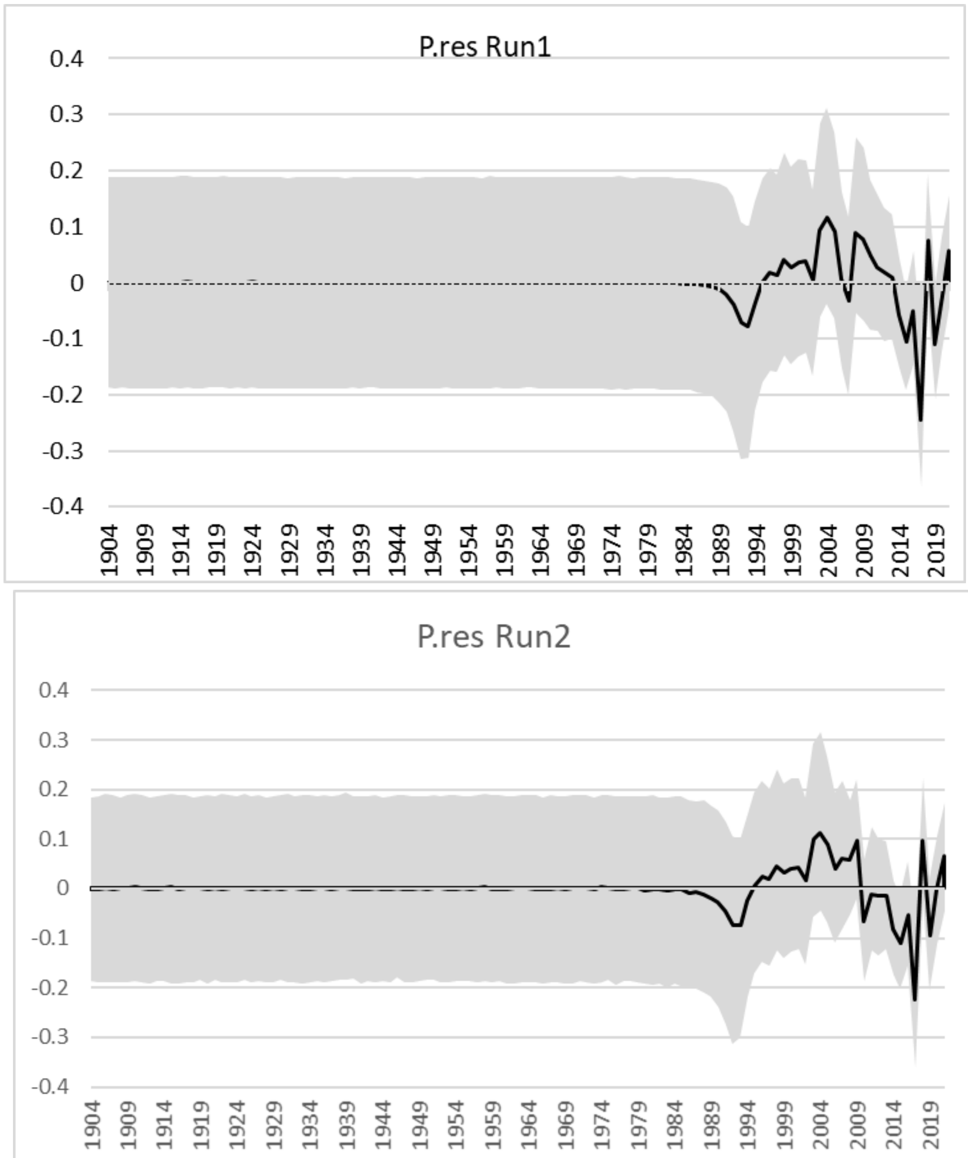


Figure 2. Process error (with 10th and 90th credible intervals) from the surplus production model fit to Disko Bay Greenland halibut in NAFO Division Inshore 1A (Top plot Run1, bottom plot Run2).

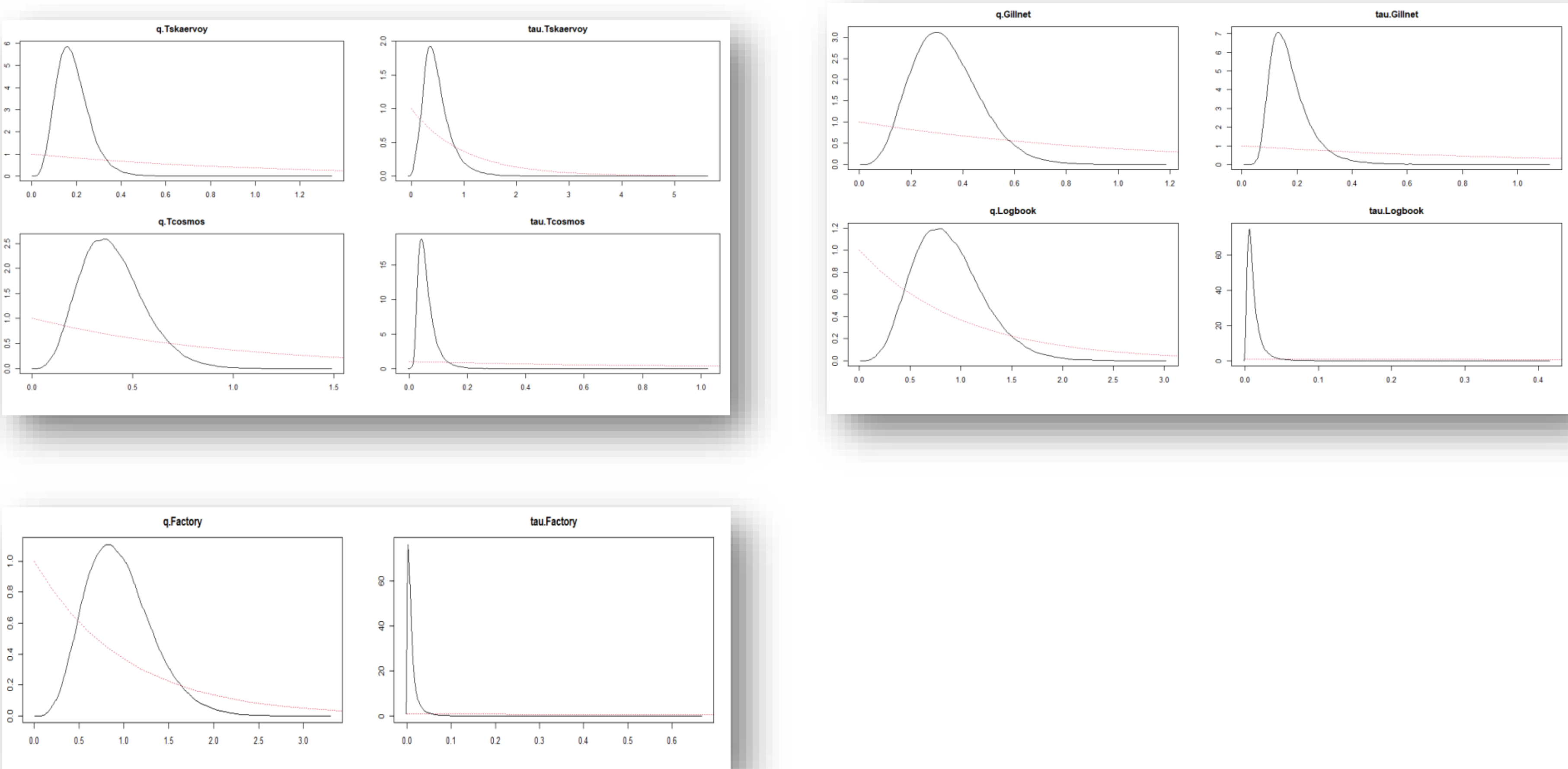


Figure 3. Observed and predicted survey indices from each of the five series used in the initial model run (Run1). For each series the left panel gives the observed and predicted values with 10th and 90th credible intervals while the right panel presents standardized residuals.

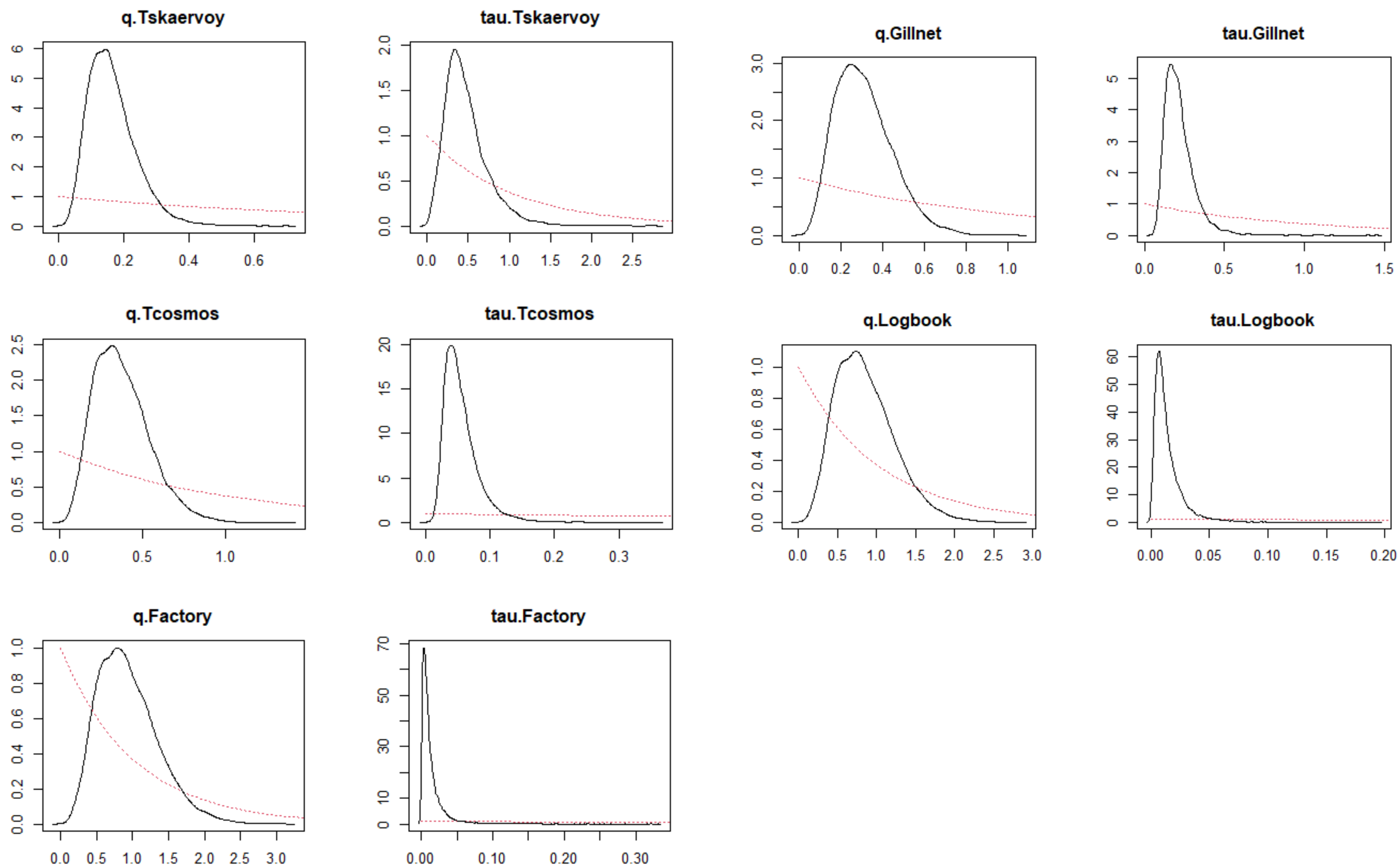


Figure 4. Observed and predicted survey indices from each of the five series used in the updated model run (Run2). For each series the left panel gives the observed and predicted values with 10th and 90th credible intervals while the right panel presents standardized residuals.

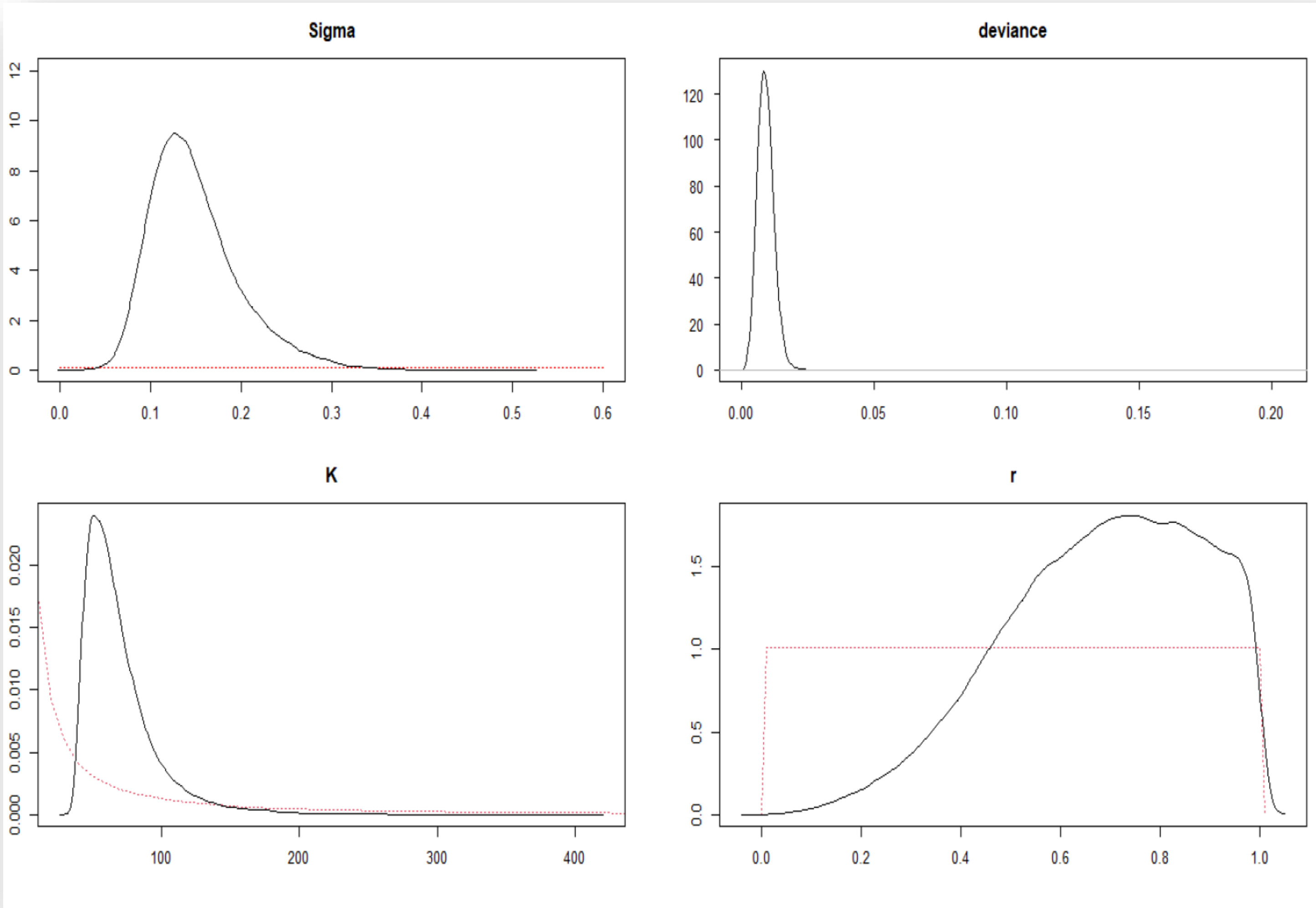


Figure 5. Run1 priors (red dotted line) and posteriors (black line) for sigma (process error), deviance, K and r.

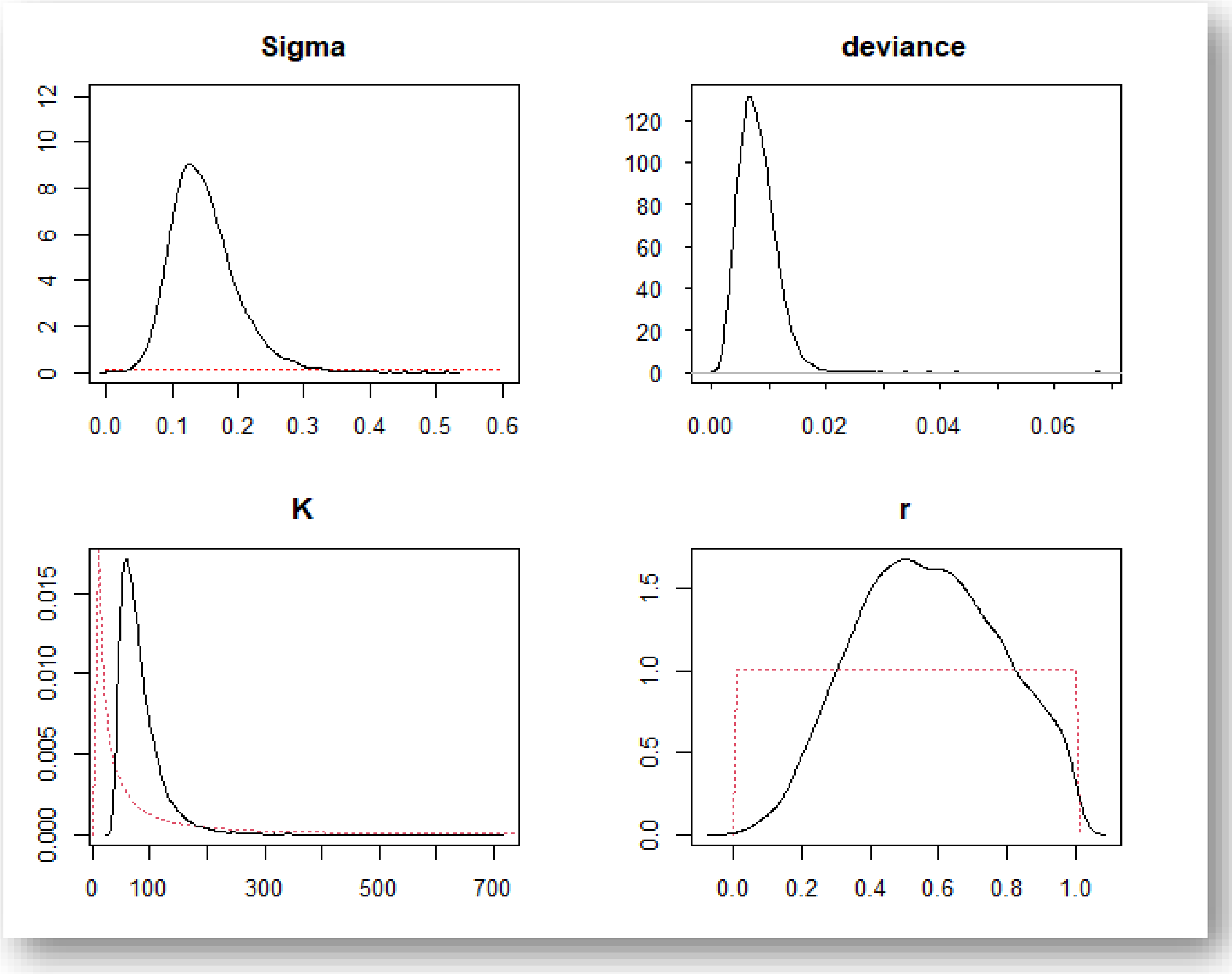
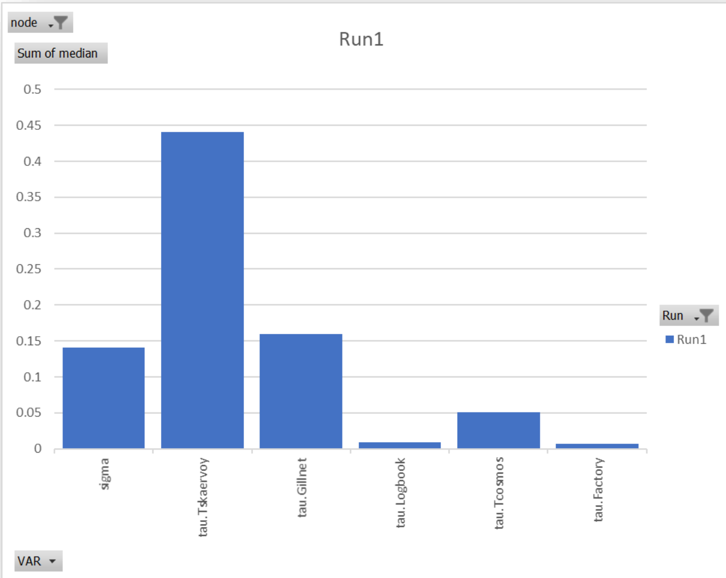


Figure 6. Run2 Priors (red dotted line) and posteriors (black line) for sigma (process error), deviance, K and r.



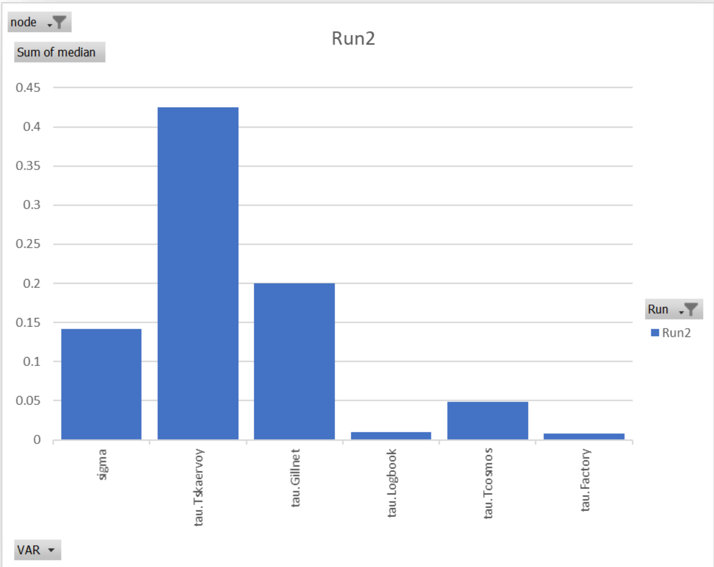


Figure 7. Error estimates for process (sigma) and for the series used in the surplus production models in a Bayesian framework for Greenland halibut in Disko Bay NAFO Division 1A Inshore (Left Run1, Right Run2)

Figure 8. Residuals for the time series, and for each of the input series used in the surplus production models in a Bayesian framework for Greenland halibut in Disko Bay NAFO Division 1A Inshore (Run1)

Figure 9. Residuals for the time series, and for each of the input series used in the surplus production models in a Bayesian framework for Greenland halibut in Disko Bay NAFO Division 1A Inshore (Run2)

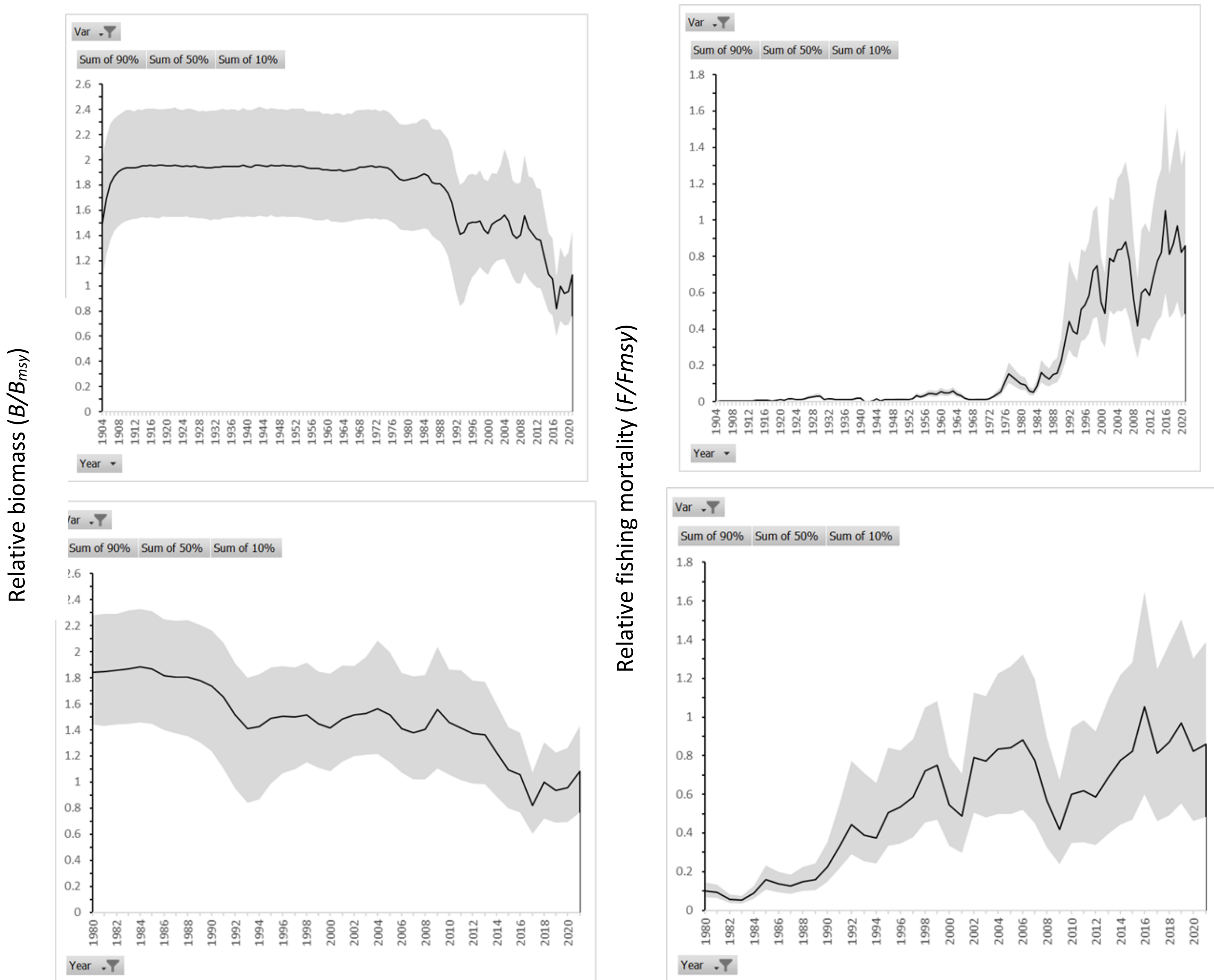


Figure 10. Greenland halibut in Disko Bay NAFO Division Inshore 1A (Run2): Median relative biomass (*Biomass/B_{MSY}*) and mean relative fishing mortality (*F/F_{MSY}*) with 10th and 90th percentiles (top panels 1904-2021, bottom panels 1980-2021). The horizontal lines are B_{msy} and $B_{lim}=30\%B_{msy}$ and $F_{lim}=F_{MSY}$.

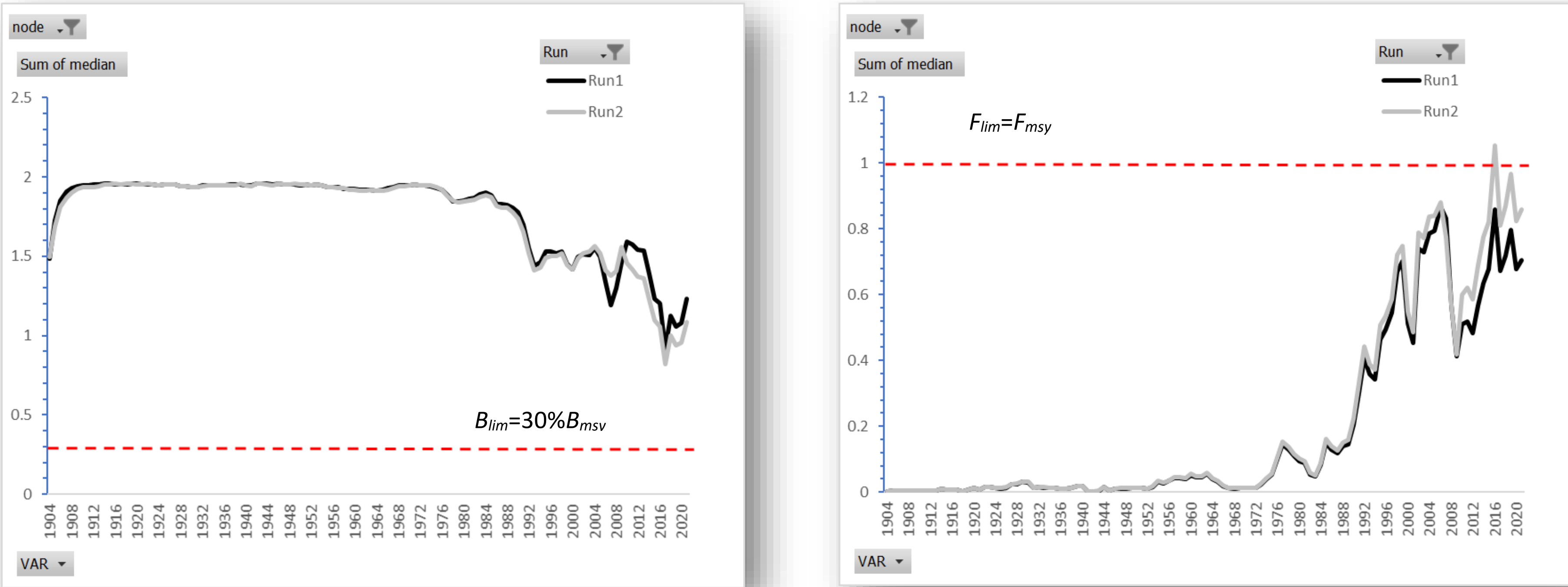


Figure 11. Relative B (B/B_{msy}) for two exploratory runs of a surplus production model in a Bayesian framework for Greenland halibut in Disko Bay NAFO Division 1A Inshore. Two possible reference points are shown, B_{lim} =30% B_{msy} and F_{lim} = F_{msy}.

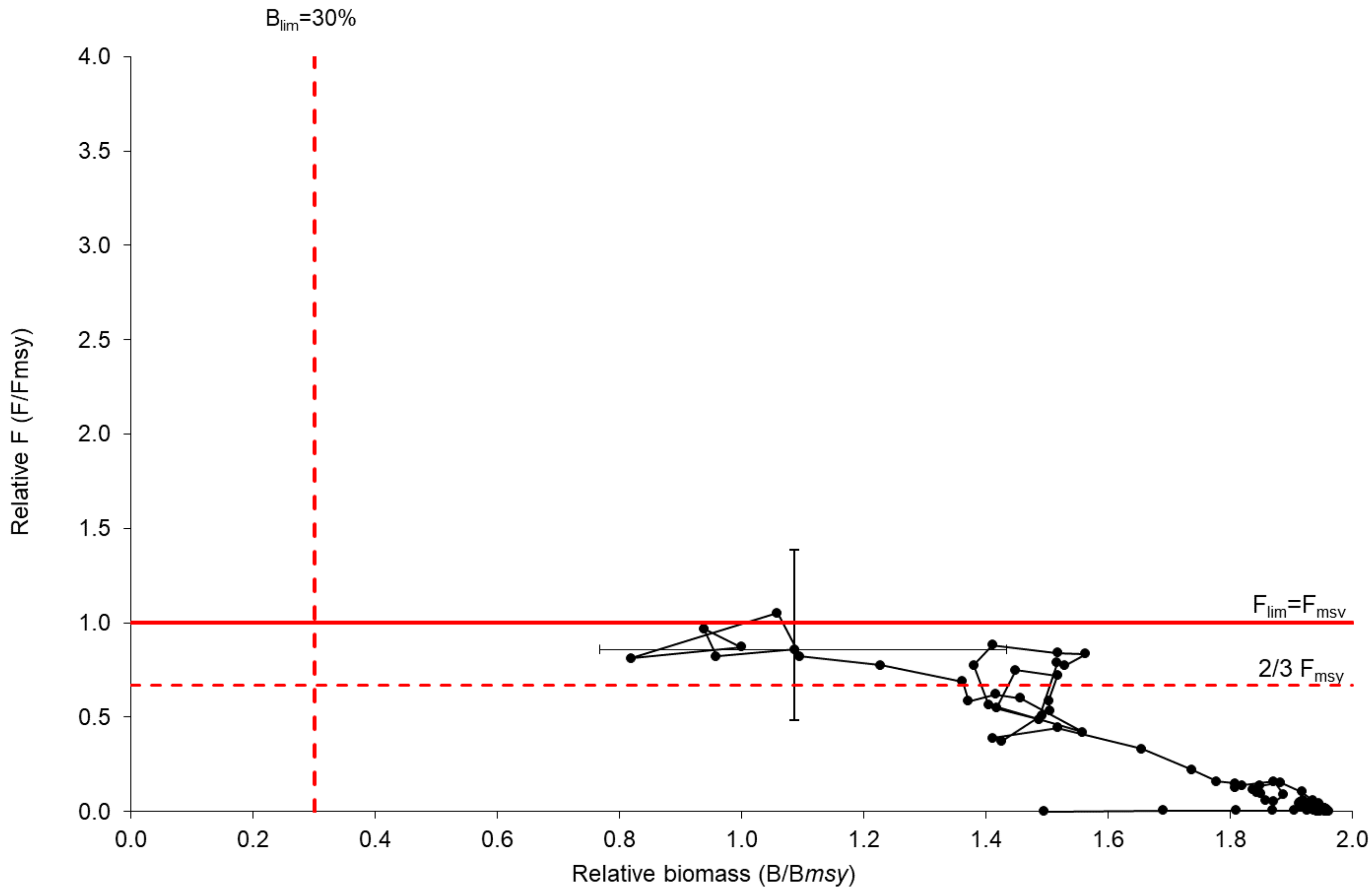


Figure 12. Greenland halibut in Disko Bay NAFO Division Inshore 1A: an example stock trajectory estimated in the surplus production analysis, under a precautionary approach framework (Run2).

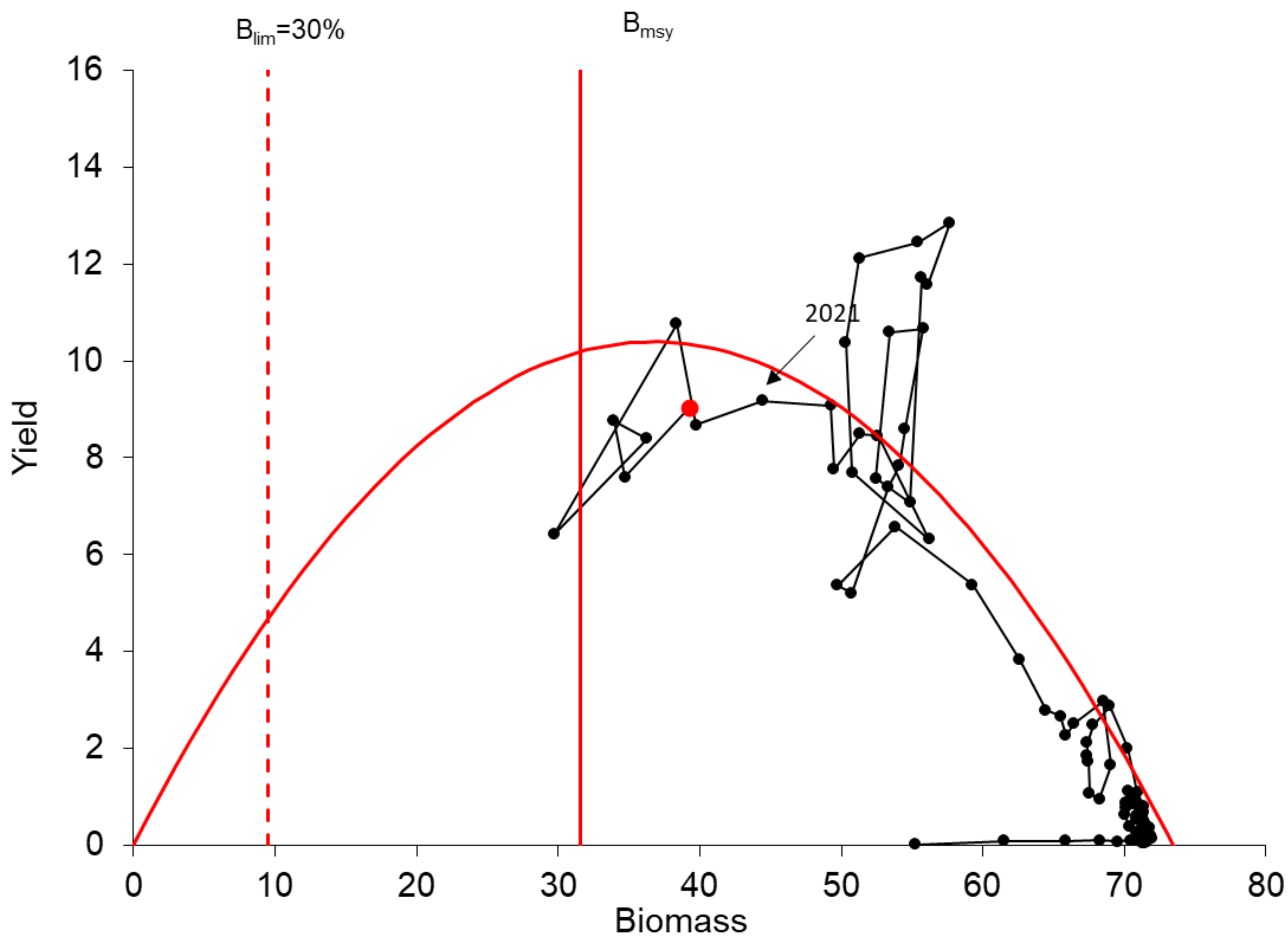


Figure 13. Greenland halibut in Disko Bay NAFO Division Inshore 1A: example of a Catch/Biomass plot.

Appendix 1.

Table A1. Complete catch series for Greenland halibut in NAFO DIvision Inshore 1A 1904-2021.

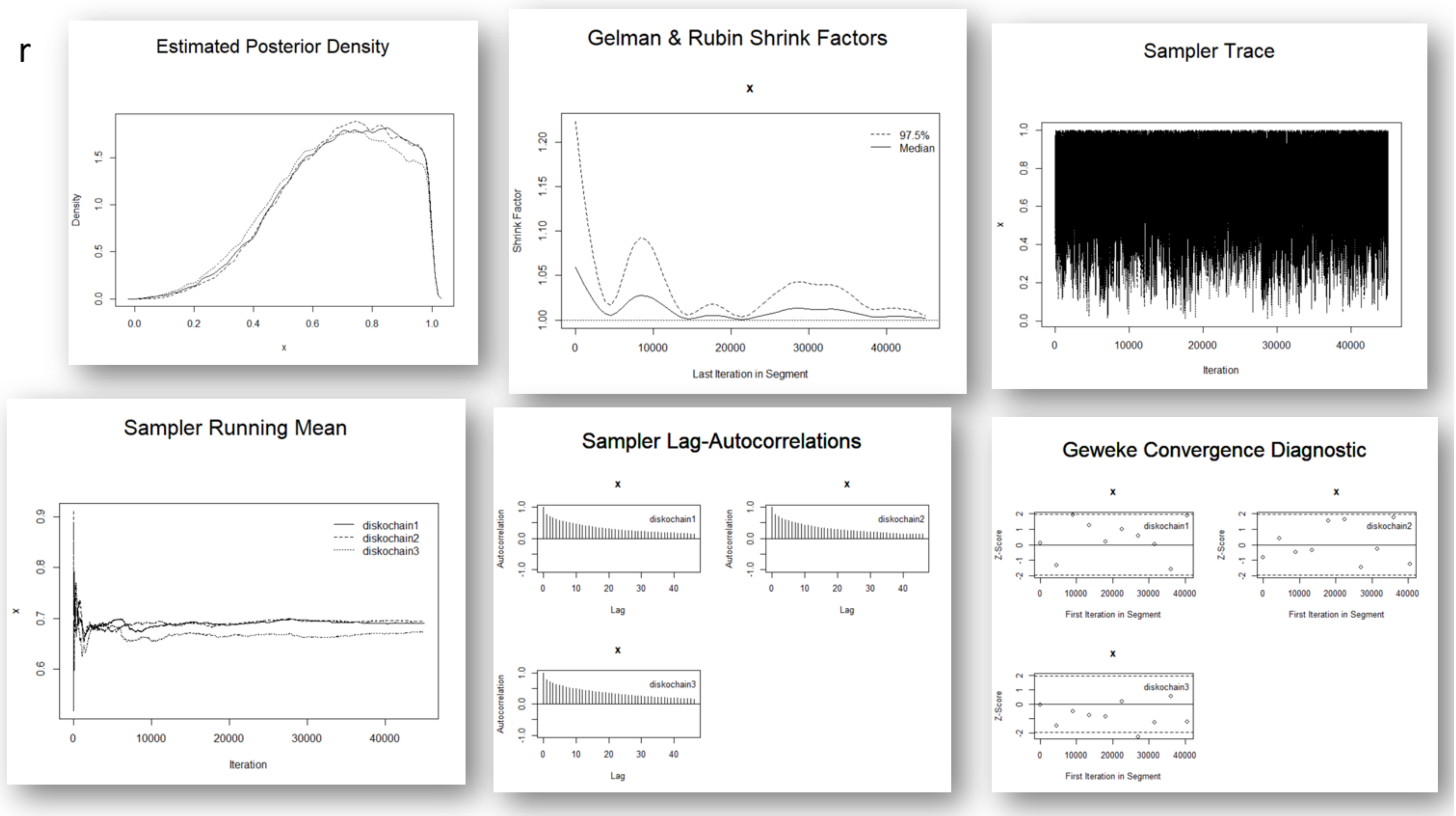
Year	Catch ('000 t)	Year	Catch ('000 t)	Year	Catch ('000 t)	Year	Catch ('000 t)	Year	Catch ('000 t)	Year	Catch ('000 t)
1904	0.010	1924	0.239	1944	0.298	1964	0.789	1984	1.656	2004	12.857
1905	0.089	1925	0.223	1945	0.070	1965	0.630	1985	2.970	2005	12.451
1906	0.093	1926	0.268	1946	0.202	1966	0.377	1986	2.500	2006	12.114
1907	0.099	1927	0.455	1947	0.224	1967	0.257	1987	2.258	2007	10.381
1908	0.076	1928	0.500	1948	0.229	1968	0.227	1988	2.670	2008	7.700
1909	0.106	1929	0.616	1949	0.265	1969	0.264	1989	2.781	2009	6.321
1910	0.105	1930	0.596	1950	0.250	1970	0.257	1990	3.821	2010	8.458
1911	0.094	1931	0.242	1951	0.257	1971	0.261	1991	5.372	2011	8.487
1912	0.087	1932	0.294	1952	0.201	1972	0.267	1992	6.577	2012	7.755
1913	0.106	1933	0.280	1953	0.323	1973	0.500	1993	5.367	2013	9.073
1914	0.176	1934	0.231	1954	0.673	1974	0.800	1994	5.201	2014	9.177
1915	0.147	1935	0.237	1955	0.541	1975	1.093	1995	7.400	2015	8.674
1916	0.156	1936	0.205	1956	0.670	1976	2.000	1996	7.837	2016	10.760
1917	0.136	1937	0.210	1957	0.853	1977	2.876	1997	8.601	2017	6.409
1918	0.057	1938	0.251	1958	0.870	1978	2.486	1998	10.671	2018	8.399
1919	0.135	1939	0.357	1959	0.796	1979	2.116	1999	10.593	2019	8.759
1920	0.233	1940	0.350	1960	1.045	1980	1.849	2000	7.574	2020	7.602
1921	0.146	1941	0.038	1961	0.887	1981	1.720	2001	7.072	2021	9.028
1922	0.297	1942	0.049	1962	0.906	1982	1.064	2002	11.718		
1923	0.301	1943	0.061	1963	1.124	1983	0.953	2003	11.571		

Appendix 2. Model script for 2022 Bayesian model

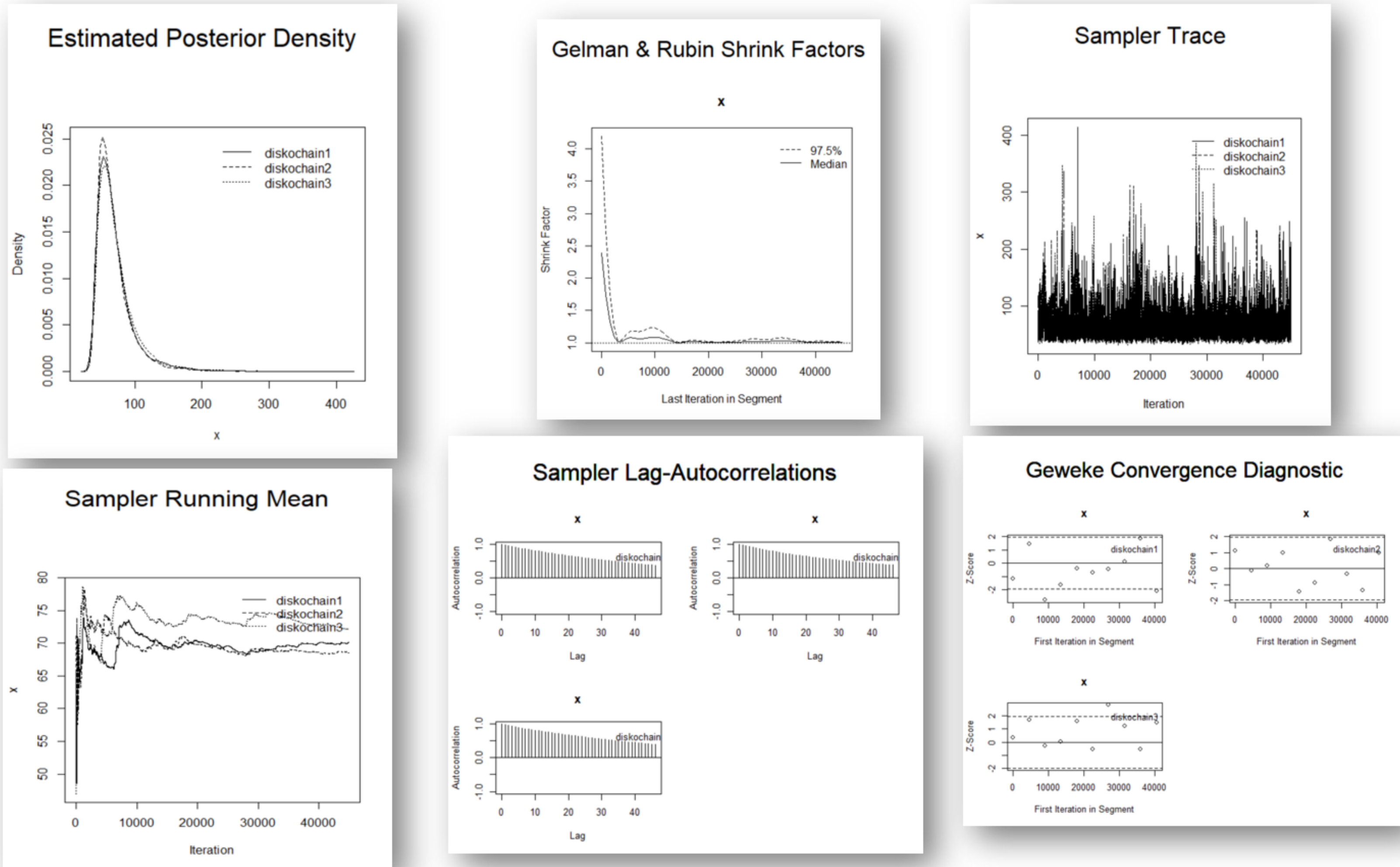
```
model
{
#prior for r mean 0.3 std 0.1
r ~ dunif(0.01,1)
# prior distribution of K
#mean 150,sd 25 run1 cv was 42% in normal scale
#this run mean of 150 and sd of 1500 CV 1000%
K~dlnorm(2.703,0.2167)
# prior distribution of q's
q.Tskaervoy~dgamma(1,1)
q.Tcosmos~dgamma(1,1)
q.Gillnet~dgamma(1,1)
q.Logbook~dgamma(1,1)
q.Factory~dgamma(1,1)
# Prior for process noise, sigma
sigma ~ dunif(0,5)
isigma2 <- pow(sigma, -2)
# Prior for observation errors, tau.
tau.Tskaervoy~dgamma(1,1)
itau2.Tskaervoy <- 1/tau.Tskaervoy
tau.Tcosmos~dgamma(1,1)
itau2.Tcosmos <- 1/tau.Tcosmos
tau.Gillnet~dgamma(1,1)
itau2.Gillnet<- 1/tau.Gillnet
tau.Logbook~dgamma(1,1)
itau2.Logbook <- 1/tau.Logbook
tau.Factory~dgamma(1,1)
itau2.Factory <- 1/tau.Factory
# Prior for initial population size as proportion of K, P[1].
Pin~dunif(0.5, 1)
Pm[1] <- log(Pin)
P[1] ~ dlnorm(Pm[1], isigma2)I(0.001,5)
P.res[1]<-log(P[1])-Pm[1]
# State equation - SP Model.
for (t in 2:(N))   {
Pm[t] <- log(max(P[t-1] + r*P[t-1]*(1-P[t-1]) - L[t-1]/K, 0.0001))
P[t] ~ dlnorm(Pm[t], isigma2)I(0.001,5)
P.res[t]<-log(P[t])-Pm[t]
}
# Observation equations
for (t in 89:(101)) {
Tskaervoym[t] <- log(q.Tskaervoy* K * P[t])
Tskaervoy[t] ~ dlnorm(Tskaervoym[t], itau2.Tskaervoy)
}
for (t in 102:(N)) {
Tcosmosm[t] <- log(q.Tcosmos* K * P[t])
Tcosmos[t] ~ dlnorm(Tcosmosm[t], itau2.Tcosmos)
}
for (t in 107:(N)) {
Logbookm[t] <- log(q.Logbook* K * P[t])
Logbook[t] ~ dlnorm(Logbookm[t], itau2.Logbook)
}
for (t in 110:(N)) {
Factorym[t] <- log(q.Factory* K * P[t])
Factory[t] ~ dlnorm(Factorym[t], itau2.Factory)
}
for (t in 98:(N)) {
Gillnetm[t] <- log(q.Gillnet* K * P[t])
Gillnet[t] ~ dlnorm(Gillnetm[t], itau2.Gillnet)
}
# Output. Using the proportion and K to estimate biomass, B.
for(t in 1:N) {
B[t] <- P[t] * K
F[t]<-L[t]/B[t]
}
#Biomass Ratio: Showing what percent the stock would be at if fished at MSY for a given year, t
for(t in 1:N) {
Bratio[t] <- B[t]/BMSY
}
#F Ratio: indicates the ratio of fishing mortality to that estimated for FMSY.
#e.g. 1.65=65% higher than that estimated for FMSY
for(t in 1:N) {
Fratio[t] <- F[t]/FMSY
}
# further management parameters and predictions:
MSY <- r*K/4;
FMSY<-r/2
BMSY<-K/2
#Replicate data sets code below here
#generate replicate data sets
for (i in 110:N){
	Factory.rep[i] ~ dlnorm(Factorym[i],itau2.Factory)
	p.smaller.Factory[i] <- step(log(Factory[i])-log(Factory.rep[i]))
#residuals of log values of replicate data
	res.Factory.rep[i] <- log(Factory[i])-log(Factory.rep[i])
}
#generate replicate data sets
for (i in 89:101){
	Tskaervoy.rep[i] ~ dlnorm(Tskaervoym[i],itau2.Tskaervoy)
	p.smaller.Tskaervoy[i] <- step(log(Tskaervoy[i])-log(Tskaervoy.rep[i]))
#residuals of log values of replicate data
	res.Tskaervoy.rep[i] <- log(Tskaervoy[i])-log(Tskaervoy.rep[i])
}
#generate replicate data sets
```

```
for (i in 102:N){
            Tcosmos.rep[i] ~
dlnorm(Tcosmosm[i],itau2.Tcosmos)
            p.smaller.Tcosmos[i] <-
step(log(Tcosmos[i])-log(Tcosmos.rep[i]))
#residuals of log values of replicate data
            res.Tcosmos.rep[i] <- log(Tcosmos[i])-
log(Tcosmos.rep[i])
}
#generate replicate data sets
for (i in 107:N){
            Logbook.rep[i] ~
dlnorm(Logbookm[i],itau2.Logbook)
            p.smaller.Logbook[i] <-
step(log(Logbook[i])-log(Logbook.rep[i]))
#residuals of log values of replicate data
            res.Logbook.rep[i] <- log(Logbook[i])-
log(Logbook.rep[i])
}
#generate replicate data sets
for (i in 98:N){
            Gillnet.rep[i] ~
dlnorm(Gillnetm[i],itau2.Gillnet)
            p.smaller.Gillnet[i] <- step(log(Gillnet[i])-
log(Gillnet.rep[i]))
#residuals of log values of replicate data
            res.Gillnet.rep[i] <- log(Gillnet[i])-
log(Gillnet.rep[i])
}
} ## END
```

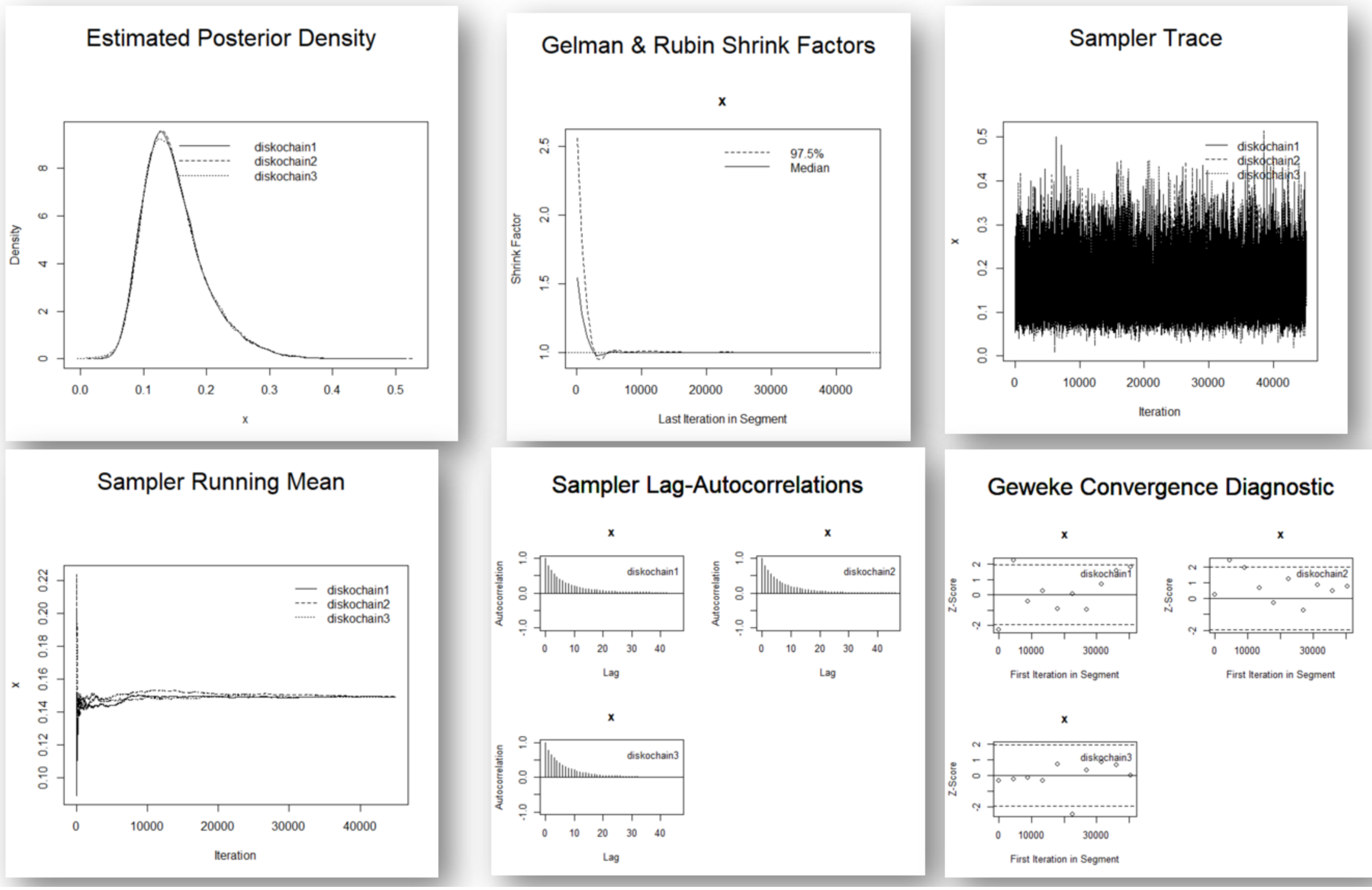
Appendix 3. Diagnostic plots for initial model run Greenland halibut in NAFO Division 1A Inshore



K


Estimated Posterior Density
diskochain1
diskochain2
diskochain3
Density
x
Gelman & Rubin Shrink Factors
x
97.5%
Median
Shrink Factor
Last Iteration in Segment
Sampler Trace
diskochain1
diskochain2
diskochain3
x
Iteration
Sampler Running Mean
diskochain1
diskochain2
diskochain3
x
Iteration
Sampler Lag-Autocorrelations
x
Autocorrelation
diskochain
Lag
Geweke Convergence Diagnostic
x
Z-Score
diskochain1
diskochain2
diskochain3
First Iteration in Segment

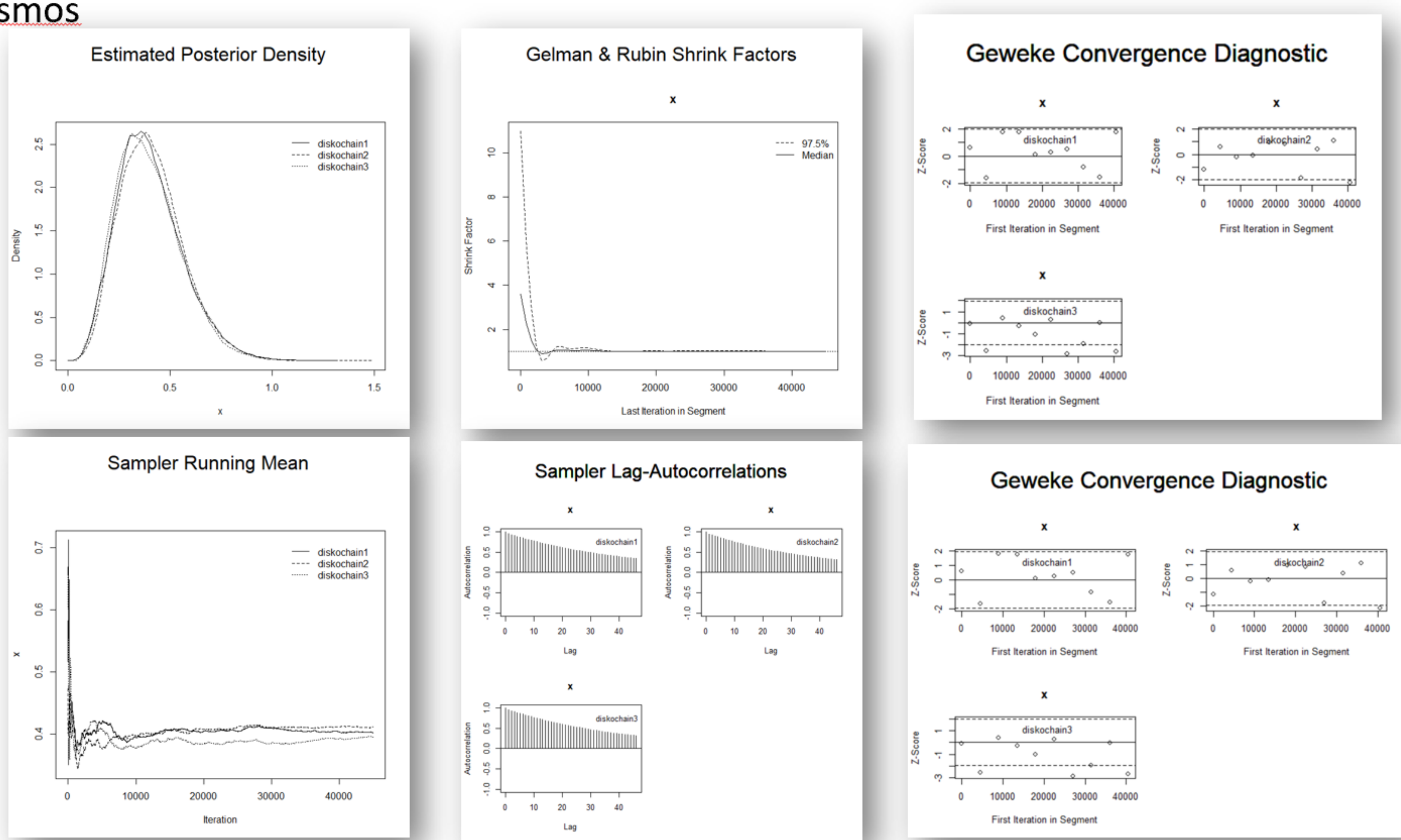
sigma

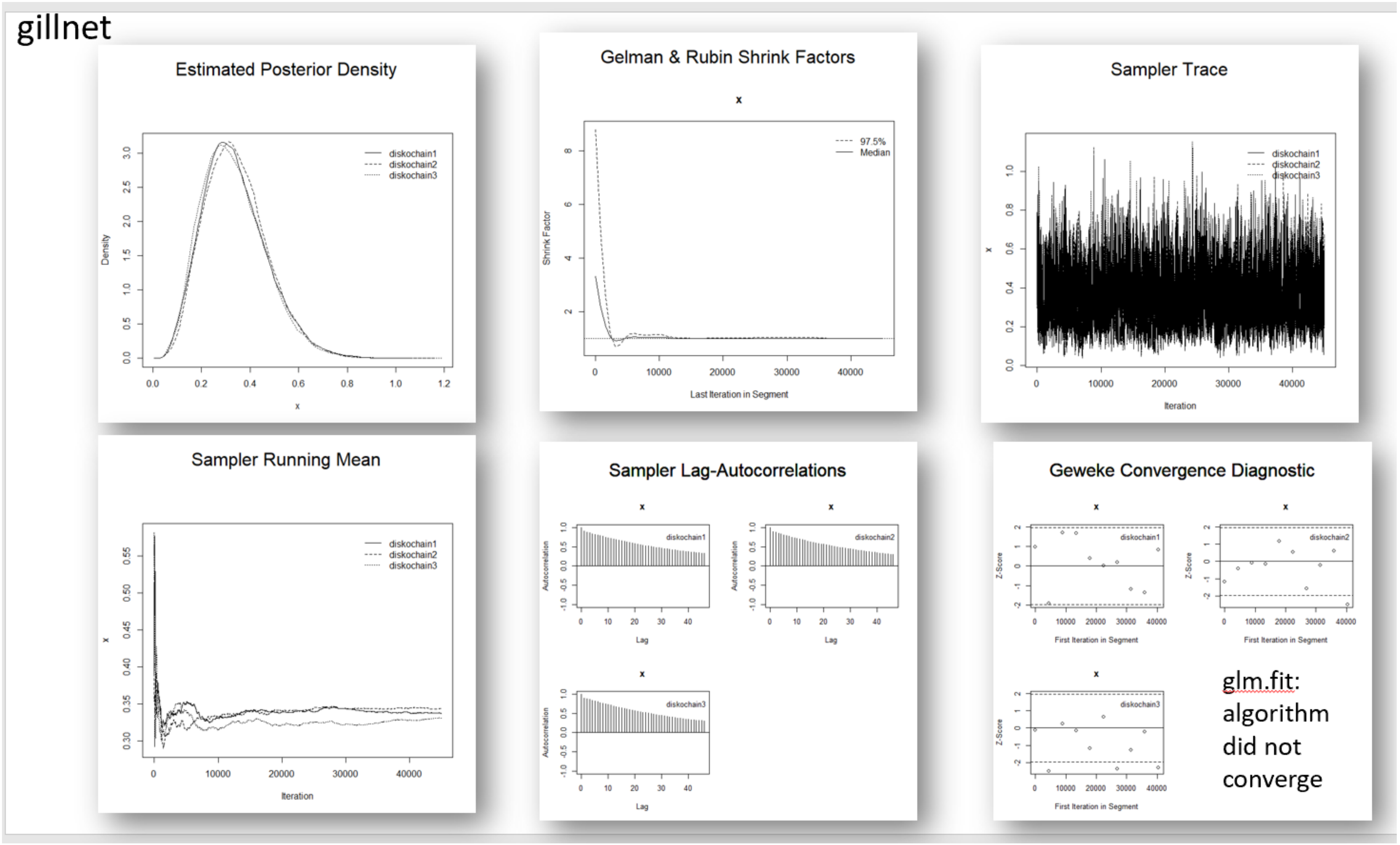

Estimated Posterior Density
diskochain1
diskochain2
diskochain3
Density
x
Gelman & Rubin Shrink Factors
x
97.5%
Median
Shrink Factor
Last Iteration in Segment
Sampler Trace
diskochain1
diskochain2
diskochain3
x
Iteration
Sampler Running Mean
diskochain1
diskochain2
diskochain3
x
Iteration
Sampler Lag-Autocorrelations
x
diskochain1
diskochain2
diskochain3
Autocorrelation
Lag
Geweke Convergence Diagnostic
x
diskochain1
diskochain2
diskochain3
Z-Score
First Iteration in Segment

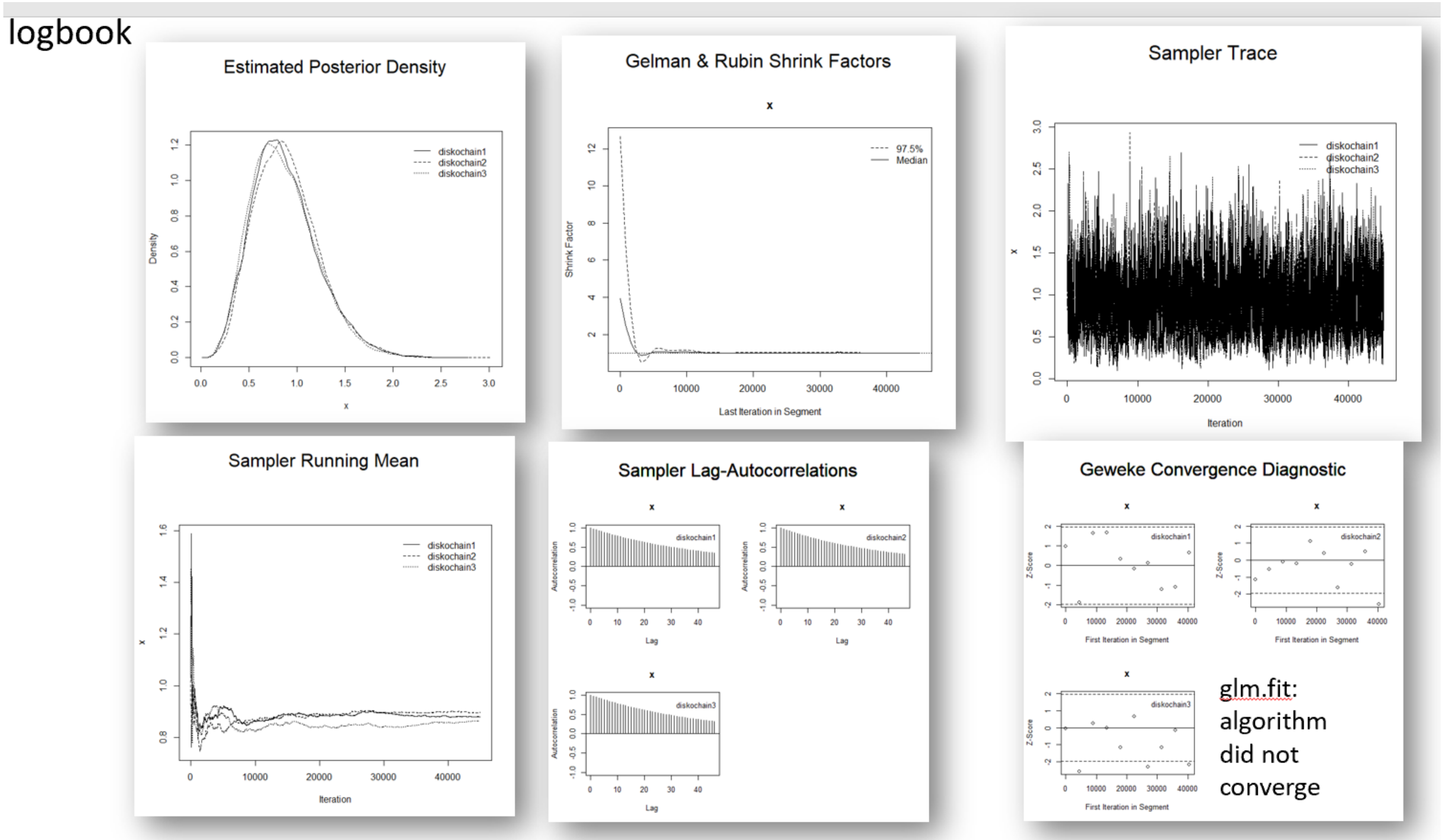
tskaervoy

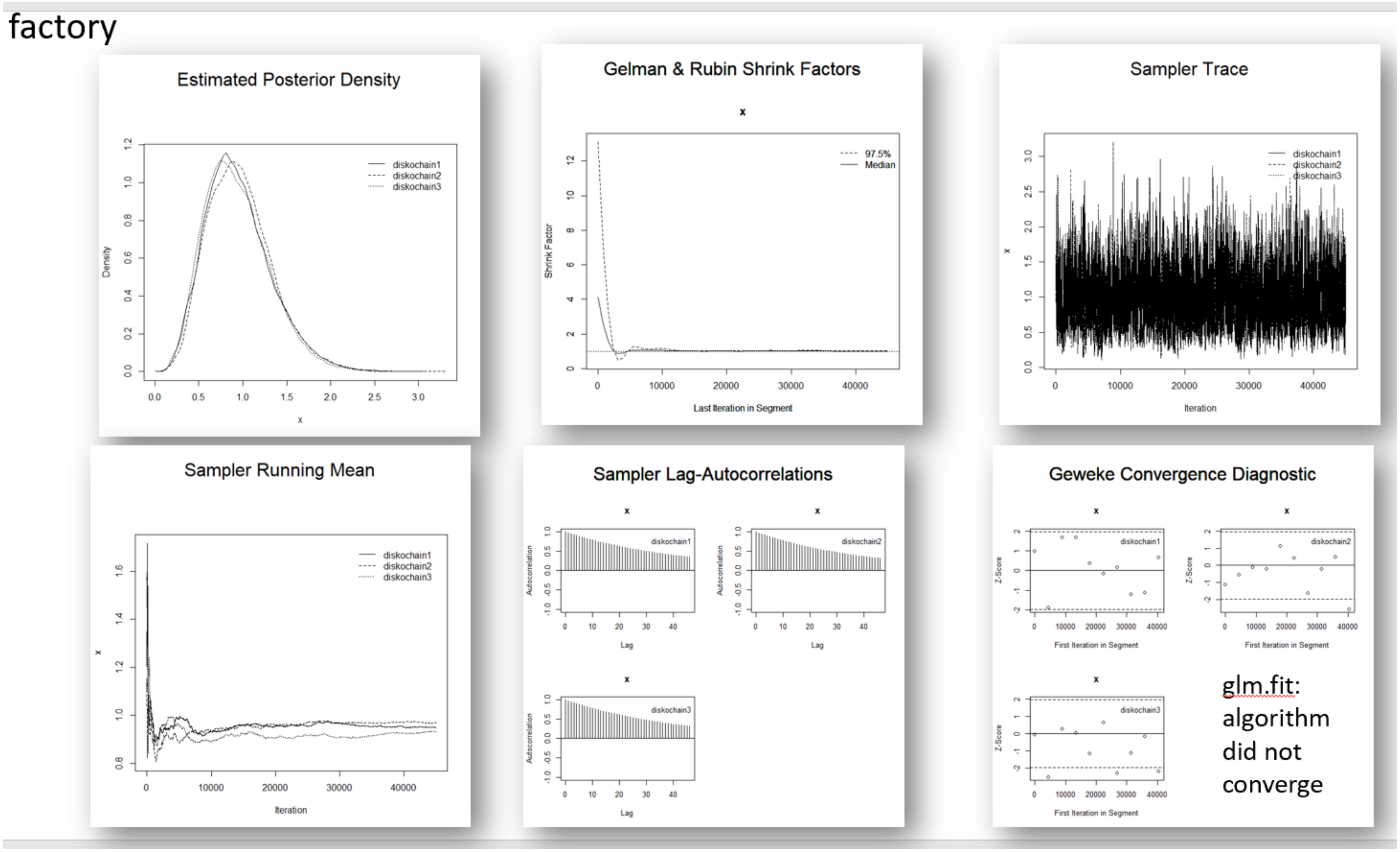
Estimated Posterior Density
Density
x
diskochain1
diskochain2
diskochain3
Gelman & Rubin Shrink Factors
x
97.5%
Median
Shrink Factor
Last Iteration in Segment
Sampler Trace
x
Iteration
Sampler Running Mean
x
Iteration
Sampler Lag-Autocorrelations
Autocorrelation
Lag
Geweke Convergence Diagnostic
Z-Score
First Iteration in Segment
glm.fit:
algorithm
did not
converge

tcosmos


Estimated Posterior Density
diskochain1
diskochain2
diskochain3
Density
x
Gelman & Rubin Shrink Factors
x
97.5%
Median
Shrink Factor
Last Iteration in Segment
Geweke Convergence Diagnostic
x
diskochain1
diskochain2
diskochain3
Z-Score
First Iteration in Segment
Sampler Running Mean
diskochain1
diskochain2
diskochain3
x
Iteration
Sampler Lag-Autocorrelations
x
diskochain1
diskochain2
diskochain3
Autocorrelation
Lag
Geweke Convergence Diagnostic
x
diskochain1
diskochain2
diskochain3
Z-Score
First Iteration in Segment

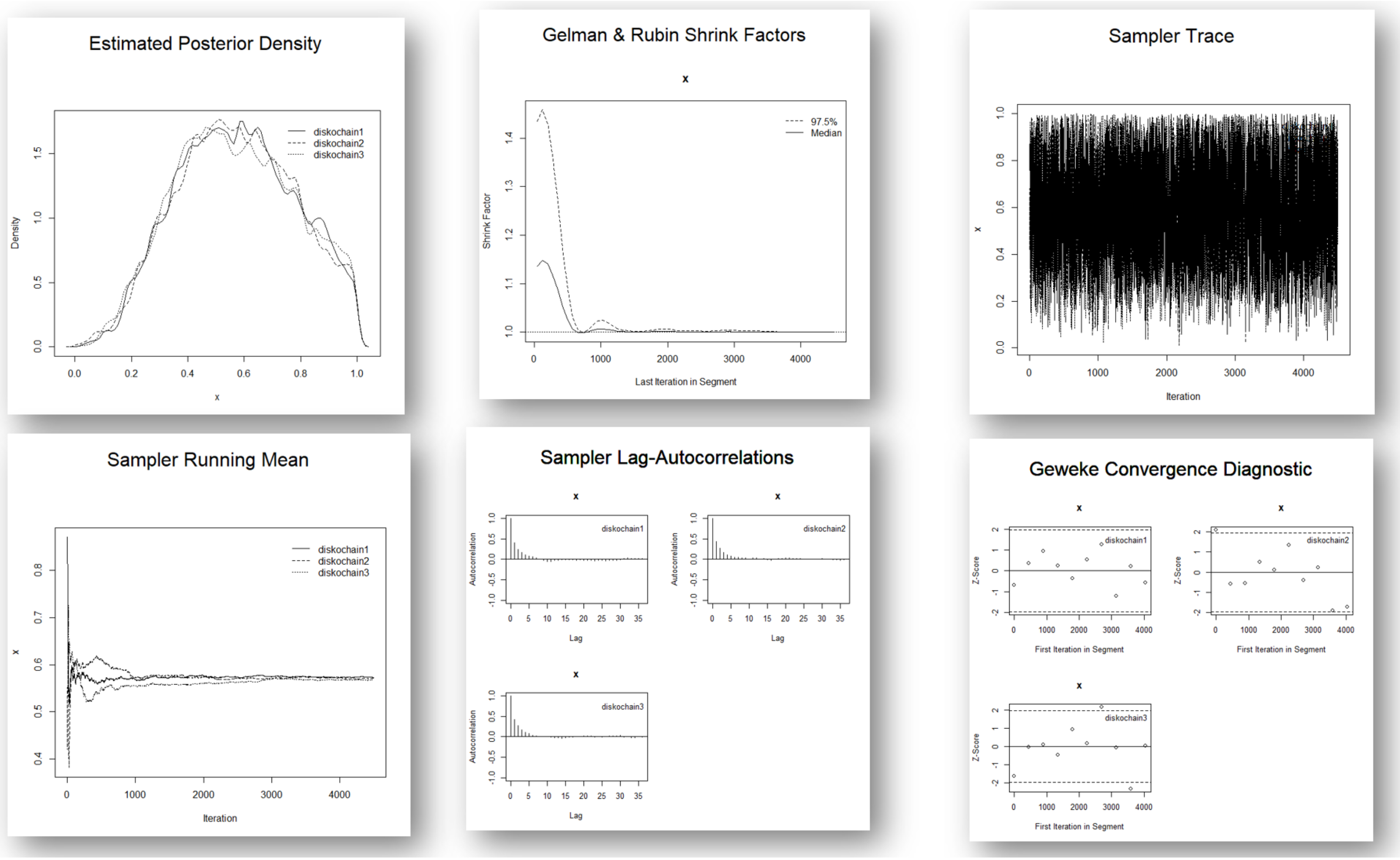

gillnet
Estimated Posterior Density
Density
x
diskochain1
diskochain2
diskochain3
Gelman & Rubin Shrink Factors
x
Shrink Factor
97.5%
Median
Last Iteration in Segment
Sampler Trace
x
Iteration
diskochain1
diskochain2
diskochain3
Sampler Running Mean
x
Iteration
diskochain1
diskochain2
diskochain3
Sampler Lag-Autocorrelations
x
Autocorrelation
Lag
diskochain1
diskochain2
diskochain3
Geweke Convergence Diagnostic
x
Z-Score
First Iteration in Segment
diskochain1
diskochain2
diskochain3
glm.fit:
algorithm
did not
converge


logbook
Estimated Posterior Density
diskochain1
diskochain2
diskochain3
Density
x
Gelman & Rubin Shrink Factors
x
97.5%
Median
Shrink Factor
Last Iteration in Segment
Sampler Trace
diskochain1
diskochain2
diskochain3
Iteration
Sampler Running Mean
diskochain1
diskochain2
diskochain3
Iteration
Sampler Lag-Autocorrelations
Autocorrelation
Lag
diskochain1
diskochain2
diskochain3
Geweke Convergence Diagnostic
Z-Score
First Iteration in Segment
diskochain1
diskochain2
diskochain3
glm.fit:
algorithm
did not
converge

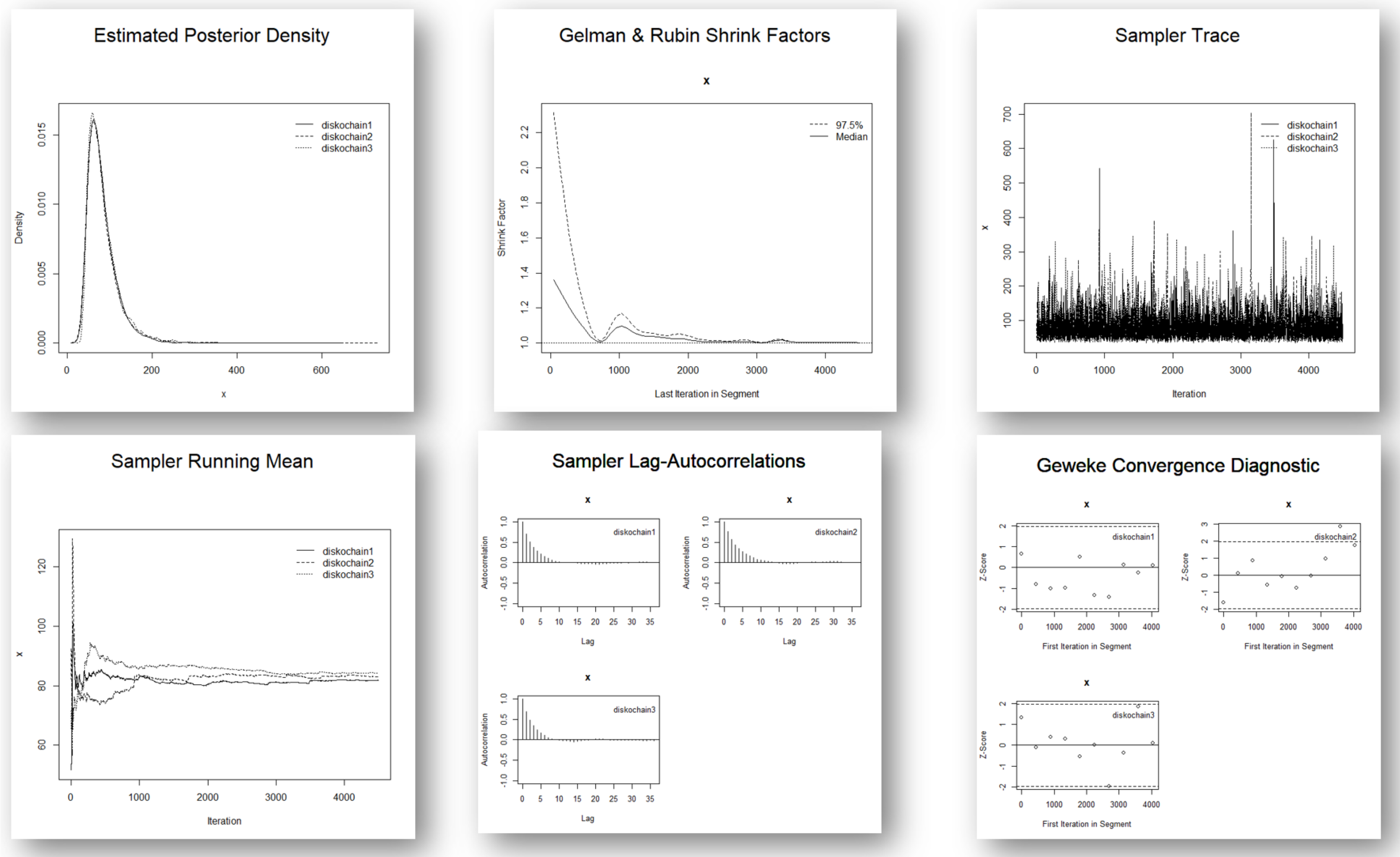

factory
Estimated Posterior Density
Density
diskochain1
diskochain2
diskochain3
Gelman & Rubin Shrink Factors
Shrink Factor
97.5%
Median
Last Iteration in Segment
Sampler Trace
Iteration
Sampler Running Mean
Iteration
Sampler Lag-Autocorrelations
Autocorrelation
Lag
Geweke Convergence Diagnostic
Z-Score
First Iteration in Segment
glm.fit:
algorithm
did not
converge

Appendix 4. Diagnostics for Updated model run of Greenland halibut in Disko Bay NAFO division 1A Inshore.

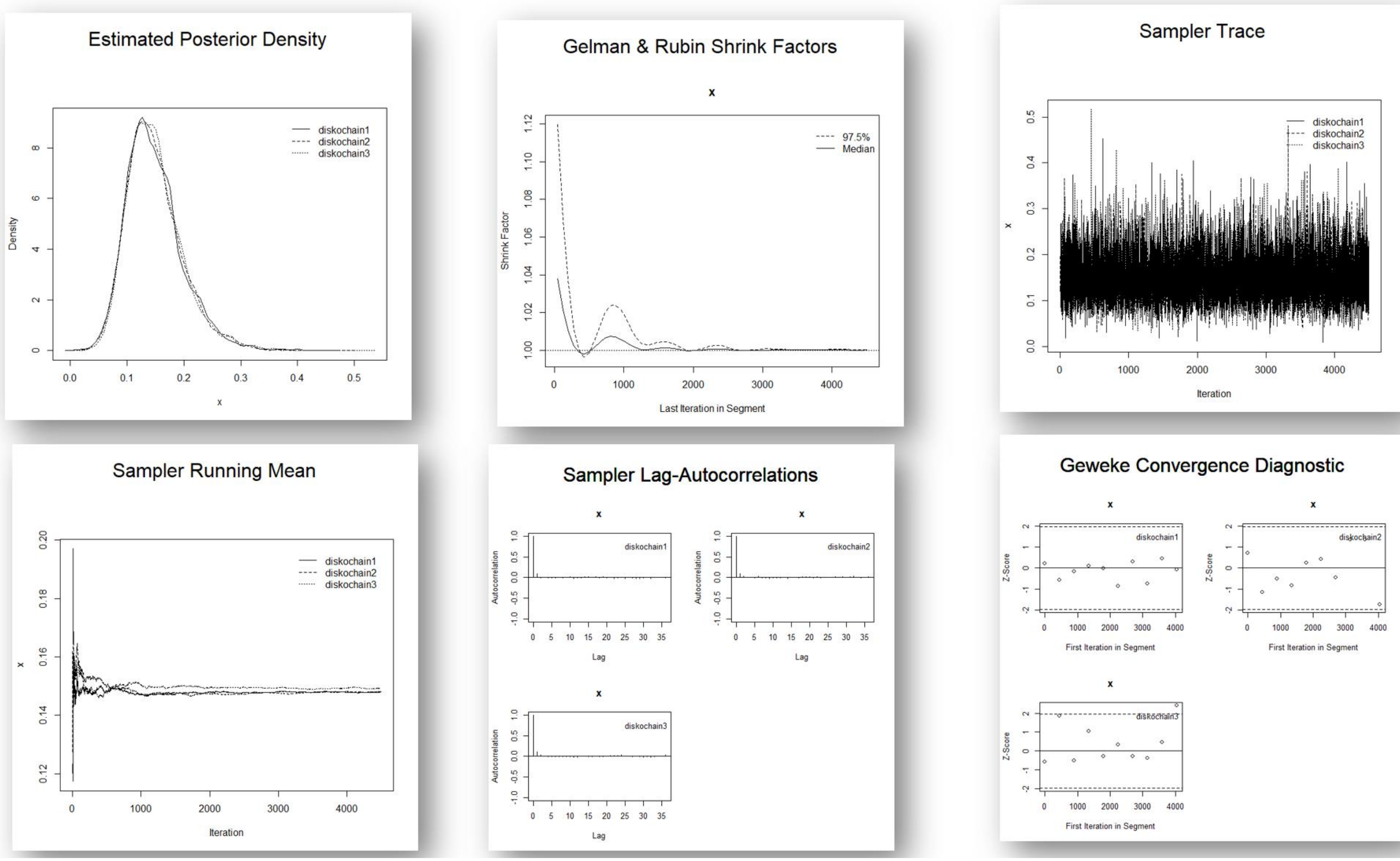
Diagnostics for r.



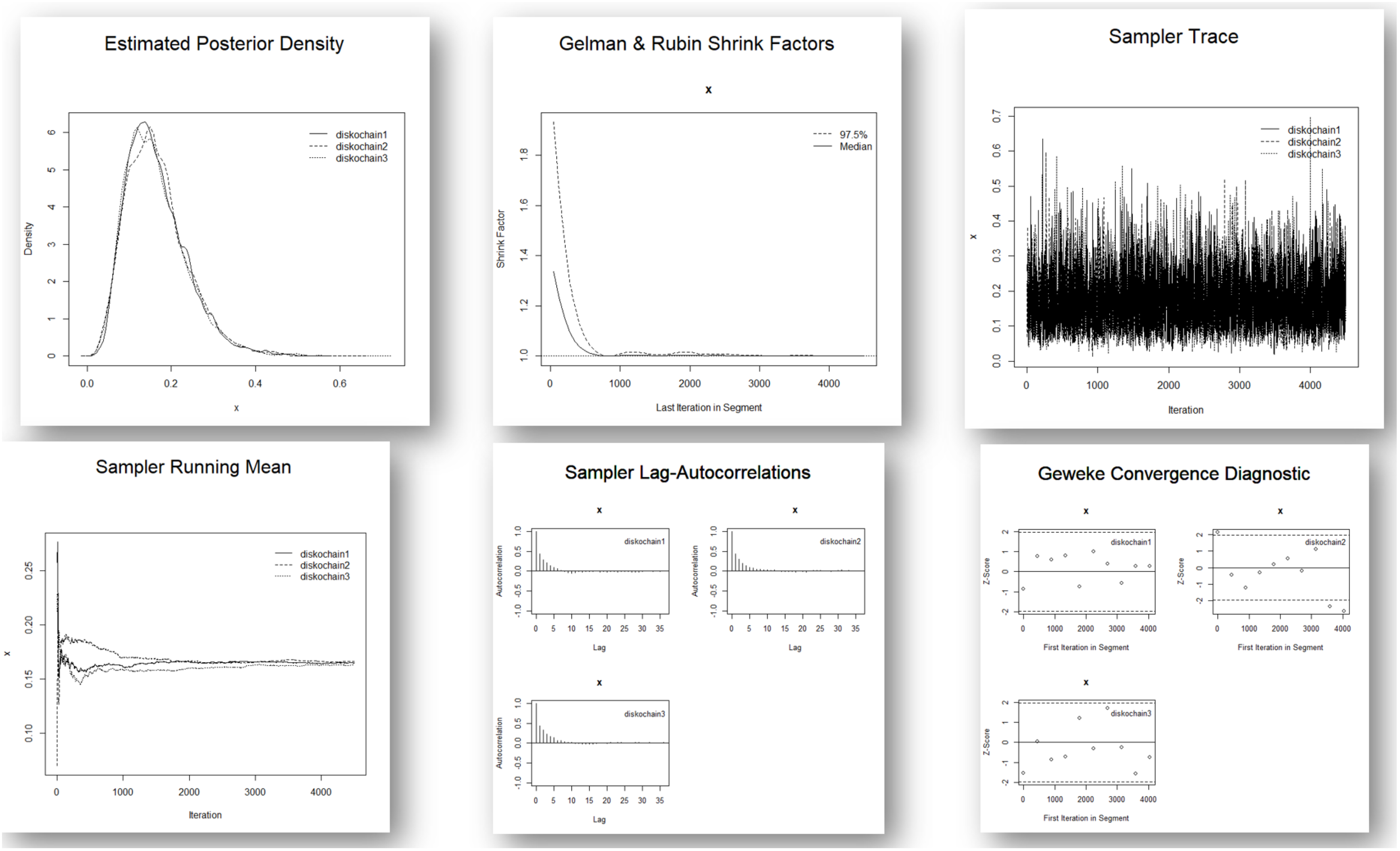
Diagnostics for K.



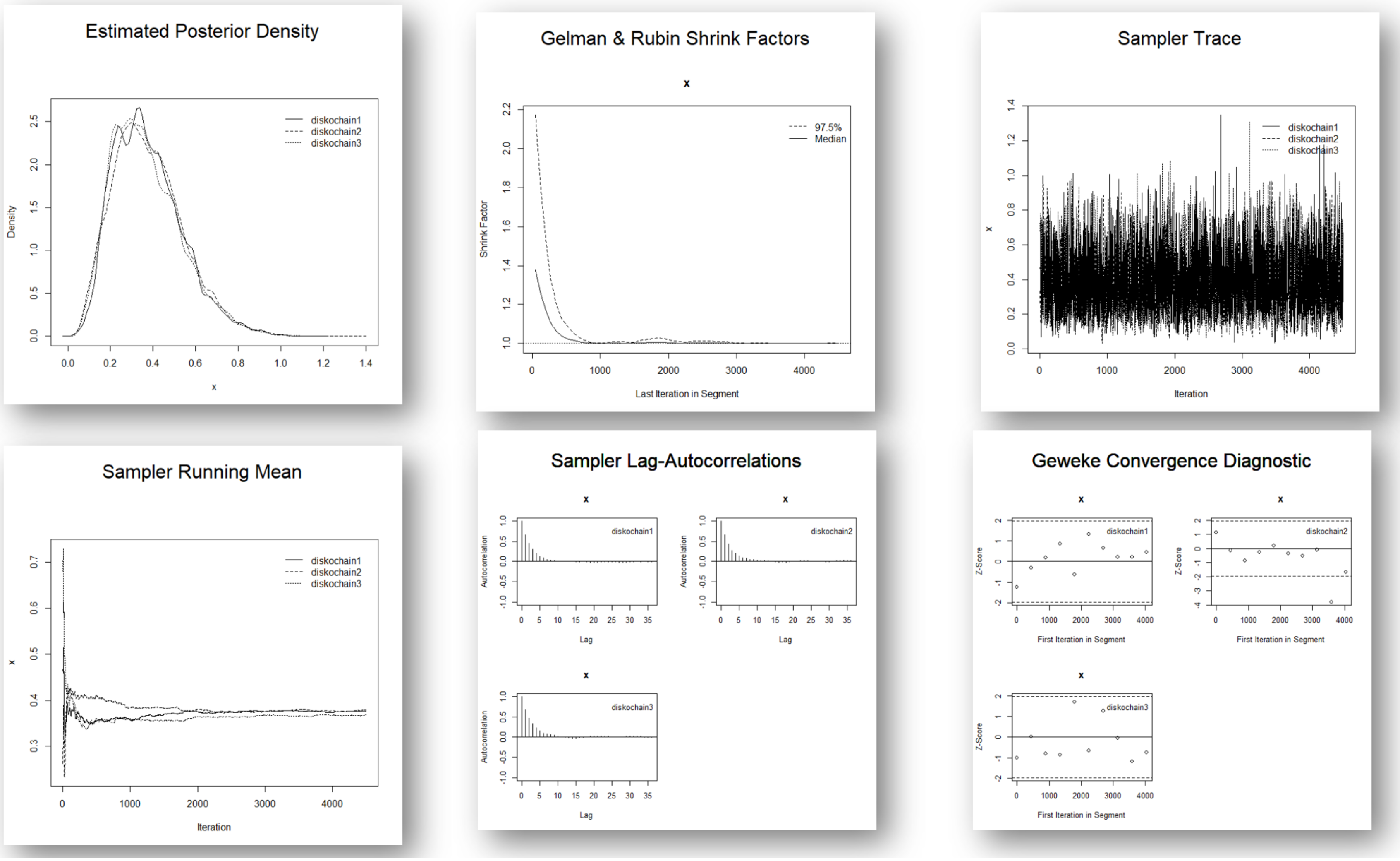
Diagnostics for sigma.



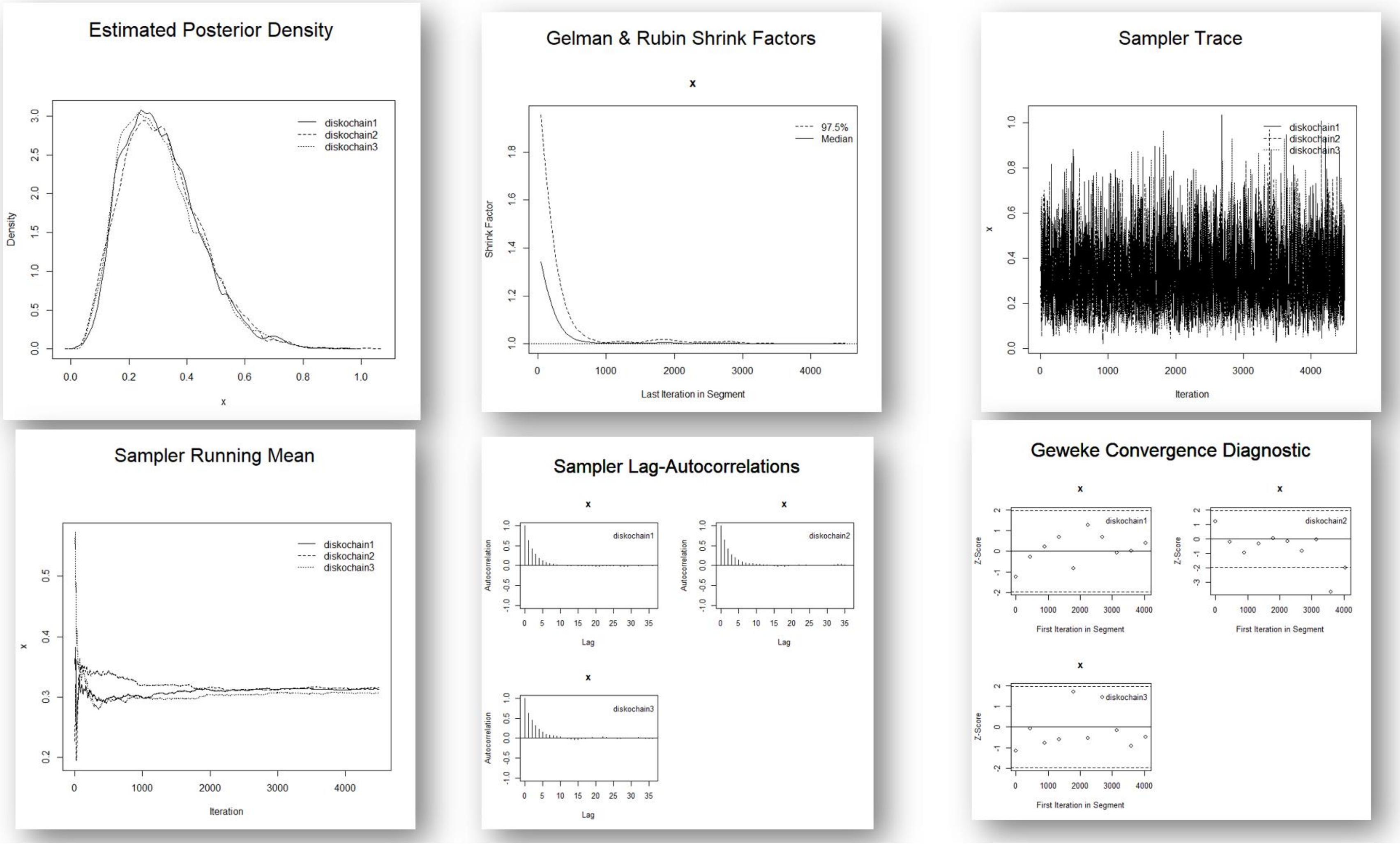
Diagnostics for Tskaervoy.



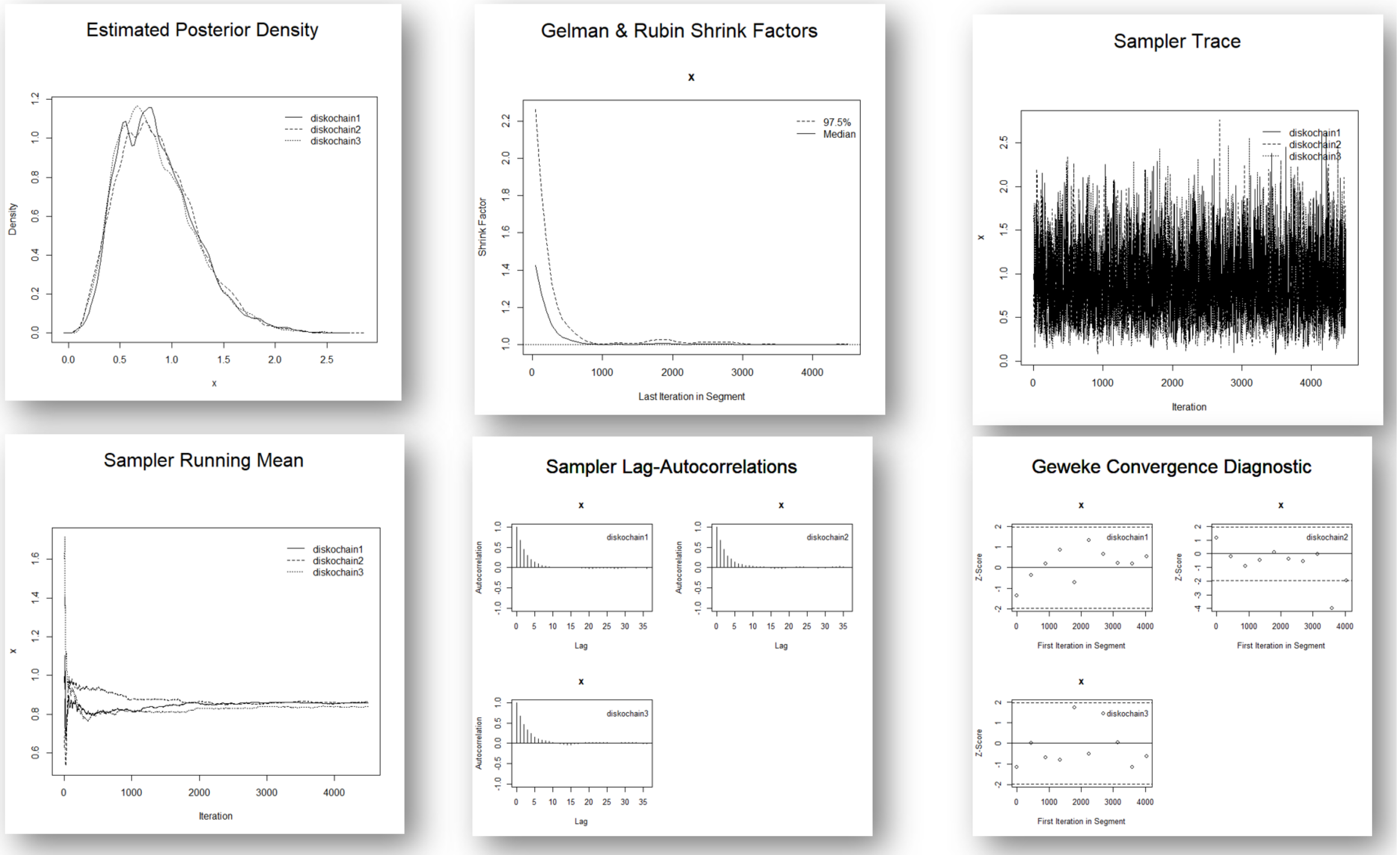
Diagnostics for Tcosmos.



Diagnostics for gillnet.



Diagnostics for logbook.



Diagnostics for Factory.