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Note

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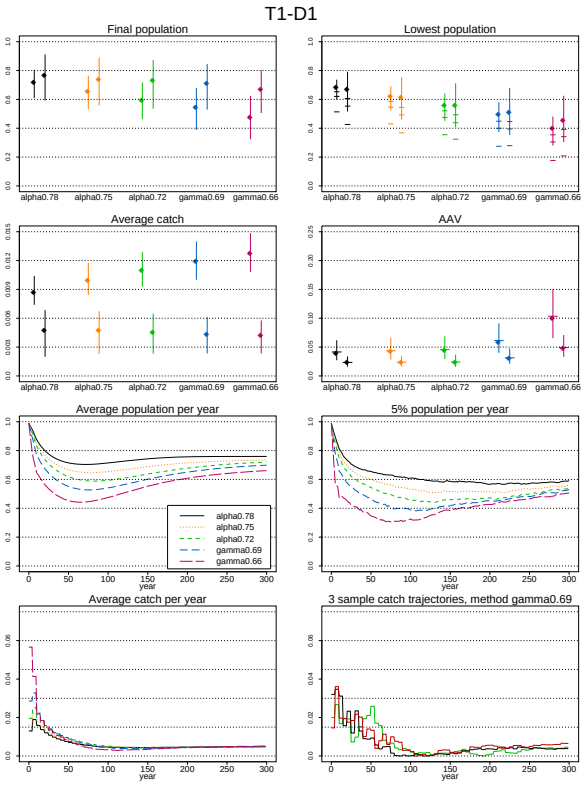
Simulation trials 2007 for a re-tuned Catch Limit Algorithm



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Abstract

The catch limit algorithm (CLA) is a central part of the revised management procedure (RMP) for whaling developed by the International Whaling Commission (IWC). The CLA has previously been tuned to a specified final depletion after 100 years of management, based on simulations from a population model with maximum sustainable yield (MSY) at 1% of the mature component of the stock (i.e. $MSYR^{mature}$=1%). According to the "old" tuning procedure, median depletion after 100 years is set to 60%, 66% or 72% of carrying capacity.

In Aldrin, Huseby and Schweder (2006), we presented two new versions of the CLA, using another tuning parameter than the traditional one, and tuned to lower levels (0.54 and 0.48 median depletion after 100 years). The two new versions were compared to the three traditional ones in a set of simulation trials where MSYR was defined relative to the 1+ population, and results were reported for time horizons of both 100 and 300 years.

At the meeting of the Scientific Committee of IWC in 2006, the CLA trials group (IWC 2006) defined a set of required trials that must be run to demonstrate whether a candidate procedure is an improvement compared to the current version of RMP. In these trials MSYR is defined relative to the mature population, and the time horizon are 100 years.

In this paper we run all these trials for the five versions of the CLA. All results are presented as specified by the CLA trials group. In addition, some results are presented in the same way as in Aldrin, Huseby and Schweder (2006) for both the 100 and the 300 years horizon .

Keywords

Target group

Availability

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Contents

1 Introduction

The catch limit algorithm (CLA) is a central part of the revised management procedure (RMP) for whaling developed by the International Whaling Commission (IWC). The CLA has previously been tuned to a specified final depletion after 100 years of management, based on simulations from a population model with maximum sustainable yield (MSY) at 1% of the mature component of the stock (i.e. $MSYR^{mature}$=1%). According to the "old" tuning procedure, median depletion after 100 years is set to 60%, 66% or 72% of carrying capacity.

In Aldrin, Huseby and Schweder (2006), hereafter called AHS, presented to the Scientific Committee of IWC 2006, we changed the horizon from 100 to 300 years, allowing the managed population to come closer to a stable level. We also measured productivity of the stock (MSYR) in terms of the total stock, excluding calves. Our "new" tuning procedure assumed $MSYR^{1+}$=1%, and targeted a given level of depletion after 300 years of management.

In the traditional versions of CLA, a tuning parameter α (or PPROB, see equation (6) below for an interpretation of this parameter), is varied until the the specified tuning level is met. In AHS, we used another parameter γ (or PSLOPE, see equation (5)), as tuning parameter. We defined two new versions of the CLA, tuned to 0.66 and 0.69 by the "new" tuning procedure. We named the five versions of the CLA by combining the name of tuning parameter and the tuning level with the "new" procedure. The "old" and "new" tuning levels for these five versions the CLA are displayed in Table 1. These results come from Tables 4 and 5 in AHS and Table 7 in the present paper. Note that the alpha.0.75 version by a mistake was called alpha0.76 in AHS, with a corresponding error in the "new" tuning level. The correct "new" tuning level is 0.75 and can be found in the supplementary material to AHS at `http://www.nr.no/~aldrin/whales/allresults.txt` .

name	α	γ	"Old" tuning level with $NYEAR$=100 and $MSYR^{mature}$=1%	"New" tuning level with $NYEAR$=300 and $MSYR^{1+}$=1%
alpha0.78	0.4015	3	0.72*	0.78
alpha0.75	0.4629	3	0.66*	0.75
alpha0.72	0.5222	3	0.60*	0.72
gamma0.69	0.5	4.7157	0.54	0.69*
gamma0.66	0.5	9.3443	0.48	0.66*

Table 1. "Old" and "new" tuning levels for five versions of the CLA, with corresponding levels of α and γ. Numbers with an aterisk are based on >50000 simulations. The remaining numbers are based on 400 simulations with the standard common sets of seeds.

AHS also investigated the properties of the five versions of the CLA by simulating a series of scenarios where MSYR was defined relative to the 1+ component of the population, with respect to yield and stock conservation properties

At the meeting of the Scientific Committee of IWC in 2006, the CLA trials group (IWC 2006), hereafter called CLA06, defined a set of required trials that must be run to demonstrate whether a candidate procedure is an improvement compared to the current version of RMP. In these trials the MSYR is defined relative to the mature population, and the time horizon is 100 years.

In this paper we run all these trials for the five versions of the CLA given in Table 1. All results are presented as specified in CLA06. Furthermore, some results are presented in the same way as in AHS for both the 100 and the 300 years horizon. The aim of this paper is to present the results of the simulation trials in a way that fulfils the specifications in CLA06. Therefore, we have not included any discussion or conclusion section in this paper, but hope that the Scientific Committee finds the results useful for their work.

2 Methods

2.1 The Catch Limit Algorithm (CLA)

The input data to the catch limit algorithm (IWC, 1999, p. 251-258) consists of a time series of historic annual catches and a time series of absolute abundance estimates along with their standard errors and correlations on the logarithmic scale.

The internal population model of the catch limit algorithm is defined by the following dynamics

$$\begin{aligned} P_0 &= \frac{P_T}{D_T}, \\ P_{t+1} &= P_t - C_t + 1.4184\,\mu\,P_t(1-(\frac{P_t}{P_0})^2) \quad (0 \le t < T), \end{aligned} \tag{1}$$

where

- 0 is the first year of recorded catch, and T is the current year of management (i.e. the first year of an assessment cycle). P_0 is regarded as pristine population size, and P_t is the population size in numbers at the beginning of year t,
- C_t is the catch in numbers in year t,
- $D_T = P_T/P_0$ is the ratio of the population size at the beginning of year T to the population size at the beginning of year zero, measuring stock depletion,

- μ is a parameter describing the productivity,
- the historic catch series used in assessments covers years 0 to $T-1$.

The abundance estimates are assumed to be log-normally distributed with a given (estimated) information matrix for the on the log scale. The likelihood based on the abundance data is

$$\text{Likelihood}(\mu, D_T, b) \propto \exp\left(-0.5(\mathbf{a}-\mathbf{p}-\beta\mathbf{1})'H(\mathbf{a}-\mathbf{p}-\beta\mathbf{1})\right) \tag{2}$$

where the symbol $\propto$ means proportional to, and where

- $\mathbf{a}$ is the vector of logarithms of the estimates of population size by year,
- $\mathbf{p}$ is the vector of logarithms of the modelled annual population sizes for the years with population estimates, $p_t = \ln(P_t)$,
- β is the logarithm of the bias parameter, thus $b = \exp(\beta)$;
- H is the information matrix of the $\mathbf{a}$ vector. H is assumed nonsingular, and $V = H^{-1}$ is the covariance matrix of the vector $\mathbf{a}$.

The parameters μ, D_T, and b are assigned independent uniform prior distributions making their joint prior distribution uniform over the region

$$[\mu_{\min}, \mu_{\max}] \times [D_{T,\min}, D_{T,\max}] \times [b_{\min}, b_{\max}], \tag{3}$$

where $\mu_{\min}$, $\mu_{\max}$, $D_{T,\min}$, $D_{T,\max}$, $b_{\min}$, and $b_{\max}$ are chosen constants. We will use $\mu_{\min} = 0.0$, $\mu_{\max} = 0.05$, $D_{T,\min} = 0.0$, $D_{T,\max} = 1.0$, $b_{\min} = 0.0$, and $b_{\max} = 1.6667$, which are the values used in the current implementation of the CLA.

A distinctive feature of the CLA is that abundance data are strongly down-weighted to obtain desired robustness properties. In the internal model, all variances and covariances of logarithmic abundance estimates are actually multiplied by 16. The historic catch data are furthermore assumed to be accurate, without any measurement errors. The posterior density function of the parameters μ, D_T, and b is therefore

$$\text{Posterior}(\mu, D_T, b) \propto \text{Prior}(\mu, D_T, b) \cdot \text{Likelihood}(\mu, D_T, b)^s, \quad s = 1/16 \tag{4}$$

The presence of a deflation parameter $0 < s < 1$ down-weights the survey information relative to a strict Bayesian approach.

The internal catch limit is the following function of μ, D_T, and P_T:

$$L_T = \begin{cases} 0 & \text{if } D_T \leq IPL \\ \gamma\mu(D_T - IPL)P_T & \text{if } D_T > IPL \end{cases} \tag{5}$$

where the internal protection level IPL is a control parameter. In this work IPL is fixed to 0.54. Traditionally, $\gamma = 3$. In AHS this parameter was used as a tuning parameter, whereas α (see below) was fixed to 0.5

The internal catch limit can be regarded as the catch limit in the hypothetical case of perfect knowledge of population parameters and size. However, in the Bayesian formalism, L_T is regarded as a random variable, with marginal posterior distribution obtained from the joint posterior distribution of (μ, D_T, b). The actual catch limit z is defined as a certain percentile of its distribution,

$$P(L_T < z|data) \leq \alpha \leq P(L_T \leq z|data) \tag{6}$$

for a given value of the parameter α. Traditionally, α has been used as tuning parameter.

We use the implementation of the algorithm of the Norwegian Computing Center (Huseby and Aldrin 2006). This implementation is available from the IWC secretariat. It is a FORTRAN subroutine called CATCHLIMIT, and the present version is from January 2006. The parameters α and γ above are input parameters to the subroutine, and are called IN_PPROB and IN_PSLOPE, respectively. The accuracy of the algorithm depends on parameters set by the user. We have used the same parameters values as in AHS.

2.2 Simulation trials

The performance of the five versions of the CLA, defined in Table, 1 is tested in various scenarios. These simulation trials are performed using the FORTRAN program MANTST which is available from the IWC secretariat. Our version of MANTST is based on version 11 (received from the IWC secretariat in January 2005), but modified by Andre Punt to allow for projections of more than 100 years. The MANTST program has several options, and the options used for the T1-D1 trial are shown in Appendix A.

We ran all trials specified as "Trials required the candidate procedure may be an improvement over the current version" in CLA06. A subset of the required trials is given in Table 2. The results from these trials are presented by tables and time plots over 100 years in Section 3.1. The remaining reqired trials are specified in Tables 3-6. Some of these are internally redundant or redundant with respect to some of the trials in Table 2. The corresponding results are presented by response curve plots (one per line in the tables) in Section 3.2. For each trial, we ran 400 simulations.

Description	Trial			
$MSYR^{mature}$	1%	1.5%	4.0%	7.0%
T1. Age structured model, maturity 7yrs D=Development (initial population size 0.99K)	T1-D1	T1-D1.5	T1-D4	T1-D7
R=Rehabilitation (initial population size 0.3K)	T1-R1	T1-R1.5	T1-R4	T1-R7
R=Sustainable (initial population size 0.6K)	T1-S1	T1-S1.5		
T2. Survey Bias 0.5	T2-D1	T2-D1.5		
	T2-R1	T2-R1.5		
T3. Survey Bias 1.5	T3-D1	T3-D1.5		
	T3-R1	T3-R1.5		
	T3-S1	T3-S1.5		
T4. Initial population size $P_0 = .05$K	T4-R1	T4-R1.5		
T6. Historic catch in error (1/2 true catch)	T6-R1	T6-R1.5	T6-R4	
T9. Episodic events: 2% chance each year	T9-D1	T9-D1.5	T9-D4	
that population is halved	T9-R1	T9-R1.5	T9-R4	
T12A. K doubles over management period	T12A-D1	T12A-D1.5	T12A-D4	
	T12A-R1	T12A-R1.5	T12A-R4	
T12A. K halves over management period	T12B-D1	T12B-D1.5	T12B-D4	
	T12B-R1	T12B-R1.5	T12B-R4	

Table 2. Overview of trials specified by in Table 1 in CLA06.

	Initial population size					
$MSYR^{mature}$	0.05K	0.1K	0.2K	0.3K	0.4K	0.5K
1	T4-R1	*	*	T1-R1	*	*
1.5	T4-R1.5	*	*	T1-R1.5	*	*
4	*	*	*	T1-R4	*	*

Table 3. Response curve trials with an initial population size (depletion level) ranging from 0.05K to 0.5K. Trials without specific names are marked with an asterisk.

	Initial population size					
$MSYR^{mature}$	0.05K	0.2K	0.4K	0.6K	0.8K	0.99K
1	T4-R1	*	*	T1-S1	*	T1-D1
1.5	T4-R1.5	*	*	T1-S1.5	*	T1-D1.5
4	*	*	*	T1-S4	*	T1-D4

Table 4. Response curve trials with an initial population size (depletion level) ranging from 0.05K to 0.99K. Trials without specific names are marked with an asterisk.

$MSYR^{mature}$	Init. pop.	Reported catch					
		100% C_t	80% C_t	60% C_t	40% C_t	20% C_t	1% C_t
1	0.3K	T1-R1	*	*	*	*	*
1	0.6K	T1-S1	*	*	*	*	*
1	0.99K	T1-D1	*	*	*	*	*
1.5	0.3K	T1-R1.5	*	*	*	*	*
1.5	0.6K	T1-S1.5	*	*	*	*	*
1.5	0.99K	T1-D1.5	*	*	*	*	*
4	0.3K	T1-R4	*	*	*	*	*
4	0.6K	T1-S4	*	*	*	*	*
4	0.99K	T1-D4	*	*	*	*	*

Table 5. Response curve trials with a reported catch ranging from 100% C_t to 1%C_t. Trials without specific names are marked with an aterisk.

$MSYR^{mature}$	Init. pop.	Positive bias					
		1.0 (No bias)	1.2	1.4	1.6	1.8	2.0
1	0.3K	T1-R1	*	*	*	*	*
1	0.6K	T1-S1	*	*	*	*	*
1	0.99K	T1-D1	*	*	*	*	*
1.5	0.3K	T1-R1.5	*	*	*	*	*
1.5	0.3K	T1-S1.5	*	*	*	*	*
1.5	0.3K	T1-D1.5	*	*	*	*	*
4	0.3K	T1-R4	*	*	*	*	*
4	0.6K	T1-S4	*	*	*	*	*
4	0.99K	T1-D4	*	*	*	*	*

Table 6. Response curve trials with a positive bias ranging from 1 (no bias) to 2. Trials without specific names are marked with an asterisk.

2.3 Statistics

CLA06 also specifies the statistics to be calculated. Catches are scaled by the initial carrying capacity. Population sizes are scaled by the initial carrying capacity except in trials where K varies (T12 trials) and in trials with episodic events (T9 trials). In these cases P_t and P_{min} are scaled by what the population size had been if no catch was taken in the management period. The T9 trials are not mentioned in CLA06, but in previous specifications (IWC, 1992, p. 317-318) the T9 trials are also scaled by the no-catch population size. Therefore we follow this specification here. All statistics are computed by version 9 of the MANRES program (received from Andre Punt in January 2006).

1. Total catch distribution
   - median of the 400 simulations (average of 200th and 201st value)
   - 5% value (20th)
   - 95% value (381st)
   - mean
2. Final population size
   - median
   - 5% value
   - 95% value
3. Lowest minimum population over 100 years distribution
   - median
   - 5% value
   - lowest (1st) value
4. Average annual catch variation (AAV)

$$AAV = \{\sum_{i=1}^{400}\sum_{t=0}^{98}|C_{i,t+1} - C_{i,t}|\}/\{\sum_{i=1}^{400}\sum_{t=0}^{98}C_{i,t}\}, \quad (7)$$

   where $C_{i,t}$ is the catch in year t for simulation number i.
5. Continuing catch distribution, as defined in CLA06.
   - median
   - 5% value
   - 95% value

6. RPL=realised protection level=lowest stock size for which a catch is set
    - median
    - 5% value
7. RR=relative recovery=stock level in the year when the zero catch trajectory reaches 54%
    - median
    - 5% value

3 Results of simulation trials

The results are divided into three parts. Section 3.1 displays the results of the trials in Table 2 in form of tables and trajectory plots. The results of the response curve trials are plotted in Section 3.2. Both these Sections present results for a time horizon of 100 years. Finally, Section 3.3 shows results from the trials in Table 2 for a horizon of 300 years, comparing them with the corresponding results for 100 years.

3.1 Results of trials in Table 2

The results of the trials in Table 2 for a time horizon of 100 years are given in Table 7, as requested in CLA06. The results for the CLA-version alpha.0.78 with $\alpha = 0.4015$ are very similar to the results in Allison (2002), who used $\alpha = 0.4020$.

Figures 1-43 gives trajectory plots for the mean, 5% and 95% of the population size, and the mean and the two first simulations of the catches, as specified in CLA06.

Table 7. Results of the trials from Table 2

	Init.	MSYR	CLA	Old	Total catch values				Final pop. size			Low population			100*Cont.Catch			AAV	RPL		Rel.Rec.	
Trial	pop.	(%)	Variant	TL	5%	Med	95%	Mean	5%	Med	95%	Min	5%	Med	5%	Med	95%		5%	Med	5%	Med
T1-D1	0.990	1	alpha.0.78	0.72	0.740	0.873	1.040	0.877	0.609	0.722	0.806	0.514	0.599	0.684	0.123	0.424	0.600	0.042	0.599	0.684		
	0.990	1	alpha.0.75	0.66	0.841	0.994	1.176	0.995	0.532	0.659	0.763	0.430	0.524	0.624	0.113	0.462	0.600	0.044	0.525	0.624		
Base	0.990	1	alpha.0.72	0.60	0.927	1.099	1.288	1.101	0.463	0.598	0.718	0.355	0.450	0.563	0.088	0.469	0.600	0.046	0.452	0.563		
case	0.990	1	gamma.0.69	0.54	1.000	1.188	1.398	1.192	0.389	0.543	0.680	0.275	0.374	0.495	0.000	0.380	0.599	0.061	0.374	0.496		
	0.990	1	gamma.0.66	0.48	1.081	1.280	1.485	1.281	0.324	0.477	0.625	0.177	0.280	0.399	0.000	0.219	0.580	0.103	0.280	0.399		
T1-D1.5	0.990	1.5	alpha.0.78	0.72	0.790	0.943	1.122	0.949	0.680	0.792	0.879	0.587	0.662	0.734	0.192	0.600	0.900	0.040	0.662	0.734		
	0.990	1.5	alpha.0.75	0.66	0.904	1.087	1.290	1.091	0.603	0.736	0.847	0.504	0.588	0.683	0.214	0.689	0.900	0.041	0.590	0.683		
	0.990	1.5	alpha.0.72	0.60	1.009	1.220	1.428	1.220	0.528	0.675	0.810	0.426	0.519	0.625	0.223	0.744	0.900	0.043	0.522	0.625		
	0.990	1.5	gamma.0.69	0.54	1.109	1.351	1.580	1.348	0.439	0.614	0.774	0.329	0.423	0.546	0.112	0.691	0.900	0.058	0.425	0.547		
	0.990	1.5	gamma.0.66	0.48	1.209	1.474	1.710	1.470	0.341	0.533	0.712	0.204	0.313	0.429	0.000	0.528	0.897	0.099	0.313	0.431		
T1-D4	0.990	4	alpha.0.78	0.72	0.927	1.144	1.397	1.150	0.844	0.913	0.973	0.743	0.796	0.849	0.347	0.983	1.638	0.035	0.796	0.850		
	0.990	4	alpha.0.75	0.66	1.121	1.388	1.665	1.386	0.805	0.883	0.959	0.704	0.760	0.820	0.494	1.281	1.951	0.036	0.760	0.820		
	0.990	4	alpha.0.72	0.60	1.325	1.623	1.922	1.620	0.767	0.850	0.940	0.662	0.721	0.789	0.679	1.555	2.199	0.036	0.721	0.789		
	0.990	4	gamma.0.69	0.54	1.597	1.972	2.309	1.969	0.678	0.794	0.917	0.552	0.627	0.721	0.843	1.918	2.401	0.048	0.631	0.721		
	0.990	4	gamma.0.66	0.48	2.028	2.482	2.769	2.457	0.521	0.695	0.865	0.344	0.440	0.577	0.942	2.110	2.401	0.085	0.447	0.580		
T1-D7	0.990	7	alpha.0.78	0.72	0.948	1.185	1.467	1.194	0.911	0.952	0.989	0.781	0.841	0.896	0.323	1.024	1.778	0.033	0.841	0.896		
	0.990	7	alpha.0.75	0.66	1.168	1.469	1.798	1.472	0.888	0.934	0.983	0.743	0.811	0.873	0.473	1.380	2.130	0.034	0.811	0.873		
	0.990	7	alpha.0.72	0.60	1.417	1.754	2.128	1.759	0.865	0.914	0.974	0.704	0.779	0.850	0.692	1.738	2.512	0.034	0.779	0.850		
	0.990	7	gamma.0.69	0.54	1.772	2.248	2.708	2.239	0.807	0.881	0.963	0.589	0.699	0.792	0.949	2.256	3.306	0.046	0.699	0.792		
	0.990	7	gamma.0.66	0.48	2.490	3.091	3.694	3.099	0.660	0.809	0.930	0.306	0.485	0.659	1.401	3.042	4.157	0.081	0.485	0.660		

continuing

Trial	Init. pop.	MSYR (%)	CLA Variant	Old TL	Total catch values				Final pop. size			Low population			100*Cont.Catch			AAV	RPL		Rel.Rec.	
					5%	Med	95%	Mean	5%	Med	95%	Min	5%	Med	5%	Med	95%		5%	Med	5%	Med
T1-R1	0.300	1	alpha.0.78	0.72	0.034	0.095	0.198	0.103	0.543	0.616	0.660	0.300	0.300	0.300	0.000	0.092	0.336	0.082	0.343	0.388	0.450	0.497
	0.300	1	alpha.0.75	0.66	0.076	0.157	0.272	0.164	0.483	0.567	0.625	0.300	0.300	0.300	0.000	0.124	0.399	0.075	0.300	0.372	0.404	0.460
	0.300	1	alpha.0.72	0.60	0.128	0.221	0.347	0.228	0.418	0.510	0.581	0.292	0.300	0.300	0.000	0.136	0.438	0.072	0.300	0.345	0.355	0.417
	0.300	1	gamma.0.69	0.54	0.133	0.235	0.375	0.244	0.387	0.496	0.576	0.265	0.297	0.300	0.000	0.116	0.478	0.090	0.297	0.343	0.328	0.405
	0.300	1	gamma.0.66	0.48	0.172	0.283	0.440	0.288	0.331	0.451	0.541	0.192	0.241	0.300	0.000	0.054	0.487	0.132	0.241	0.309	0.265	0.366
T1-R1.5	0.300	1.5	alpha.0.78	0.72	0.074	0.170	0.315	0.180	0.664	0.758	0.815	0.300	0.300	0.300	0.042	0.254	0.572	0.063	0.352	0.421	0.478	0.512
	0.300	1.5	alpha.0.75	0.66	0.135	0.253	0.415	0.260	0.593	0.705	0.777	0.300	0.300	0.300	0.061	0.319	0.664	0.060	0.300	0.397	0.443	0.485
	0.300	1.5	alpha.0.72	0.60	0.202	0.337	0.507	0.341	0.516	0.640	0.726	0.300	0.300	0.300	0.063	0.364	0.735	0.058	0.300	0.374	0.403	0.452
	0.300	1.5	gamma.0.69	0.54	0.214	0.371	0.568	0.377	0.461	0.611	0.717	0.293	0.300	0.300	0.010	0.385	0.830	0.074	0.300	0.374	0.379	0.439
	0.300	1.5	gamma.0.66	0.48	0.253	0.440	0.653	0.444	0.373	0.538	0.668	0.231	0.273	0.300	0.000	0.367	0.853	0.115	0.276	0.349	0.317	0.396
T1-R4	0.300	4	alpha.0.78	0.72	0.258	0.494	0.794	0.508	0.892	0.945	0.986	0.300	0.300	0.300	0.183	0.659	1.203	0.041	0.396	0.600	0.533	0.540
	0.300	4	alpha.0.75	0.66	0.407	0.692	0.990	0.698	0.864	0.919	0.971	0.300	0.300	0.300	0.342	0.946	1.472	0.037	0.300	0.525	0.519	0.539
	0.300	4	alpha.0.72	0.60	0.593	0.900	1.193	0.902	0.831	0.888	0.950	0.300	0.300	0.300	0.580	1.238	1.691	0.034	0.300	0.456	0.498	0.534
	0.300	4	gamma.0.69	0.54	0.726	1.119	1.455	1.110	0.771	0.847	0.935	0.300	0.300	0.300	0.714	1.555	2.106	0.043	0.300	0.456	0.490	0.535
	0.300	4	gamma.0.66	0.48	1.057	1.519	1.809	1.488	0.630	0.752	0.890	0.300	0.300	0.300	0.928	2.040	2.401	0.072	0.300	0.456	0.457	0.529
T1-R7	0.300	7	alpha.0.78	0.72	0.198	0.451	0.855	0.481	0.952	0.988	1.002	0.300	0.300	0.300	0.000	0.305	1.078	0.056	0.558	0.830	0.540	0.540
	0.300	7	alpha.0.75	0.66	0.376	0.701	1.148	0.727	0.931	0.974	1.000	0.300	0.300	0.300	0.042	0.587	1.471	0.048	0.448	0.690	0.535	0.540
	0.300	7	alpha.0.72	0.60	0.612	1.004	1.456	1.017	0.906	0.955	0.996	0.300	0.300	0.300	0.199	1.012	1.905	0.041	0.300	0.558	0.523	0.540
	0.300	7	gamma.0.69	0.54	0.738	1.285	1.827	1.294	0.869	0.933	0.995	0.300	0.300	0.300	0.229	1.401	2.440	0.050	0.300	0.690	0.523	0.540
	0.300	7	gamma.0.66	0.48	1.221	1.986	2.532	1.946	0.781	0.867	0.985	0.300	0.300	0.300	0.570	2.396	3.556	0.074	0.300	0.690	0.505	0.540
T1-S1	0.600	1	alpha.0.78	0.72	0.329	0.440	0.591	0.447	0.614	0.712	0.782	0.520	0.568	0.600	0.071	0.339	0.600	0.039	0.568	0.600		
	0.600	1	alpha.0.75	0.66	0.417	0.557	0.731	0.563	0.519	0.641	0.730	0.441	0.500	0.570	0.068	0.386	0.600	0.039	0.500	0.570		
	0.600	1	alpha.0.72	0.60	0.500	0.663	0.851	0.667	0.432	0.566	0.674	0.358	0.424	0.507	0.047	0.381	0.596	0.040	0.426	0.507		
	0.600	1	gamma.0.69	0.54	0.537	0.720	0.925	0.725	0.368	0.517	0.644	0.274	0.348	0.450	0.000	0.300	0.580	0.056	0.350	0.450		
	0.600	1	gamma.0.66	0.48	0.598	0.777	0.992	0.784	0.290	0.446	0.579	0.167	0.251	0.359	0.000	0.143	0.540	0.099	0.252	0.359		

continuing

Trial	Init. pop.	MSYR (%)	CLA Variant	Old TL	Total catch values 5%	Med	95%	Mean	Final pop. size 5%	Med	95%	Low population Min	5%	Med	100*Cont.Catch 5%	Med	95%	AAV	RPL 5%	Med	Rel.Rec. 5%	Med
T1-S1.5	0.600	1.5	alpha.0.78	0.72	0.380	0.521	0.701	0.529	0.716	0.812	0.885	0.561	0.600	0.600	0.145	0.510	0.900	0.036	0.600	0.600		
	0.600	1.5	alpha.0.75	0.66	0.496	0.674	0.874	0.676	0.621	0.742	0.843	0.521	0.573	0.600	0.169	0.637	0.900	0.036	0.573	0.600		
	0.600	1.5	alpha.0.72	0.60	0.603	0.814	1.012	0.811	0.532	0.667	0.793	0.444	0.511	0.582	0.183	0.711	0.900	0.036	0.511	0.582		
	0.600	1.5	gamma.0.69	0.54	0.660	0.906	1.135	0.904	0.434	0.604	0.760	0.334	0.411	0.514	0.071	0.679	0.900	0.051	0.416	0.514		
	0.600	1.5	gamma.0.66	0.48	0.716	0.986	1.248	0.987	0.324	0.522	0.702	0.211	0.289	0.403	0.000	0.489	0.892	0.093	0.290	0.403		
T1-S4	0.600	4	alpha.0.78	0.72	0.452	0.646	0.914	0.664	0.896	0.952	0.990	0.600	0.600	0.600	0.132	0.584	1.204	0.037	0.600	0.600		
	0.600	4	alpha.0.75	0.66	0.647	0.915	1.206	0.923	0.856	0.918	0.981	0.600	0.600	0.600	0.230	0.944	1.553	0.034	0.600	0.600		
	0.600	4	alpha.0.72	0.60	0.869	1.203	1.492	1.200	0.812	0.877	0.963	0.582	0.600	0.600	0.437	1.321	1.894	0.032	0.600	0.600		
	0.600	4	gamma.0.69	0.54	1.093	1.523	1.846	1.503	0.739	0.829	0.946	0.528	0.599	0.600	0.570	1.707	2.317	0.043	0.599	0.600		
	0.600	4	gamma.0.66	0.48	1.515	2.023	2.339	1.988	0.595	0.727	0.894	0.358	0.485	0.600	0.779	2.101	2.401	0.076	0.485	0.600		
T2-D1	0.990	1	alpha.0.78	0.72	0.423	0.518	0.630	0.521	0.787	0.852	0.906	0.729	0.786	0.834	0.107	0.355	0.600	0.037	0.786	0.834		
	0.990	1	alpha.0.75	0.66	0.501	0.618	0.749	0.619	0.737	0.813	0.883	0.678	0.737	0.797	0.133	0.448	0.600	0.038	0.738	0.798		
Survey	0.990	1	alpha.0.72	0.60	0.580	0.718	0.856	0.717	0.686	0.770	0.855	0.627	0.686	0.757	0.163	0.528	0.600	0.039	0.687	0.758		
Bias 0.5	0.990	1	gamma.0.69	0.54	0.672	0.850	1.018	0.847	0.611	0.715	0.832	0.535	0.610	0.697	0.140	0.568	0.600	0.052	0.611	0.698		
	0.990	1	gamma.0.66	0.48	0.808	1.041	1.231	1.031	0.497	0.632	0.792	0.390	0.490	0.601	0.037	0.525	0.600	0.090	0.494	0.602		
T2-D1.5	0.990	1.5	alpha.0.78	0.72	0.442	0.539	0.660	0.543	0.838	0.894	0.946	0.787	0.831	0.867	0.132	0.415	0.762	0.036	0.831	0.868		
	0.990	1.5	alpha.0.75	0.66	0.523	0.650	0.787	0.651	0.796	0.862	0.929	0.741	0.791	0.838	0.177	0.531	0.869	0.037	0.792	0.838		
Survey	0.990	1.5	alpha.0.72	0.60	0.610	0.759	0.909	0.759	0.755	0.825	0.908	0.696	0.751	0.806	0.224	0.638	0.900	0.038	0.752	0.806		
Bias 0.5	0.990	1.5	gamma.0.69	0.54	0.722	0.917	1.097	0.914	0.682	0.778	0.891	0.608	0.677	0.754	0.231	0.751	0.900	0.050	0.678	0.754		
	0.990	1.5	gamma.0.66	0.48	0.896	1.157	1.357	1.150	0.565	0.692	0.849	0.440	0.554	0.658	0.163	0.787	0.900	0.087	0.557	0.658		
T2-R1	0.300	1	alpha.0.78	0.72	0.000	0.000	0.014	0.002	0.675	0.685	0.685	0.300	0.300	0.300	0.000	0.000	0.020	0.189	0.455		0.534	0.540
	0.300	1	alpha.0.75	0.66	0.000	0.001	0.045	0.008	0.654	0.685	0.685	0.300	0.300	0.300	0.000	0.000	0.078	0.157	0.420	0.636	0.519	0.540
Survey	0.300	1	alpha.0.72	0.60	0.000	0.017	0.089	0.026	0.623	0.673	0.685	0.300	0.300	0.300	0.000	0.000	0.139	0.133	0.388	0.437	0.496	0.534
Bias 0.5	0.300	1	gamma.0.69	0.54	0.000	0.012	0.090	0.024	0.620	0.677	0.685	0.300	0.300	0.300	0.000	0.000	0.157	0.159	0.404	0.473	0.493	0.537
	0.300	1	gamma.0.66	0.48	0.000	0.019	0.126	0.035	0.594	0.671	0.685	0.300	0.300	0.300	0.000	0.000	0.211	0.194	0.399	0.471	0.468	0.534

continuing

Trial	Init. pop.	MSYR (%)	CLA Variant	Old TL	Total catch values				Final pop. size			Low population			100*Cont.Catch			AAV	RPL		Rel.Rec.	
					5%	Med	95%	Mean	5%	Med	95%	Min	5%	Med	5%	Med	95%		5%	Med	5%	Med
T2-R1.5	0.300	1.5	alpha.0.78	0.72	0.000	0.001	0.051	0.010	0.829	0.857	0.858	0.300	0.300	0.300	0.000	0.000	0.147	0.132	0.500	0.812	0.538	0.540
	0.300	1.5	alpha.0.75	0.66	0.000	0.016	0.098	0.028	0.801	0.849	0.858	0.300	0.300	0.300	0.000	0.018	0.224	0.116	0.472	0.586	0.529	0.540
Survey	0.300	1.5	alpha.0.72	0.60	0.004	0.052	0.164	0.063	0.766	0.830	0.856	0.300	0.300	0.300	0.000	0.065	0.295	0.099	0.421	0.500	0.513	0.536
Bias 0.5	0.300	1.5	gamma.0.69	0.54	0.001	0.051	0.179	0.064	0.753	0.830	0.857	0.300	0.300	0.300	0.000	0.051	0.349	0.120	0.446	0.528	0.511	0.538
	0.300	1.5	gamma.0.66	0.48	0.002	0.076	0.248	0.091	0.711	0.815	0.857	0.300	0.300	0.300	0.000	0.059	0.522	0.154	0.446	0.528	0.492	0.536
T3-D1	0.990	1	alpha.0.78	0.72	0.955	1.092	1.260	1.096	0.484	0.607	0.702	0.361	0.456	0.555	0.081	0.345	0.600	0.047	0.456	0.555		
	0.990	1	alpha.0.75	0.66	1.045	1.190	1.362	1.195	0.410	0.543	0.646	0.274	0.381	0.487	0.038	0.313	0.590	0.050	0.381	0.488		
Survey	0.990	1	alpha.0.72	0.60	1.116	1.272	1.446	1.274	0.343	0.478	0.591	0.199	0.309	0.420	0.000	0.270	0.569	0.053	0.309	0.421		
Bias 1.5	0.990	1	gamma.0.69	0.54	1.158	1.313	1.481	1.315	0.298	0.437	0.547	0.140	0.247	0.357	0.000	0.175	0.540	0.070	0.247	0.357		
	0.990	1	gamma.0.66	0.48	1.213	1.347	1.513	1.353	0.253	0.378	0.478	0.089	0.160	0.276	0.000	0.037	0.477	0.114	0.161	0.278		
T3-D1.5	0.990	1.5	alpha.0.78	0.72	1.036	1.206	1.404	1.210	0.554	0.695	0.804	0.423	0.515	0.611	0.172	0.570	0.900	0.044	0.515	0.611		
	0.990	1.5	alpha.0.75	0.66	1.135	1.328	1.537	1.331	0.467	0.627	0.756	0.325	0.433	0.542	0.132	0.569	0.900	0.046	0.433	0.542		
Survey	0.990	1.5	alpha.0.72	0.60	1.224	1.423	1.640	1.427	0.393	0.555	0.701	0.244	0.351	0.474	0.079	0.526	0.888	0.049	0.351	0.474		
Bias 1.5	0.990	1.5	gamma.0.69	0.54	1.267	1.475	1.691	1.479	0.333	0.506	0.660	0.157	0.275	0.400	0.000	0.422	0.858	0.066	0.275	0.400		
	0.990	1.5	gamma.0.66	0.48	1.306	1.508	1.718	1.512	0.287	0.435	0.578	0.092	0.170	0.297	0.000	0.280	0.804	0.111	0.175	0.299		
T3-R1	0.300	1	alpha.0.78	0.72	0.147	0.230	0.349	0.237	0.414	0.504	0.569	0.284	0.300	0.300	0.009	0.182	0.478	0.060	0.300	0.343	0.366	0.420
	0.300	1	alpha.0.75	0.66	0.205	0.300	0.427	0.306	0.341	0.435	0.511	0.239	0.276	0.300	0.000	0.164	0.452	0.061	0.276	0.314	0.303	0.367
Survey	0.300	1	alpha.0.72	0.60	0.264	0.357	0.486	0.365	0.273	0.372	0.450	0.173	0.223	0.288	0.000	0.123	0.406	0.062	0.223	0.288	0.242	0.310
Bias 1.5	0.300	1	gamma.0.69	0.54	0.271	0.370	0.505	0.378	0.240	0.351	0.434	0.147	0.185	0.260	0.000	0.063	0.403	0.081	0.185	0.260	0.204	0.286
	0.300	1	gamma.0.66	0.48	0.294	0.395	0.524	0.400	0.187	0.304	0.396	0.080	0.131	0.209	0.000	0.000	0.389	0.128	0.131	0.210	0.146	0.245
T3-R1.5	0.300	1.5	alpha.0.78	0.72	0.218	0.343	0.510	0.350	0.517	0.636	0.715	0.300	0.300	0.300	0.118	0.427	0.812	0.049	0.300	0.374	0.405	0.454
	0.300	1.5	alpha.0.75	0.66	0.289	0.429	0.608	0.435	0.422	0.556	0.650	0.268	0.300	0.300	0.086	0.434	0.813	0.050	0.300	0.352	0.352	0.410
Survey	0.300	1.5	alpha.0.72	0.60	0.346	0.497	0.670	0.502	0.336	0.473	0.578	0.219	0.271	0.300	0.019	0.369	0.753	0.052	0.271	0.300	0.295	0.361
Bias 1.5	0.300	1.5	gamma.0.69	0.54	0.350	0.514	0.712	0.523	0.297	0.438	0.552	0.170	0.219	0.300	0.000	0.310	0.754	0.071	0.219	0.300	0.258	0.333
	0.300	1.5	gamma.0.66	0.48	0.380	0.526	0.710	0.537	0.239	0.377	0.486	0.088	0.152	0.235	0.000	0.163	0.722	0.118	0.152	0.237	0.187	0.274

continuing

Trial	Init. pop.	MSYR (%)	CLA Variant	Old TL	Total catch values 5%	Med	95%	Mean	Final pop. size 5%	Med	95%	Low population Min	5%	Med	100*Cont.Catch 5%	Med	95%	AAV	RPL 5%	Med	Rel.Rec. 5%	Med
T3-S1	0.600	1	alpha.0.78	0.72	0.514	0.643	0.814	0.652	0.463	0.581	0.667	0.376	0.436	0.515	0.067	0.363	0.598	0.037	0.436	0.515		
	0.600	1	alpha.0.75	0.66	0.598	0.746	0.921	0.751	0.367	0.497	0.600	0.269	0.345	0.437	0.018	0.309	0.573	0.040	0.345	0.437		
Survey	0.600	1	alpha.0.72	0.60	0.667	0.821	0.994	0.824	0.295	0.426	0.533	0.187	0.269	0.368	0.000	0.223	0.529	0.043	0.270	0.368		
Bias 1.5	0.600	1	gamma.0.69	0.54	0.686	0.835	1.013	0.840	0.250	0.391	0.496	0.121	0.206	0.310	0.000	0.105	0.484	0.061	0.206	0.310		
	0.600	1	gamma.0.66	0.48	0.729	0.847	1.009	0.853	0.208	0.336	0.434	0.075	0.143	0.238	0.000	0.000	0.436	0.106	0.143	0.239		
T3-S1.5	0.600	1.5	alpha.0.78	0.72	0.604	0.781	0.974	0.783	0.558	0.686	0.791	0.447	0.515	0.588	0.183	0.651	0.900	0.034	0.515	0.588		
	0.600	1.5	alpha.0.75	0.66	0.712	0.913	1.118	0.914	0.448	0.595	0.729	0.347	0.417	0.511	0.139	0.638	0.900	0.036	0.418	0.511		
Survey	0.600	1.5	alpha.0.72	0.60	0.785	1.006	1.218	1.004	0.354	0.510	0.662	0.245	0.329	0.433	0.050	0.542	0.879	0.039	0.329	0.433		
Bias 1.5	0.600	1.5	gamma.0.69	0.54	0.798	1.014	1.248	1.024	0.288	0.465	0.626	0.151	0.246	0.361	0.000	0.385	0.842	0.057	0.246	0.361		
	0.600	1.5	gamma.0.66	0.48	0.810	1.010	1.224	1.017	0.253	0.401	0.546	0.092	0.158	0.264	0.000	0.186	0.772	0.102	0.158	0.264		
T4-R1	0.050	1	alpha.0.78	0.72	0.000	0.000	0.000	0.000	0.202	0.202	0.202	0.050	0.050	0.050	0.000	0.000	0.000	0.000				
	0.050	1	alpha.0.75	0.66	0.000	0.000	0.000	0.000	0.202	0.202	0.202	0.050	0.050	0.050	0.000	0.000	0.000	0.400				
Init.	0.050	1	alpha.0.72	0.60	0.000	0.000	0.000	0.000	0.202	0.202	0.202	0.050	0.050	0.050	0.000	0.000	0.000	0.250				
pop. 0.05K	0.050	1	gamma.0.69	0.54	0.000	0.000	0.000	0.000	0.202	0.202	0.202	0.050	0.050	0.050	0.000	0.000	0.000	0.251				
	0.050	1	gamma.0.66	0.48	0.000	0.000	0.000	0.000	0.202	0.202	0.202	0.050	0.050	0.050	0.000	0.000	0.000	0.238				
T4-R1.5	0.050	1.5	alpha.0.78	0.72	0.000	0.000	0.000	0.000	0.309	0.309	0.309	0.050	0.050	0.050	0.000	0.000	0.000	0.000				
	0.050	1.5	alpha.0.75	0.66	0.000	0.000	0.000	0.000	0.309	0.309	0.309	0.050	0.050	0.050	0.000	0.000	0.000	0.228				
Init.	0.050	1.5	alpha.0.72	0.60	0.000	0.000	0.014	0.002	0.296	0.309	0.309	0.050	0.050	0.050	0.000	0.000	0.041	0.177	0.186			
pop. 0.05K	0.050	1.5	gamma.0.69	0.54	0.000	0.000	0.012	0.001	0.300	0.309	0.309	0.050	0.050	0.050	0.000	0.000	0.022	0.217	0.211			
	0.050	1.5	gamma.0.66	0.48	0.000	0.000	0.020	0.002	0.294	0.309	0.309	0.050	0.050	0.050	0.000	0.000	0.007	0.250	0.211			
T6-R1	0.300	1	alpha.0.78	0.72	0.156	0.224	0.315	0.228	0.444	0.512	0.561	0.299	0.300	0.300	0.059	0.229	0.464	0.043	0.300	0.343	0.395	0.432
	0.300	1	alpha.0.75	0.66	0.208	0.293	0.400	0.296	0.371	0.450	0.510	0.276	0.300	0.300	0.057	0.263	0.491	0.043	0.300	0.300	0.344	0.390
Historic	0.300	1	alpha.0.72	0.60	0.263	0.356	0.470	0.359	0.301	0.388	0.456	0.240	0.275	0.300	0.039	0.268	0.469	0.043	0.275	0.300	0.294	0.346
catch in	0.300	1	gamma.0.69	0.54	0.277	0.389	0.522	0.392	0.251	0.350	0.431	0.186	0.228	0.288	0.000	0.230	0.448	0.059	0.228	0.288	0.252	0.313
error	0.300	1	gamma.0.66	0.48	0.309	0.425	0.568	0.429	0.189	0.293	0.378	0.107	0.157	0.229	0.000	0.118	0.400	0.102	0.158	0.230	0.188	0.258

continuing

Trial	Init. pop.	MSYR (%)	CLA Variant	Old TL	Total catch values				Final pop. size			Low population			100*Cont.Catch			AAV	RPL		Rel.Rec.	
					5%	Med	95%	Mean	5%	Med	95%	Min	5%	Med	5%	Med	95%		5%	Med	5%	Med
T6-R1.5	0.300	1.5	alpha.0.78	0.72	0.219	0.312	0.428	0.316	0.577	0.659	0.717	0.300	0.300	0.300	0.179	0.439	0.671	0.036	0.300	0.352	0.425	0.463
	0.300	1.5	alpha.0.75	0.66	0.286	0.405	0.530	0.404	0.488	0.585	0.658	0.296	0.300	0.300	0.206	0.524	0.784	0.035	0.300	0.300	0.386	0.431
Historic	0.300	1.5	alpha.0.72	0.60	0.351	0.487	0.617	0.485	0.404	0.505	0.596	0.268	0.300	0.300	0.203	0.570	0.807	0.036	0.300	0.300	0.345	0.396
catch in	0.300	1.5	gamma.0.69	0.54	0.377	0.546	0.704	0.543	0.324	0.438	0.555	0.233	0.278	0.300	0.115	0.567	0.793	0.050	0.278	0.300	0.307	0.364
error	0.300	1.5	gamma.0.66	0.48	0.406	0.592	0.771	0.592	0.218	0.346	0.482	0.145	0.189	0.265	0.000	0.430	0.724	0.091	0.189	0.265	0.241	0.306
T6-R4	0.300	4	alpha.0.78	0.72	0.526	0.670	0.821	0.669	0.892	0.916	0.943	0.300	0.300	0.300	0.682	0.993	1.247	0.026	0.300	0.396	0.490	0.522
	0.300	4	alpha.0.75	0.66	0.697	0.855	1.013	0.857	0.863	0.893	0.922	0.300	0.300	0.300	0.944	1.222	1.517	0.025	0.300	0.300	0.468	0.510
Historic	0.300	4	alpha.0.72	0.60	0.876	1.038	1.207	1.038	0.830	0.867	0.896	0.300	0.300	0.300	1.161	1.442	1.781	0.025	0.300	0.300	0.442	0.493
catch in	0.300	4	gamma.0.69	0.54	1.099	1.302	1.510	1.300	0.747	0.814	0.859	0.300	0.300	0.300	1.369	1.824	2.288	0.035	0.300	0.300	0.417	0.481
error	0.300	4	gamma.0.66	0.48	1.410	1.682	1.910	1.673	0.548	0.685	0.783	0.208	0.296	0.300	1.559	2.160	2.401	0.066	0.296	0.300	0.353	0.442
T9-D1	0.990	1	alpha.0.78	0.72	0.432	0.999	1.636	1.010	0.535	0.755	0.911	0.089	0.524	0.701				0.043				
	0.990	1	alpha.0.75	0.66	0.487	1.140	1.903	1.164	0.468	0.698	0.877	0.084	0.460	0.647				0.044				
Episodic	0.990	1	alpha.0.72	0.60	0.523	1.269	2.154	1.306	0.406	0.643	0.841	0.079	0.392	0.594				0.045				
events	0.990	1	gamma.0.69	0.54	0.580	1.418	2.518	1.487	0.360	0.590	0.797	0.068	0.345	0.534				0.059				
	0.990	1	gamma.0.66	0.48	0.710	1.593	2.836	1.683	0.305	0.515	0.721	0.047	0.276	0.437				0.097				
T9-D1.5	0.990	1.5	alpha.0.78	0.72	0.456	0.998	1.546	1.004	0.589	0.814	0.945	0.093	0.562	0.738				0.043				
	0.990	1.5	alpha.0.75	0.66	0.518	1.159	1.821	1.170	0.529	0.767	0.925	0.088	0.505	0.688				0.044				
Episodic	0.990	1.5	alpha.0.72	0.60	0.567	1.319	2.095	1.329	0.461	0.713	0.899	0.083	0.428	0.634				0.045				
events	0.990	1.5	gamma.0.69	0.54	0.648	1.520	2.513	1.544	0.407	0.666	0.871	0.071	0.379	0.578				0.058				
	0.990	1.5	gamma.0.66	0.48	0.778	1.762	2.977	1.814	0.338	0.585	0.799	0.049	0.297	0.480				0.095				
T9-D4	0.990	4	alpha.0.78	0.72	0.628	1.042	1.399	1.029	0.765	0.928	1.002	0.034	0.666	0.823				0.040				
	0.990	4	alpha.0.75	0.66	0.716	1.250	1.683	1.236	0.713	0.905	0.994	0.028	0.611	0.785				0.041				
Episodic	0.990	4	alpha.0.72	0.60	0.803	1.465	2.004	1.446	0.649	0.881	0.987	0.023	0.549	0.743				0.042				
events	0.990	4	gamma.0.69	0.54	0.964	1.786	2.517	1.775	0.602	0.850	0.976	0.086	0.489	0.694				0.055				
	0.990	4	gamma.0.66	0.48	1.135	2.350	3.435	2.336	0.494	0.778	0.941	0.060	0.365	0.576				0.091				

continuing

Trial	Init. pop.	MSYR (%)	CLA Variant	Old TL	Total catch values 5%	Med	95%	Mean	Final pop. size 5%	Med	95%	Low population Min	5%	Med	100*Cont.Catch 5%	Med	95%	AAV	RPL 5%	Med	Rel.Rec. 5%	Med
T9-R1	0.300	1	alpha.0.78	0.72	0.000	0.210	0.673	0.269	0.697	0.889	1.000	0.491	0.691	0.865				0.045				
	0.300	1	alpha.0.75	0.66	0.008	0.289	0.826	0.353	0.606	0.836	0.977	0.152	0.597	0.800				0.044				
Episodic	0.300	1	alpha.0.72	0.60	0.037	0.367	0.960	0.438	0.516	0.768	0.922	0.122	0.500	0.724				0.045				
events	0.300	1	gamma.0.69	0.54	0.034	0.416	1.171	0.512	0.460	0.720	0.918	0.100	0.435	0.678				0.055				
	0.300	1	gamma.0.66	0.48	0.050	0.516	1.433	0.628	0.350	0.611	0.886	0.055	0.347	0.566				0.087				
T9-R1.5	0.300	1.5	alpha.0.78	0.72	0.002	0.289	0.759	0.326	0.716	0.911	0.995	0.517	0.702	0.877				0.043				
	0.300	1.5	alpha.0.75	0.66	0.019	0.393	0.915	0.426	0.638	0.864	0.971	0.198	0.621	0.818				0.042				
Episodic	0.300	1.5	alpha.0.72	0.60	0.051	0.490	1.078	0.529	0.548	0.797	0.923	0.148	0.525	0.751				0.042				
events	0.300	1.5	gamma.0.69	0.54	0.051	0.567	1.318	0.627	0.494	0.768	0.918	0.105	0.477	0.706				0.052				
	0.300	1.5	gamma.0.66	0.48	0.077	0.701	1.659	0.786	0.389	0.670	0.884	0.073	0.369	0.597				0.082				
T9-R4	0.300	4	alpha.0.78	0.72	0.090	0.438	0.865	0.451	0.841	0.959	1.003	0.598	0.787	0.915				0.049				
	0.300	4	alpha.0.75	0.66	0.147	0.638	1.098	0.626	0.778	0.939	1.003	0.450	0.713	0.872				0.045				
Episodic	0.300	4	alpha.0.72	0.60	0.217	0.833	1.346	0.817	0.719	0.916	1.000	0.029	0.633	0.816				0.041				
events	0.300	4	gamma.0.69	0.54	0.251	1.026	1.682	1.006	0.669	0.889	0.991	0.062	0.567	0.779				0.050				
	0.300	4	gamma.0.66	0.48	0.333	1.434	2.291	1.389	0.584	0.831	0.953	0.112	0.473	0.696				0.077				
T12A-D1	0.990	1	alpha.0.78	0.72	0.805	0.970	1.160	0.975	0.484	0.583	0.674	0.406	0.484	0.581				0.039				
	0.990	1	alpha.0.75	0.66	0.895	1.085	1.281	1.091	0.412	0.518	0.621	0.333	0.412	0.515				0.042				
K	0.990	1	alpha.0.72	0.60	0.985	1.189	1.395	1.191	0.349	0.458	0.571	0.270	0.349	0.452				0.044				
doubles	0.990	1	gamma.0.69	0.54	1.046	1.267	1.497	1.269	0.285	0.404	0.524	0.208	0.279	0.392				0.060				
	0.990	1	gamma.0.66	0.48	1.108	1.322	1.545	1.330	0.224	0.342	0.464	0.133	0.220	0.327				0.102				
T12A-D1.5	0.990	1.5	alpha.0.78	0.72	0.916	1.120	1.331	1.126	0.532	0.635	0.733	0.452	0.532	0.628				0.036				
	0.990	1.5	alpha.0.75	0.66	1.030	1.272	1.486	1.268	0.452	0.567	0.678	0.376	0.452	0.560				0.038				
K	0.990	1.5	alpha.0.72	0.60	1.135	1.400	1.603	1.389	0.384	0.500	0.625	0.313	0.384	0.495				0.040				
doubles	0.990	1.5	gamma.0.69	0.54	1.215	1.512	1.744	1.501	0.302	0.427	0.577	0.230	0.299	0.415				0.055				
	0.990	1.5	gamma.0.66	0.48	1.289	1.578	1.837	1.575	0.217	0.351	0.502	0.152	0.211	0.330				0.097				

continuing

Trial	Init. pop.	MSYR (%)	CLA Variant	Old TL	Total catch values				Final pop. size			Low population			100*Cont.Catch			AAV	RPL		Rel.Rec.	
					5%	Med	95%	Mean	5%	Med	95%	Min	5%	Med	5%	Med	95%		5%	Med	5%	Med
T12A-D4	0.990	4	alpha.0.78	0.72	1.429	1.703	2.020	1.705	0.787	0.846	0.896	0.721	0.771	0.821				0.030				
	0.990	4	alpha.0.75	0.66	1.692	1.982	2.317	1.986	0.740	0.811	0.869	0.660	0.724	0.784				0.031				
K	0.990	4	alpha.0.72	0.60	1.936	2.242	2.590	2.245	0.685	0.774	0.839	0.592	0.675	0.745				0.032				
doubles	0.990	4	gamma.0.69	0.54	2.307	2.691	3.064	2.689	0.552	0.684	0.785	0.403	0.544	0.652				0.043				
	0.990	4	gamma.0.66	0.48	2.744	3.159	3.536	3.155	0.335	0.521	0.682	0.175	0.322	0.474				0.079				
T12A-R1	0.300	1	alpha.0.78	0.72	0.041	0.104	0.212	0.113	0.762	0.878	0.952	0.644	0.762	0.877				0.078				
	0.300	1	alpha.0.75	0.66	0.084	0.167	0.287	0.175	0.668	0.798	0.890	0.566	0.668	0.798				0.073				
K	0.300	1	alpha.0.72	0.60	0.138	0.230	0.360	0.238	0.568	0.709	0.817	0.483	0.567	0.707				0.070				
doubles	0.300	1	gamma.0.69	0.54	0.145	0.246	0.394	0.256	0.525	0.684	0.807	0.417	0.520	0.681				0.088				
	0.300	1	gamma.0.66	0.48	0.179	0.292	0.450	0.300	0.445	0.614	0.751	0.306	0.436	0.607				0.131				
T12A-R1.5	0.300	1.5	alpha.0.78	0.72	0.097	0.203	0.357	0.212	0.711	0.835	0.918	0.601	0.711	0.835				0.057				
	0.300	1.5	alpha.0.75	0.66	0.159	0.286	0.452	0.293	0.619	0.758	0.854	0.515	0.619	0.757				0.055				
K	0.300	1.5	alpha.0.72	0.60	0.224	0.368	0.544	0.373	0.521	0.669	0.778	0.449	0.521	0.668				0.055				
doubles	0.300	1.5	gamma.0.69	0.54	0.235	0.413	0.608	0.415	0.458	0.623	0.761	0.374	0.458	0.622				0.070				
	0.300	1.5	gamma.0.66	0.48	0.273	0.480	0.693	0.481	0.365	0.531	0.691	0.269	0.359	0.529				0.111				
T12A-R4	0.300	4	alpha.0.78	0.72	0.553	0.818	1.041	0.807	0.884	0.910	0.937	0.804	0.838	0.884				0.027				
	0.300	4	alpha.0.75	0.66	0.731	1.006	1.220	0.991	0.858	0.889	0.919	0.758	0.793	0.844				0.026				
K	0.300	4	alpha.0.72	0.60	0.925	1.185	1.399	1.173	0.825	0.864	0.898	0.690	0.741	0.796				0.025				
doubles	0.300	4	gamma.0.69	0.54	1.153	1.470	1.716	1.452	0.736	0.806	0.859	0.608	0.661	0.739				0.032				
	0.300	4	gamma.0.66	0.48	1.565	1.912	2.131	1.887	0.528	0.659	0.767	0.420	0.484	0.603				0.058				
T12B-D1	0.990	1	alpha.0.78	0.72	0.677	0.786	0.925	0.793	0.763	0.867	0.926	0.618	0.668	0.733				0.044				
	0.990	1	alpha.0.75	0.66	0.775	0.903	1.069	0.908	0.691	0.825	0.906	0.541	0.605	0.686				0.046				
K	0.990	1	alpha.0.72	0.60	0.866	1.014	1.179	1.017	0.618	0.777	0.879	0.459	0.543	0.636				0.048				
halves	0.990	1	gamma.0.69	0.54	0.948	1.117	1.305	1.117	0.555	0.738	0.861	0.344	0.458	0.563				0.063				
	0.990	1	gamma.0.66	0.48	1.039	1.230	1.420	1.229	0.477	0.676	0.825	0.232	0.326	0.450				0.105				

continuing

Trial	Init. pop.	MSYR (%)	CLA Variant	Old TL	Total catch values				Final pop. size			Low population			100*Cont.Catch			AAV	RPL		Rel.Rec.	
					5%	Med	95%	Mean	5%	Med	95%	Min	5%	Med	5%	Med	95%		5%	Med	5%	Med
T12B-D1.5	0.990	1.5	alpha.0.78	0.72	0.690	0.808	0.951	0.814	0.824	0.921	0.971	0.669	0.718	0.776				0.043				
	0.990	1.5	alpha.0.75	0.66	0.800	0.937	1.107	0.945	0.762	0.892	0.962	0.612	0.664	0.734				0.045				
K	0.990	1.5	alpha.0.72	0.60	0.906	1.069	1.256	1.073	0.697	0.853	0.949	0.537	0.603	0.688				0.047				
halves	0.990	1.5	gamma.0.69	0.54	1.004	1.208	1.414	1.205	0.627	0.827	0.944	0.415	0.514	0.616				0.061				
	0.990	1.5	gamma.0.66	0.48	1.130	1.360	1.585	1.358	0.538	0.769	0.925	0.282	0.365	0.493				0.102				
T12B-D4	0.990	4	alpha.0.78	0.72	0.704	0.842	1.018	0.849	0.927	0.981	1.001	0.745	0.808	0.863				0.041				
	0.990	4	alpha.0.75	0.66	0.843	1.014	1.232	1.023	0.896	0.972	1.001	0.708	0.773	0.838				0.042				
K	0.990	4	alpha.0.72	0.60	0.995	1.204	1.457	1.210	0.855	0.958	1.000	0.668	0.738	0.810				0.043				
halves	0.990	4	gamma.0.69	0.54	1.171	1.457	1.782	1.463	0.801	0.945	1.006	0.565	0.661	0.746				0.056				
	0.990	4	gamma.0.66	0.48	1.479	1.902	2.261	1.882	0.693	0.915	1.010	0.348	0.470	0.616				0.095				
T12B-R1	0.300	1	alpha.0.78	0.72	0.025	0.084	0.178	0.090	0.847	0.936	0.980	0.733	0.817	0.914				0.088				
	0.300	1	alpha.0.75	0.66	0.068	0.144	0.252	0.150	0.774	0.883	0.949	0.640	0.730	0.848				0.079				
K	0.300	1	alpha.0.72	0.60	0.120	0.208	0.330	0.215	0.688	0.817	0.901	0.559	0.631	0.765				0.074				
halves	0.300	1	gamma.0.69	0.54	0.125	0.221	0.359	0.230	0.647	0.802	0.898	0.503	0.580	0.739				0.093				
	0.300	1	gamma.0.66	0.48	0.155	0.266	0.412	0.273	0.567	0.745	0.856	0.369	0.478	0.662				0.135				
T12B-R1.5	0.300	1.5	alpha.0.78	0.72	0.049	0.131	0.263	0.141	0.872	0.952	0.986	0.738	0.821	0.910				0.074				
	0.300	1.5	alpha.0.75	0.66	0.105	0.210	0.360	0.218	0.811	0.916	0.968	0.667	0.742	0.848				0.067				
K	0.300	1.5	alpha.0.72	0.60	0.173	0.295	0.459	0.301	0.739	0.870	0.941	0.588	0.652	0.774				0.063				
halves	0.300	1.5	gamma.0.69	0.54	0.183	0.323	0.513	0.330	0.690	0.851	0.936	0.516	0.591	0.741				0.081				
	0.300	1.5	gamma.0.66	0.48	0.221	0.390	0.592	0.394	0.593	0.794	0.908	0.361	0.464	0.647				0.122				
T12B-R4	0.300	4	alpha.0.78	0.72	0.103	0.250	0.477	0.266	0.966	0.999	1.005	0.853	0.888	0.933				0.068				
	0.300	4	alpha.0.75	0.66	0.202	0.392	0.665	0.411	0.938	0.994	1.006	0.817	0.850	0.901				0.059				
K	0.300	4	alpha.0.72	0.60	0.341	0.569	0.874	0.583	0.902	0.981	1.007	0.752	0.806	0.863				0.053				
halves	0.300	4	gamma.0.69	0.54	0.384	0.682	1.042	0.697	0.871	0.979	1.011	0.684	0.751	0.827				0.065				
	0.300	4	gamma.0.66	0.48	0.535	0.968	1.393	0.965	0.781	0.957	1.015	0.516	0.622	0.730				0.096				

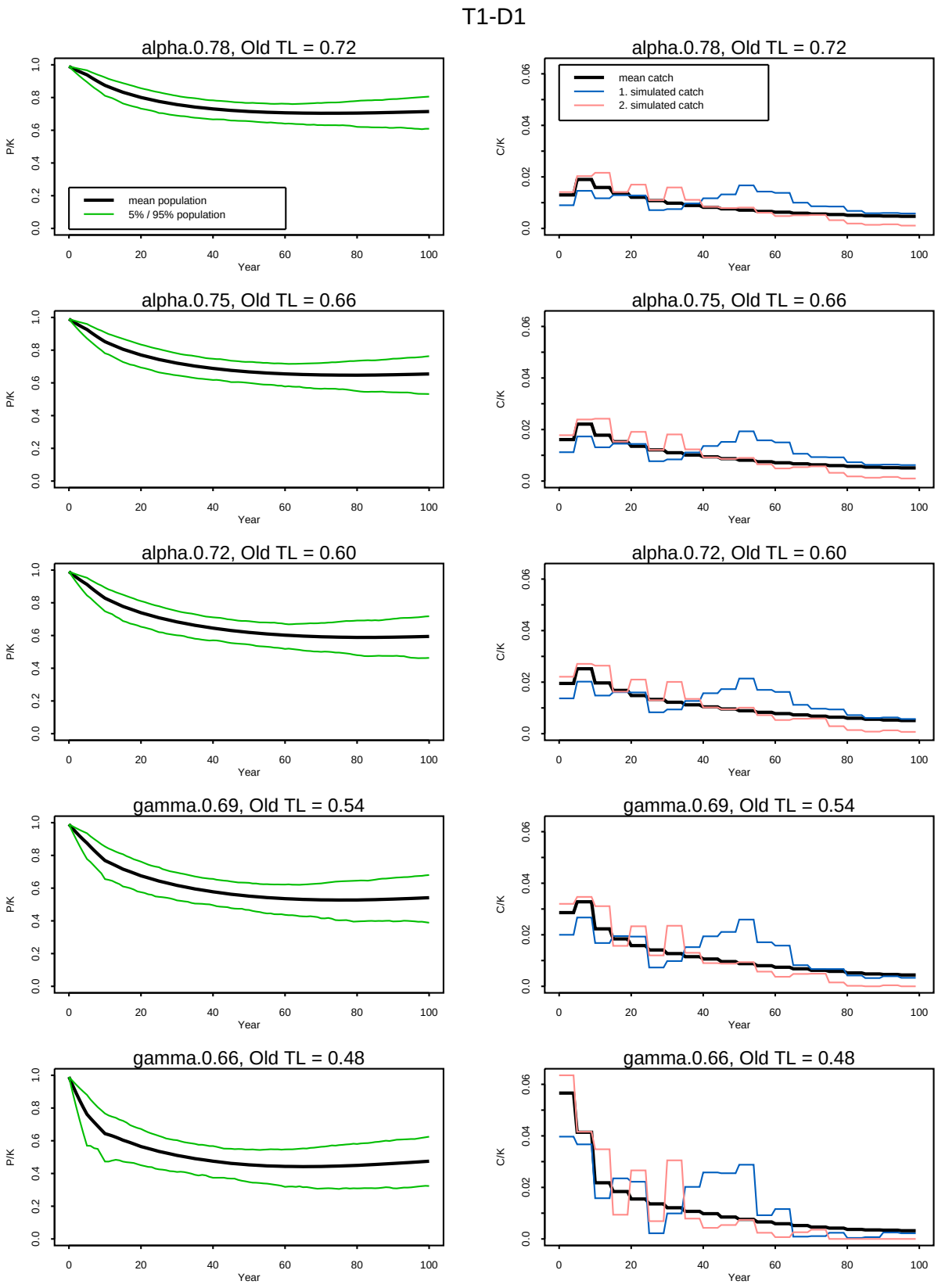


Figure 1. Trial T1-D1. Base case. Population (left) and catch (right) trajectory (left) for the five versions of CLA.

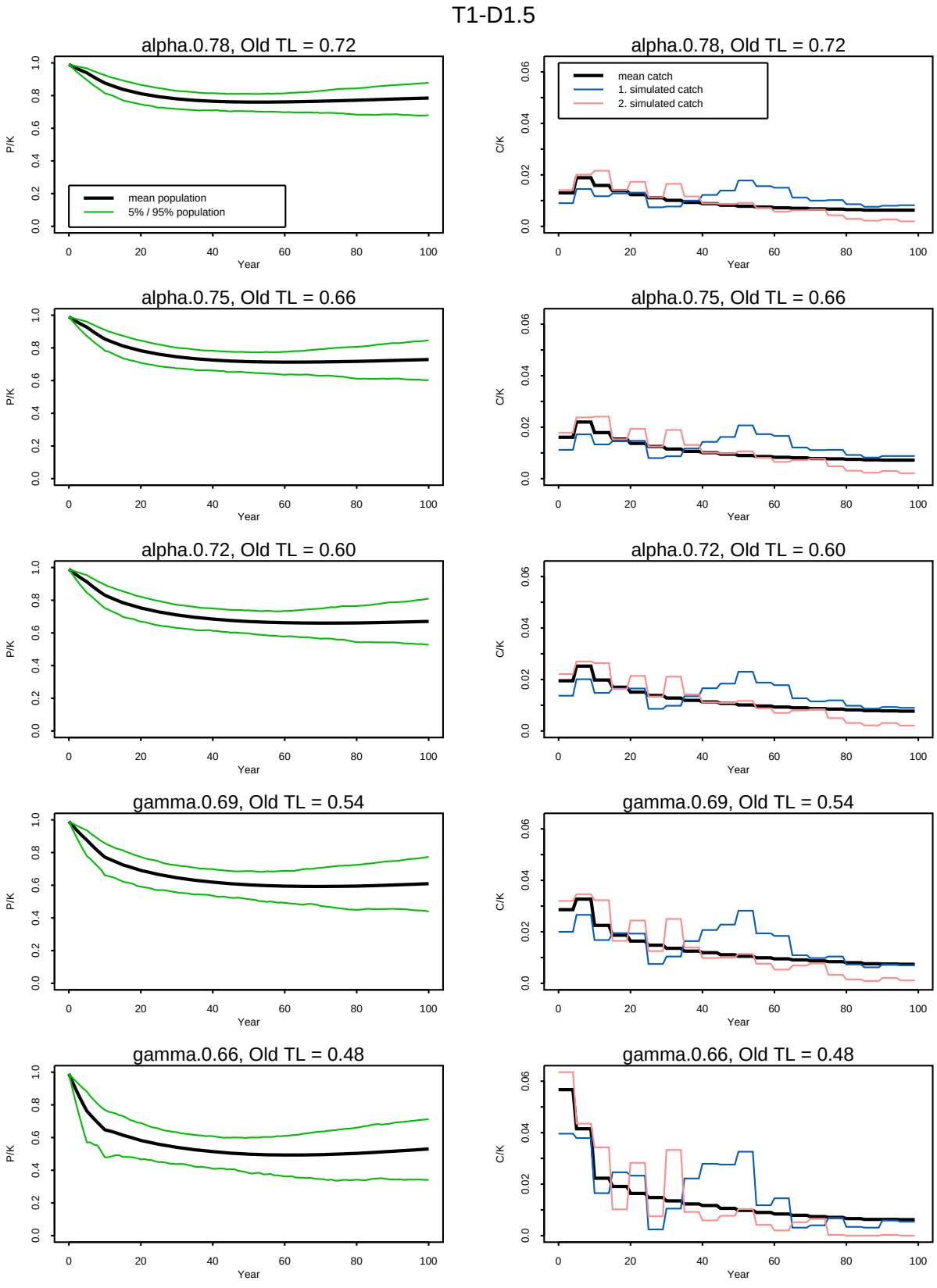


Figure 2. Trial T1-D1.5. Base case.

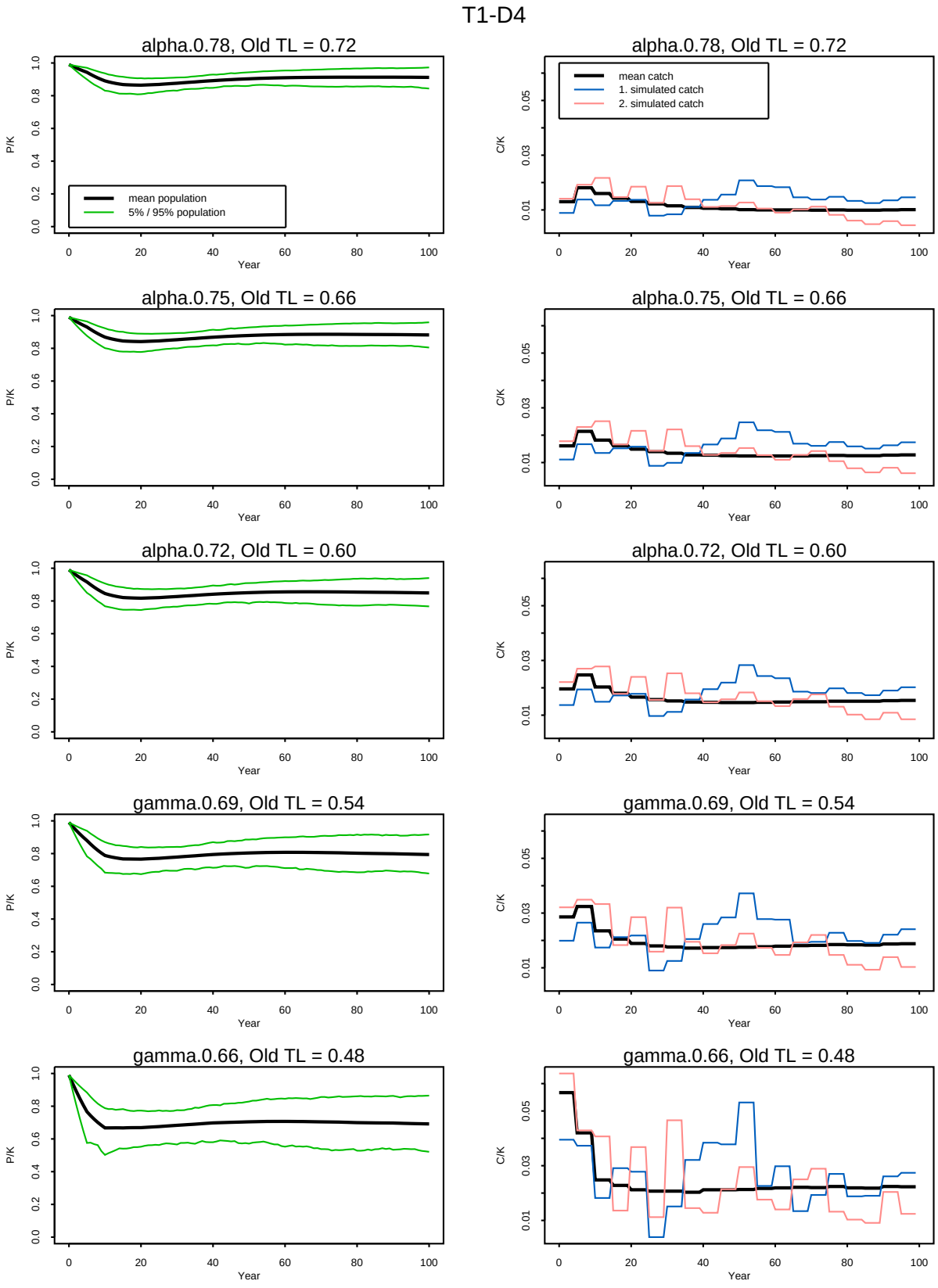


Figure 3. Trial T1-D4. Base case.

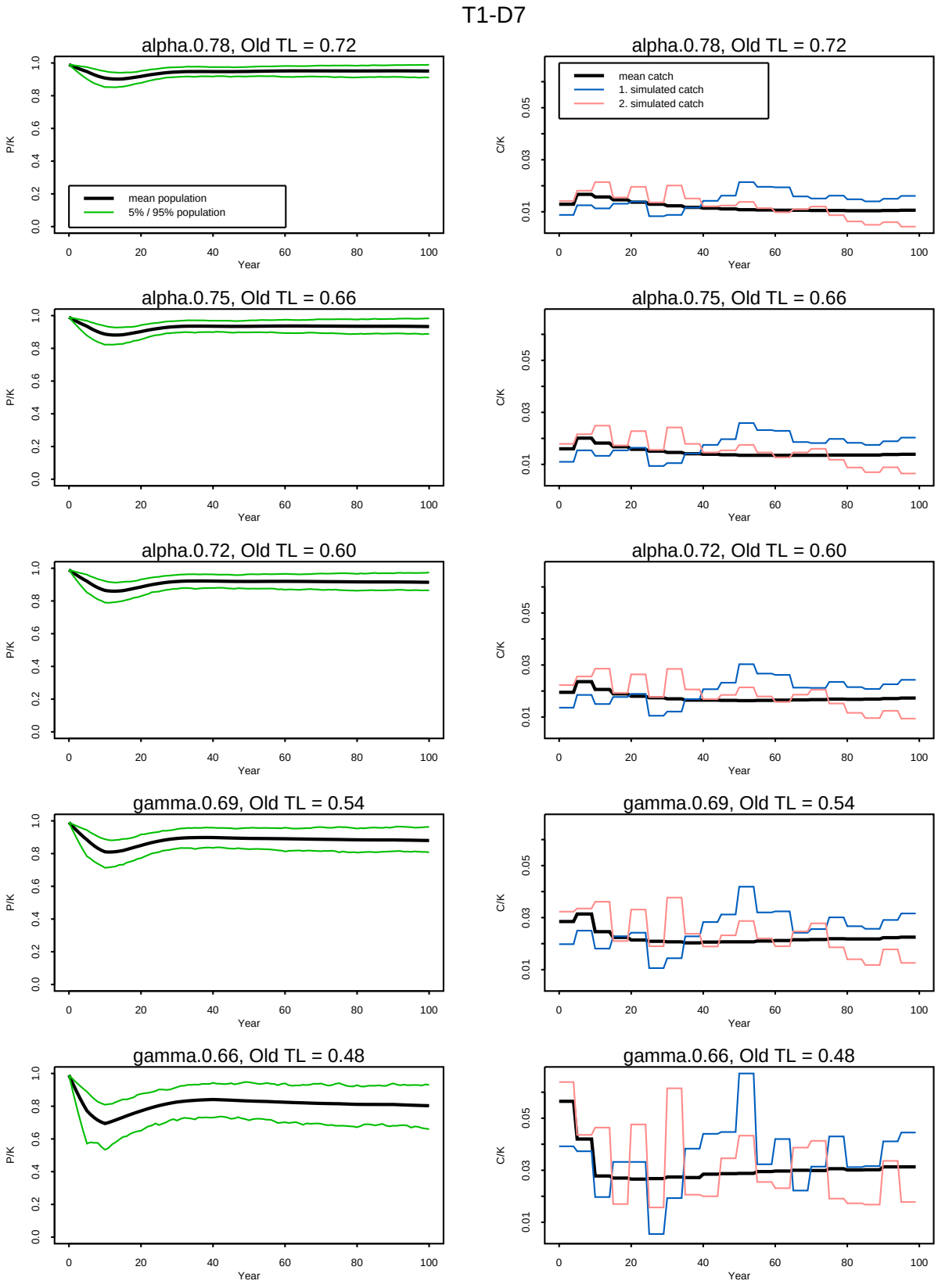


Figure 4. Trial T1-D7. Base case.

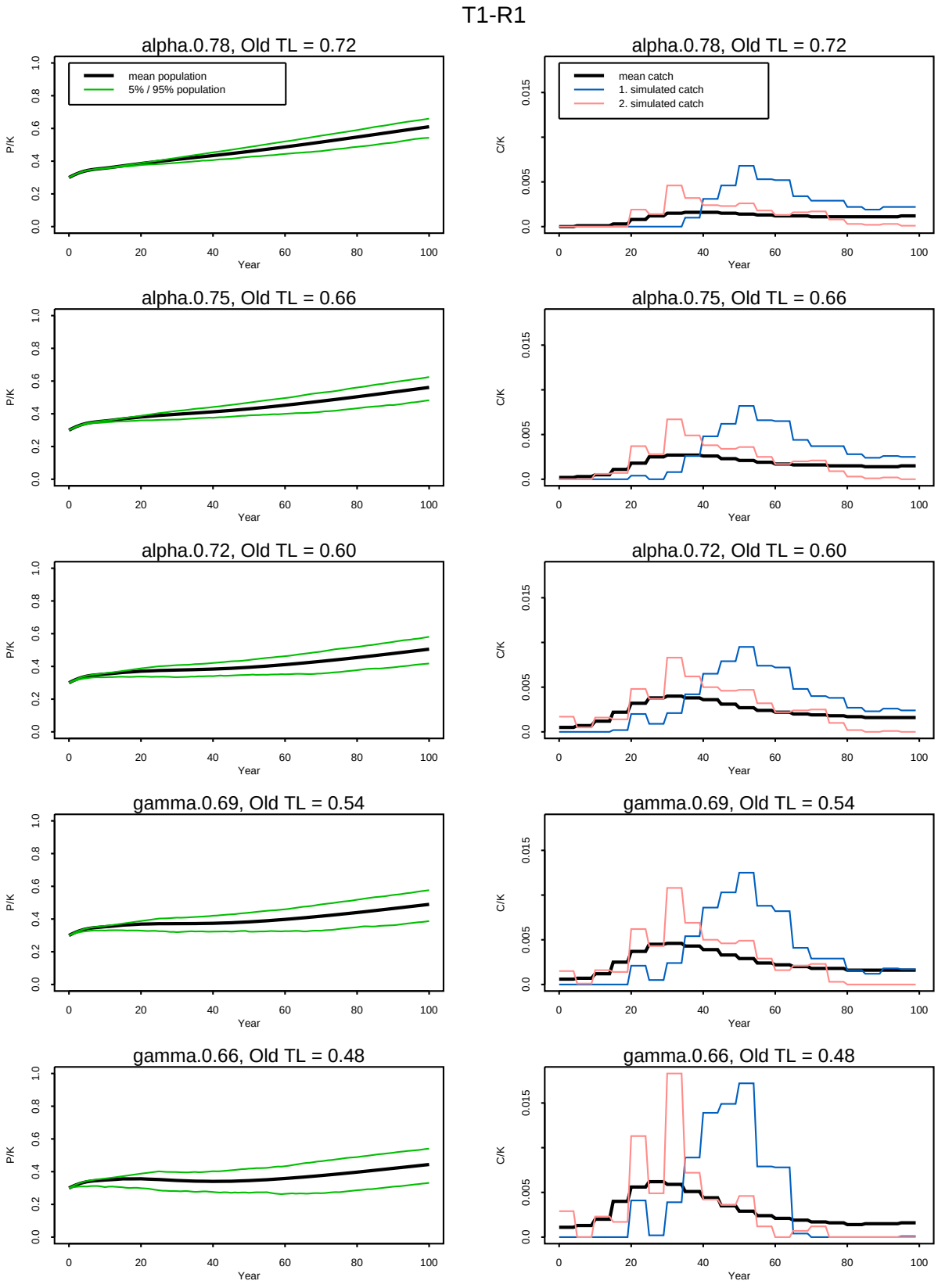


Figure 5. Trial T1-R1. Base case.

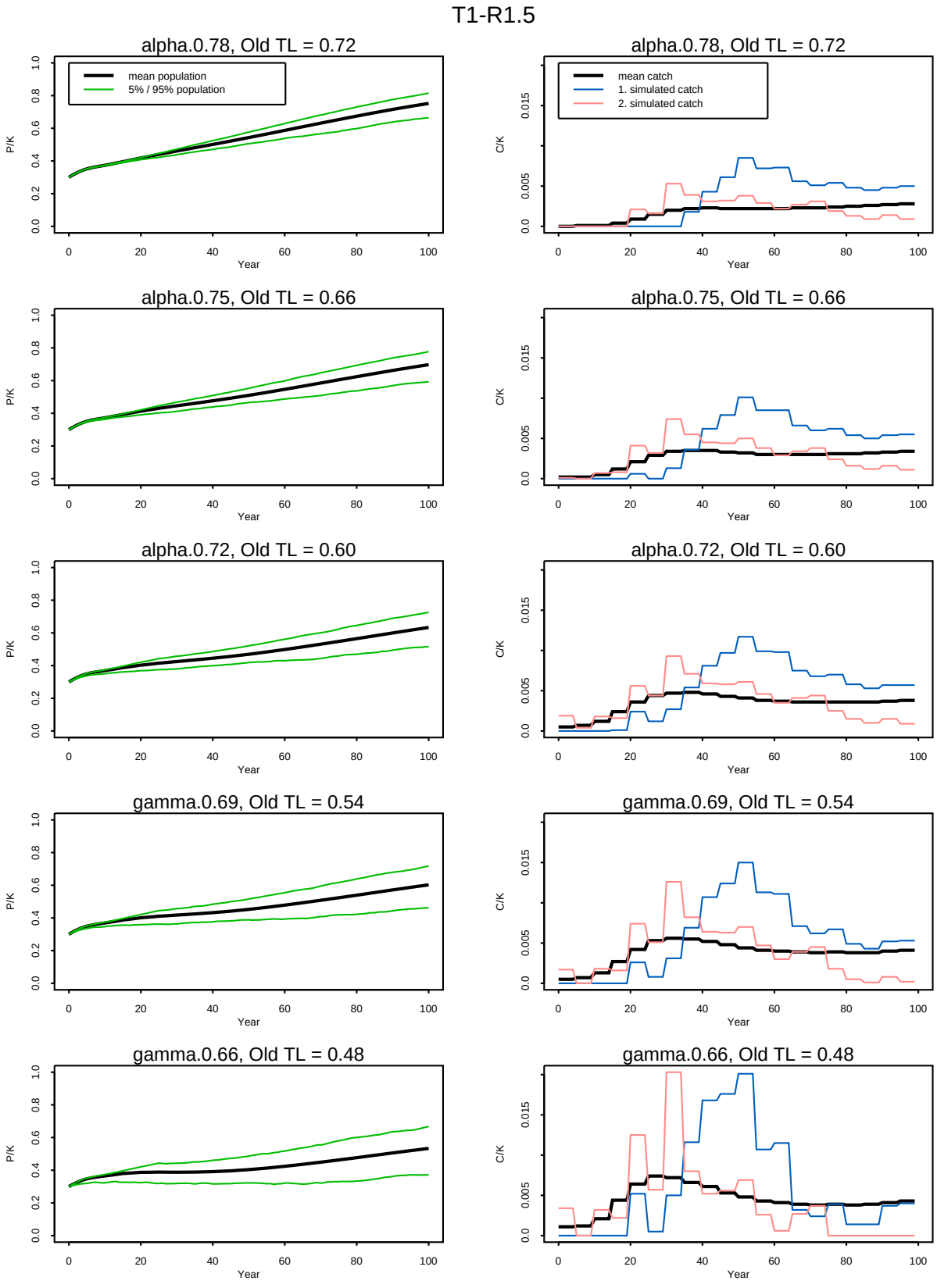


Figure 6. Trial T1-R1.5. Base case.

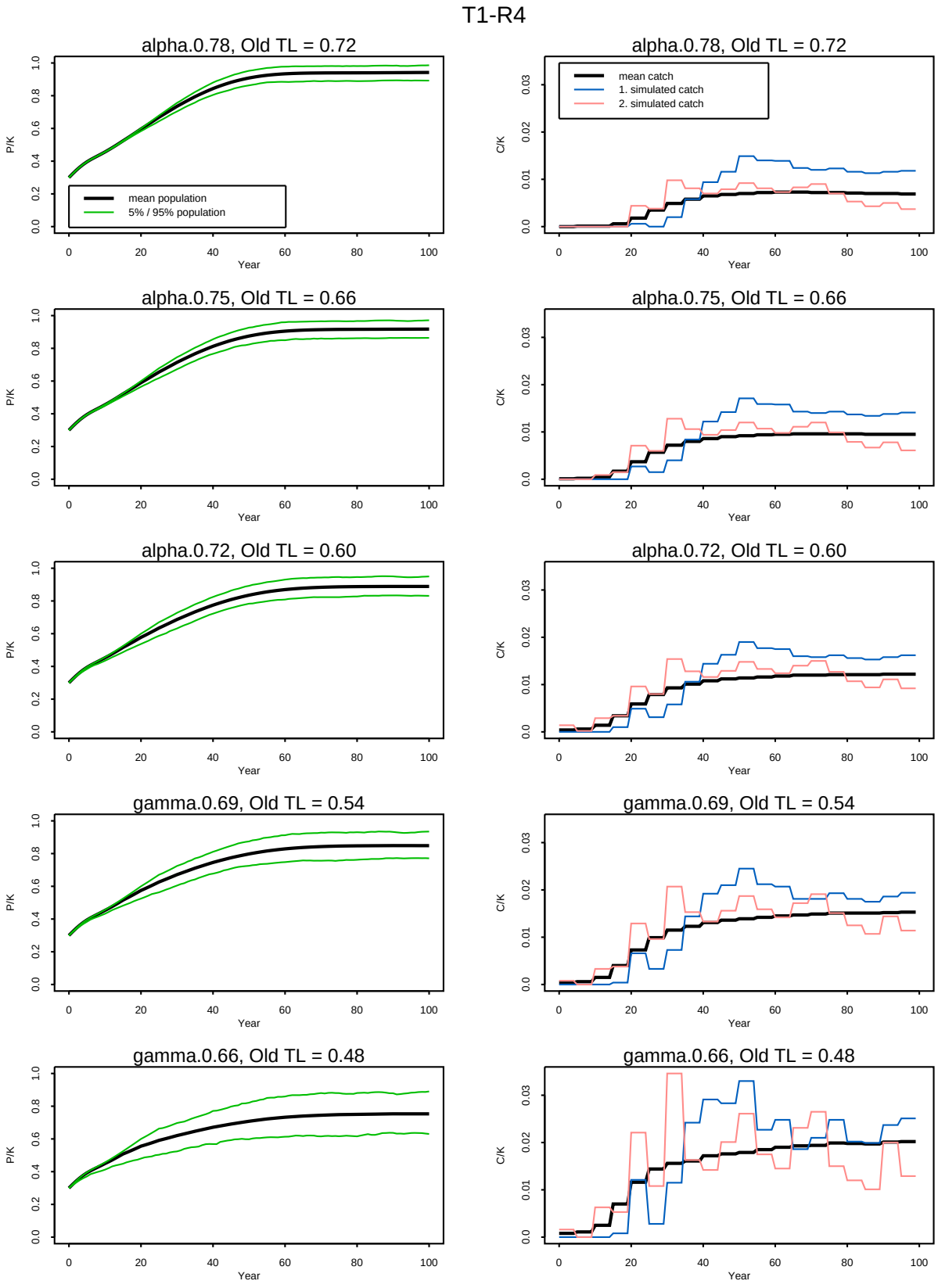


Figure 7. Trial T1-R4. Base case.

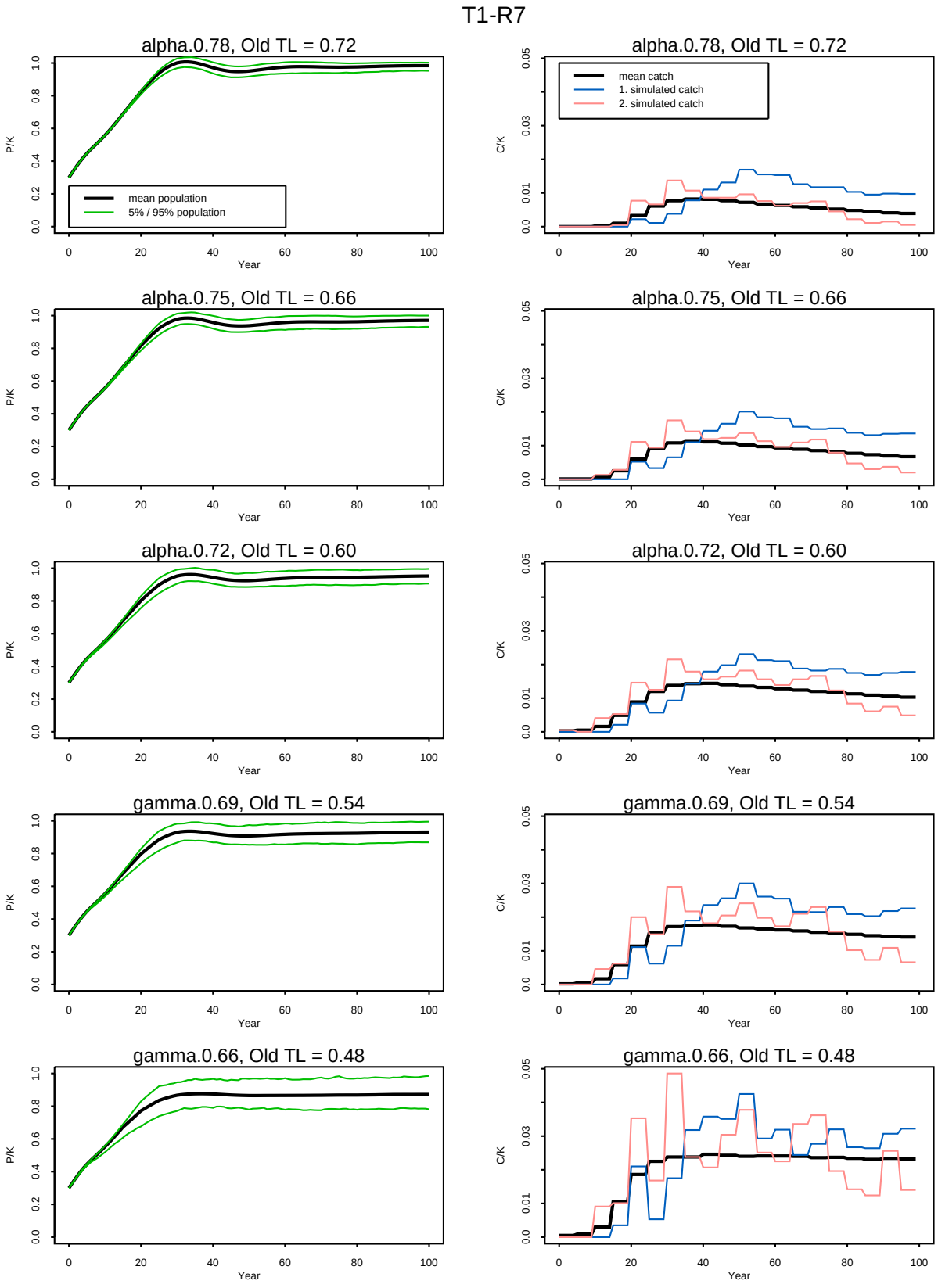


Figure 8. Trial T1-R7. Base case.

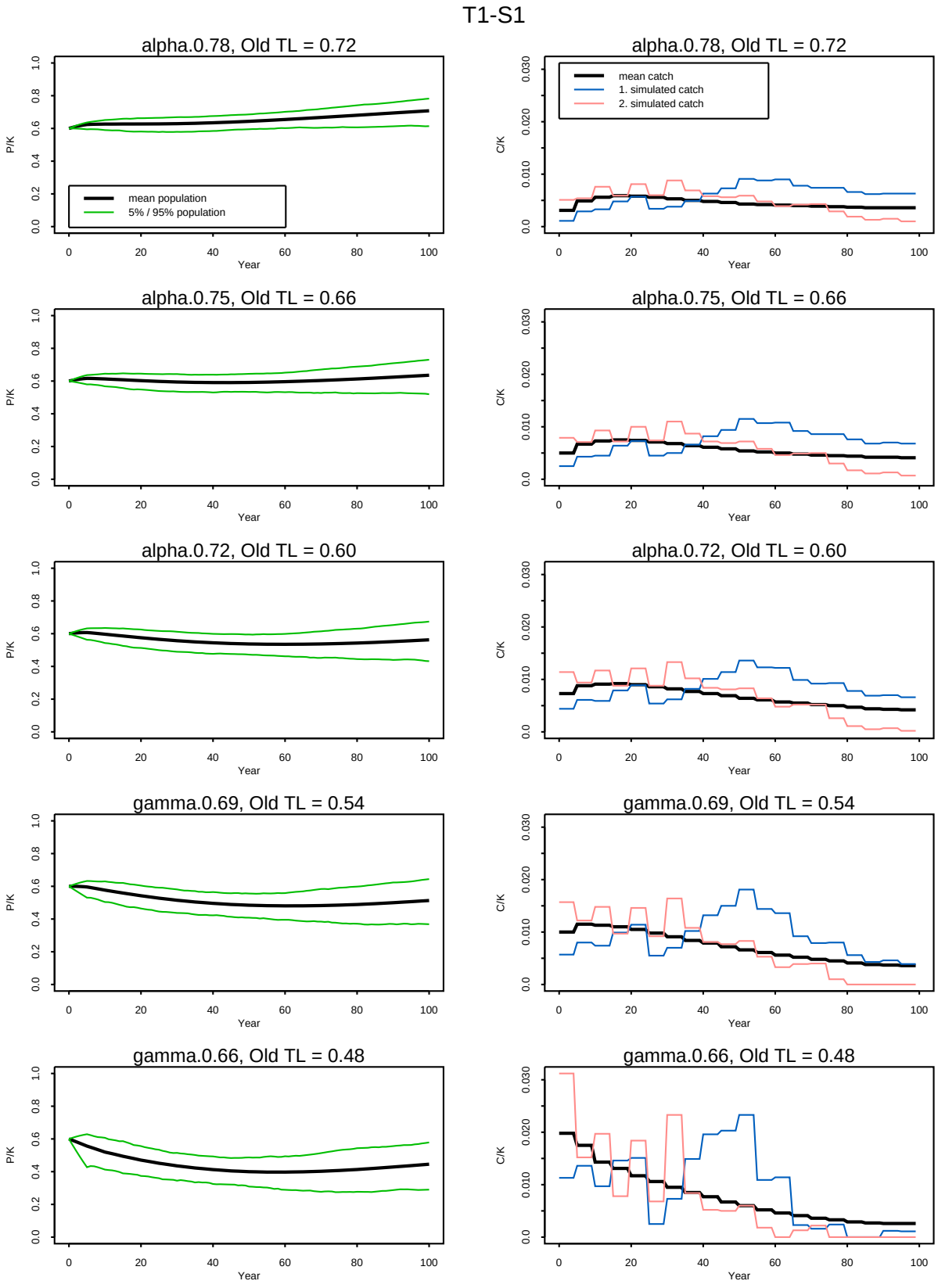


Figure 9. Trial T1-S1. Base case.

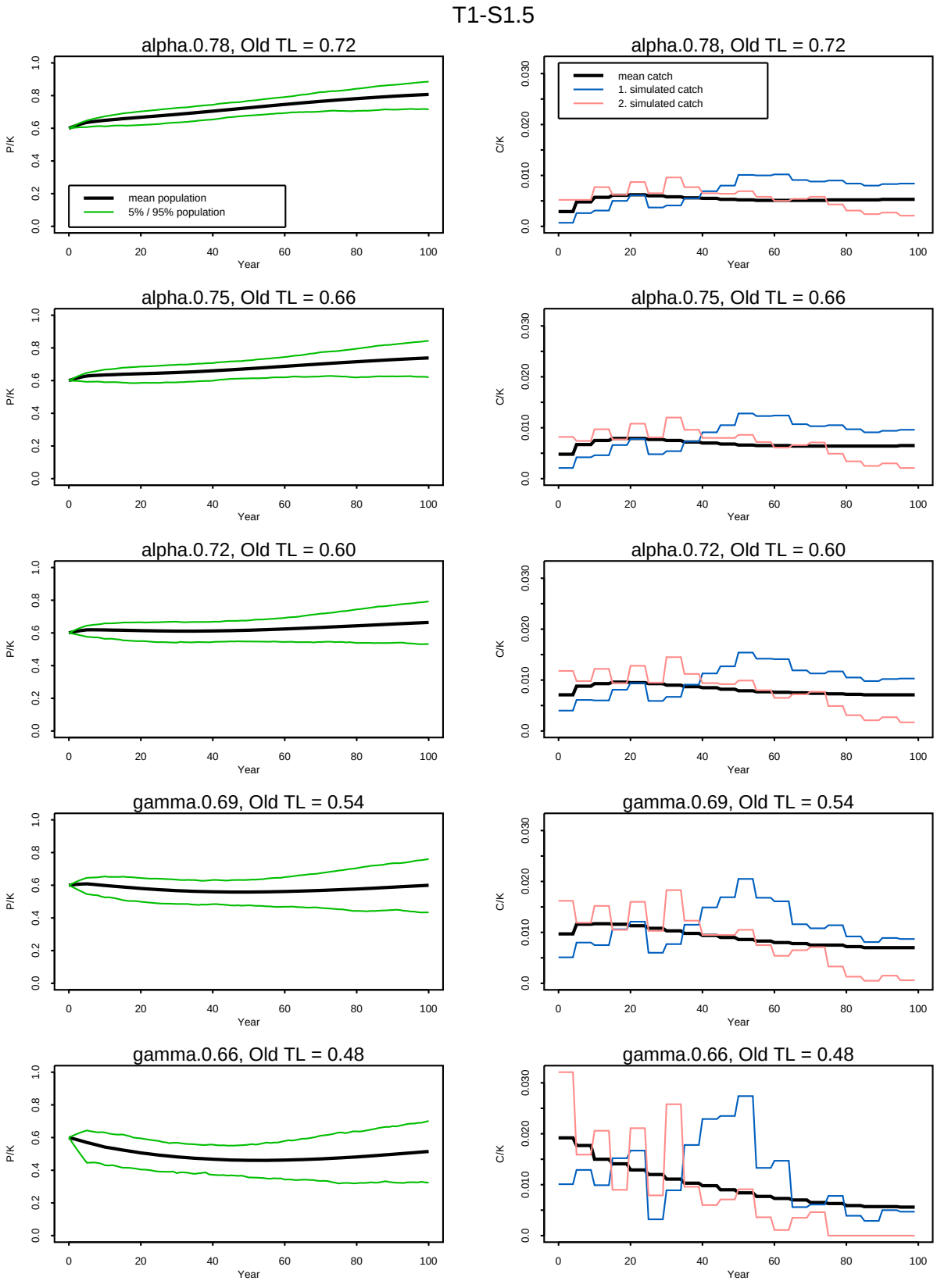


Figure 10. Trial T1-S1.5. Base case.

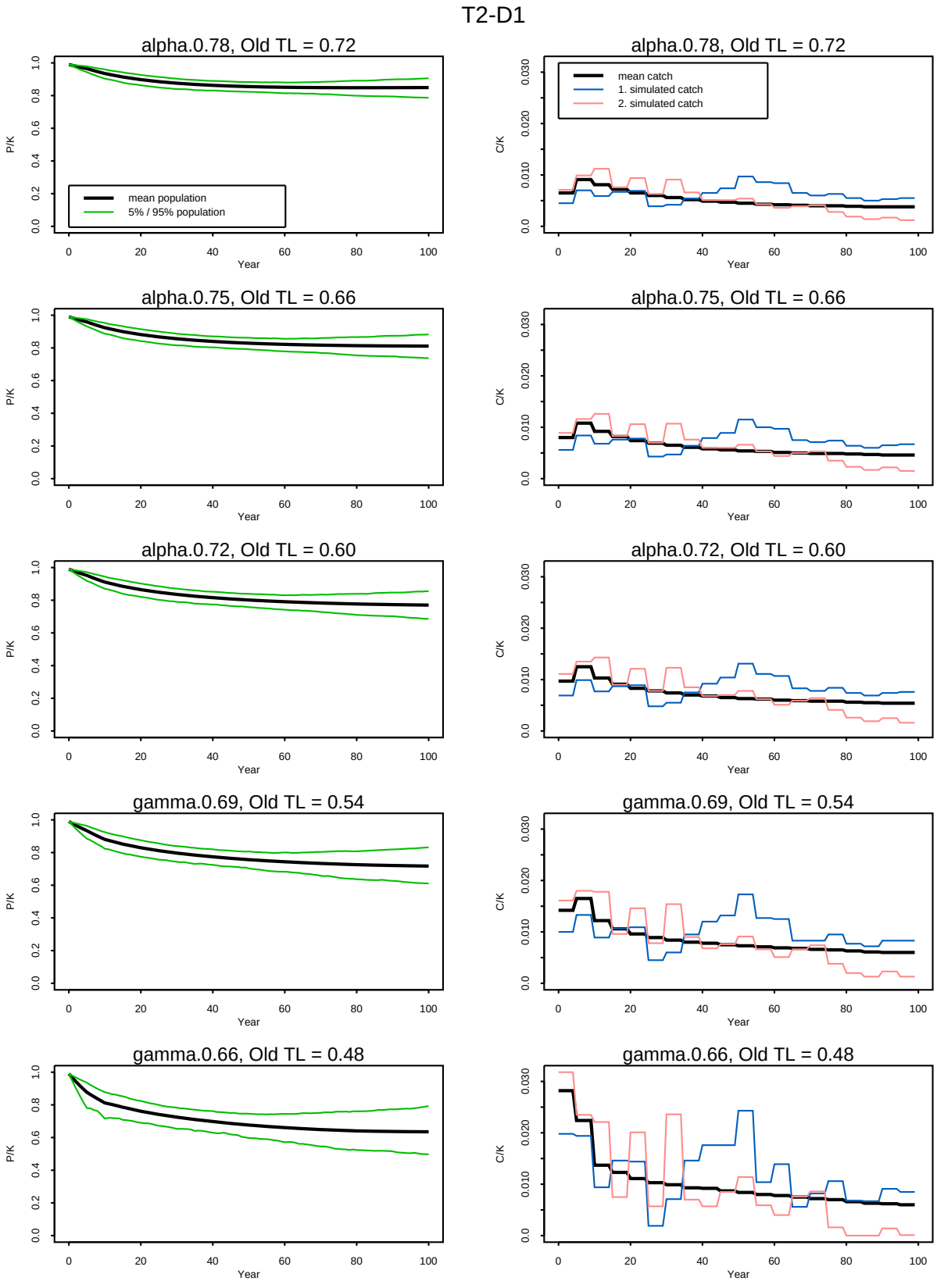


Figure 11. Trial T2-D1. 50% negative bias in abundance estimates.

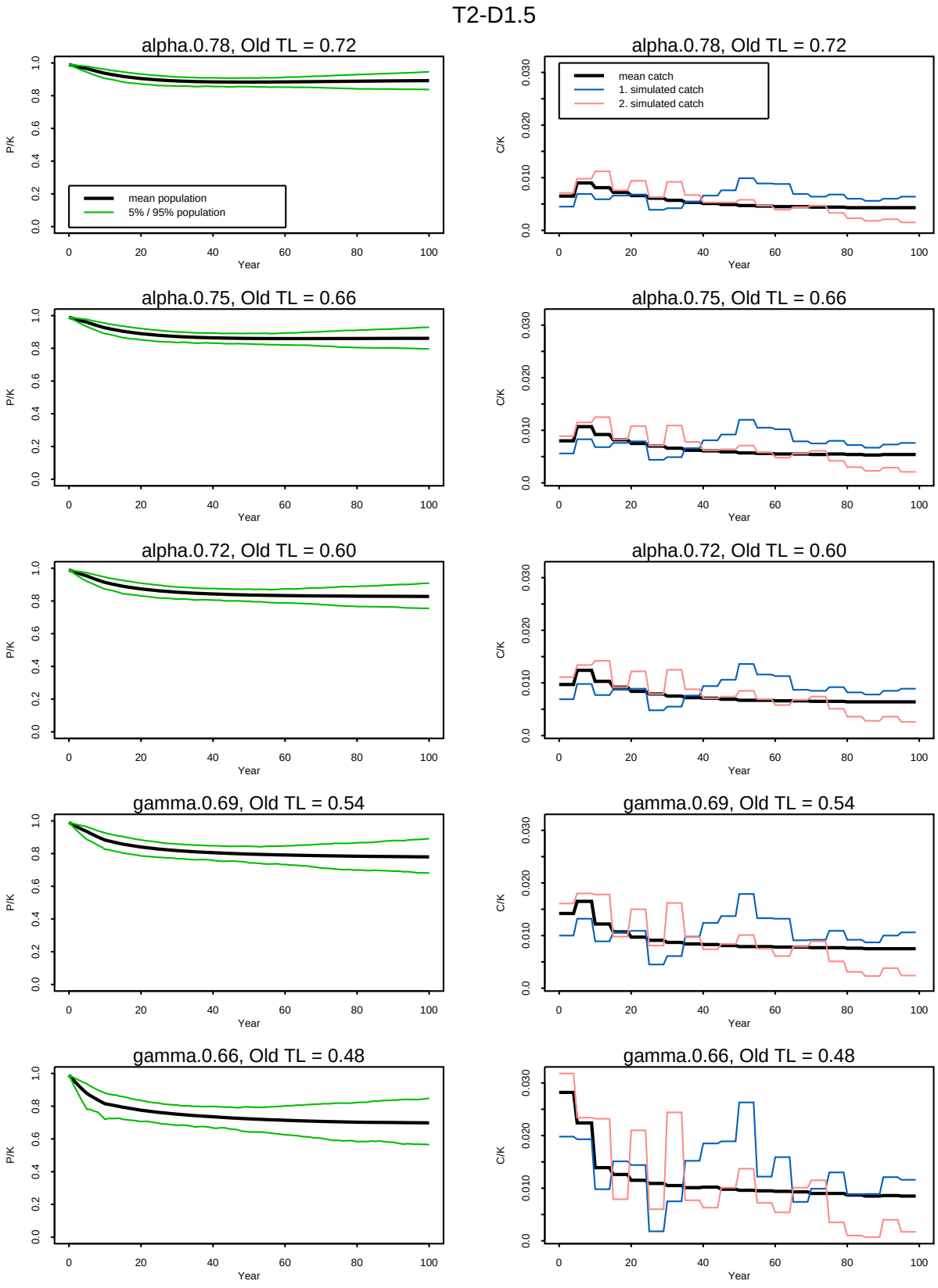


Figure 12. Trial T2-D1.5. 50% negative bias in abundance estimates.

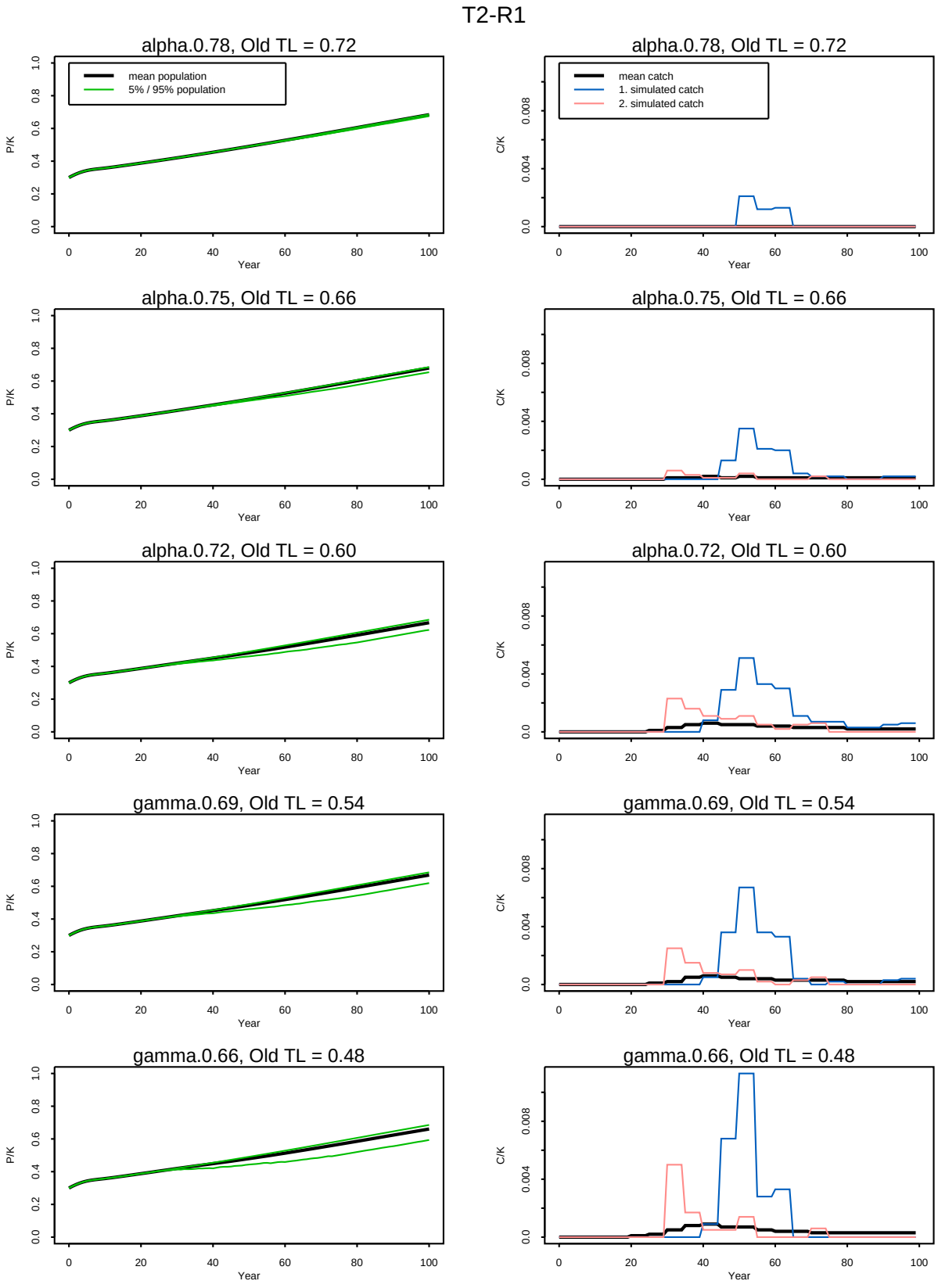


Figure 13. Trial T2-R1. 50% negative bias in abundance estimates.

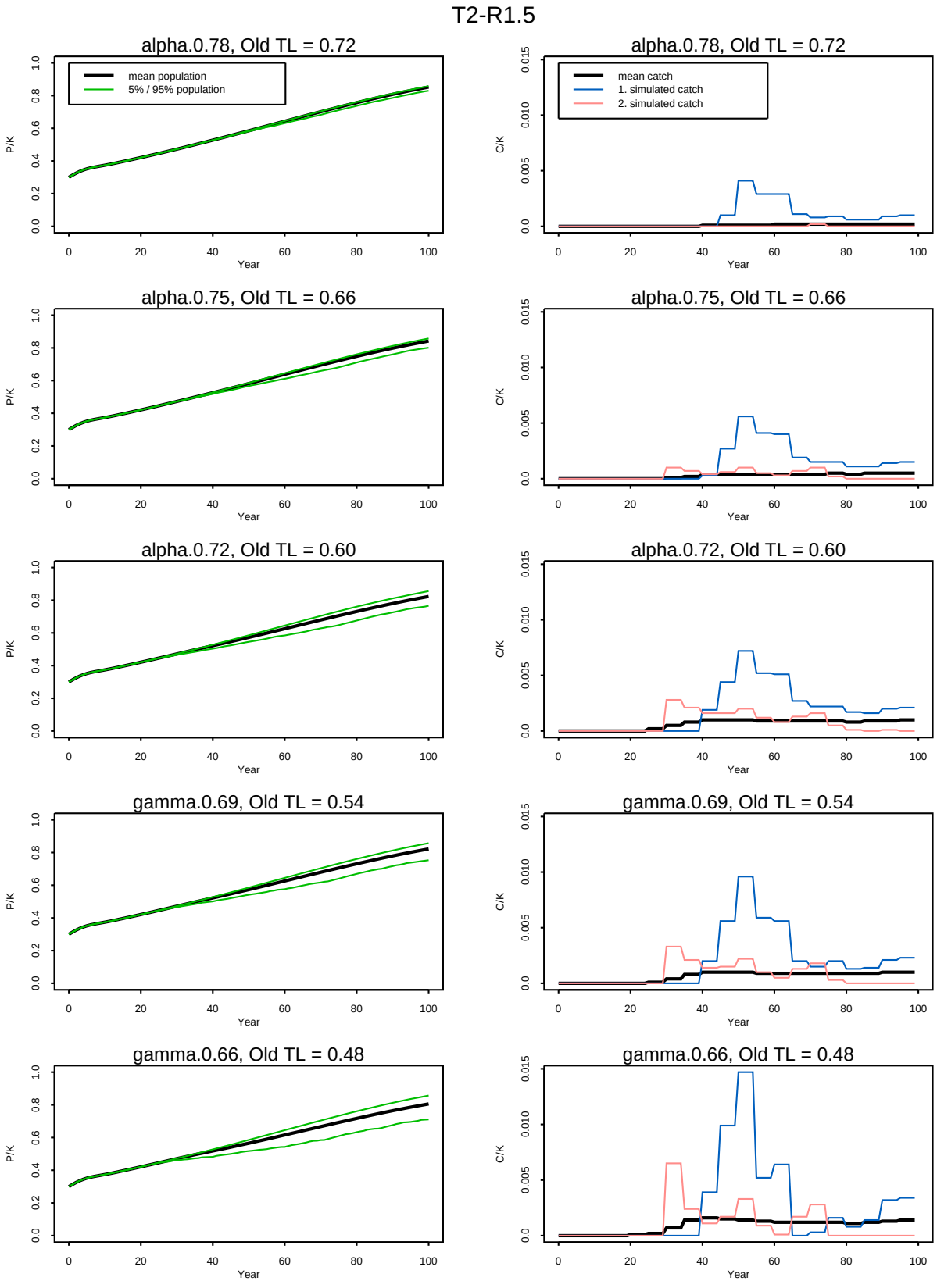


Figure 14. Trial T2-R1.5. 50% negative bias in abundance estimates.

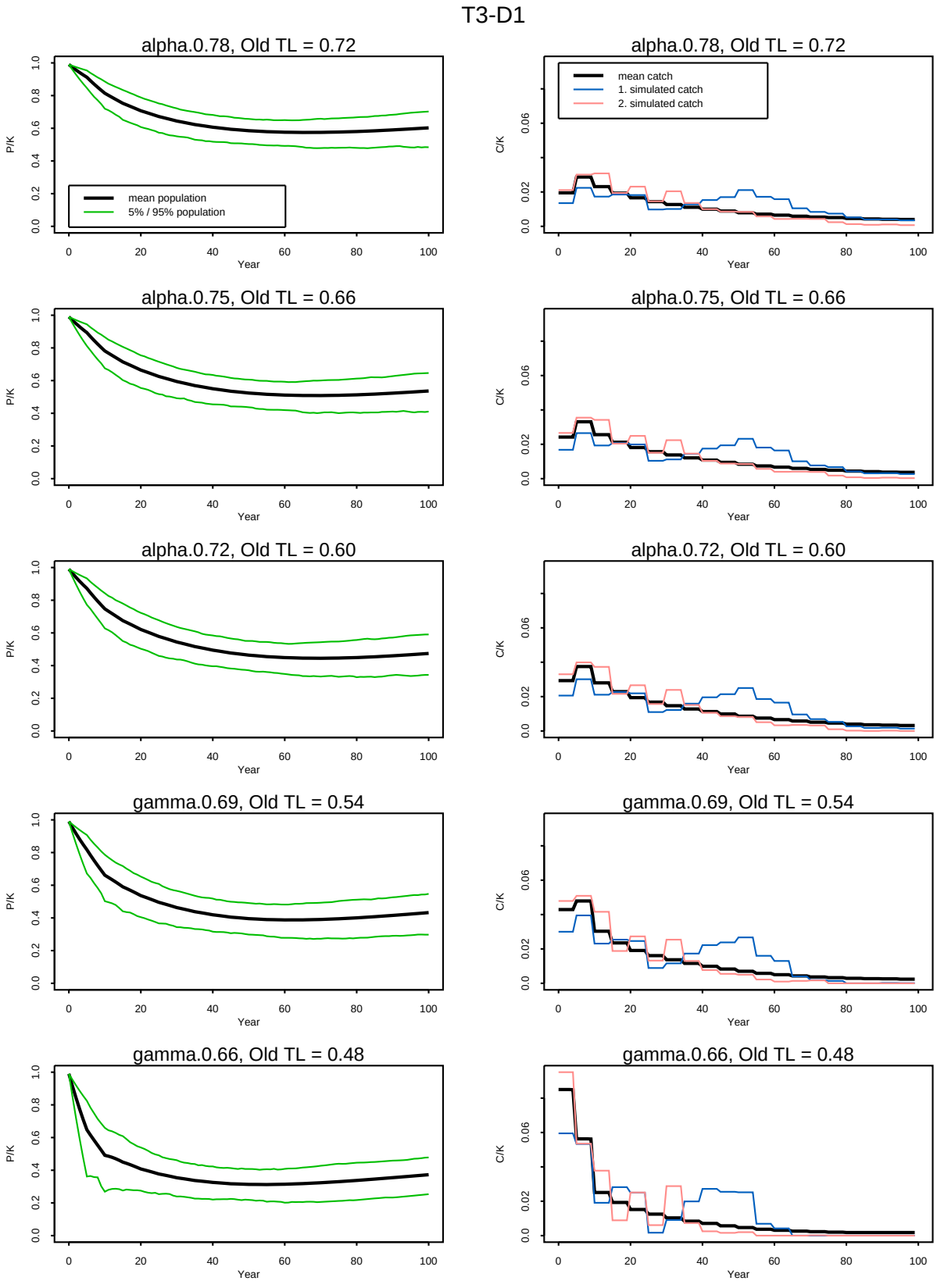


Figure 15. Trial T3-D1. 50% positive bias in abundance estimates.

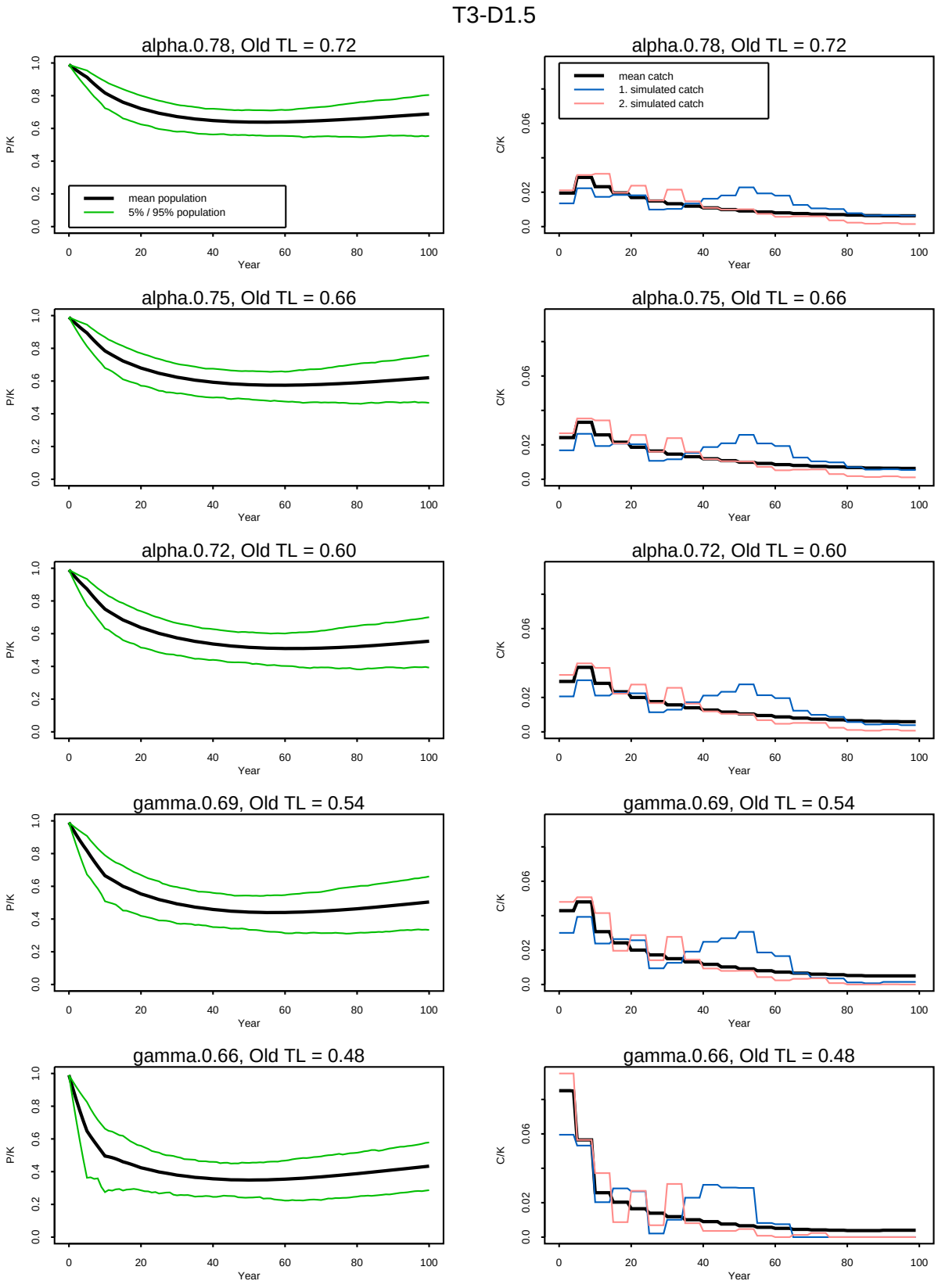


Figure 16. Trial T3-D1.5. 50% positive bias in abundance estimates.

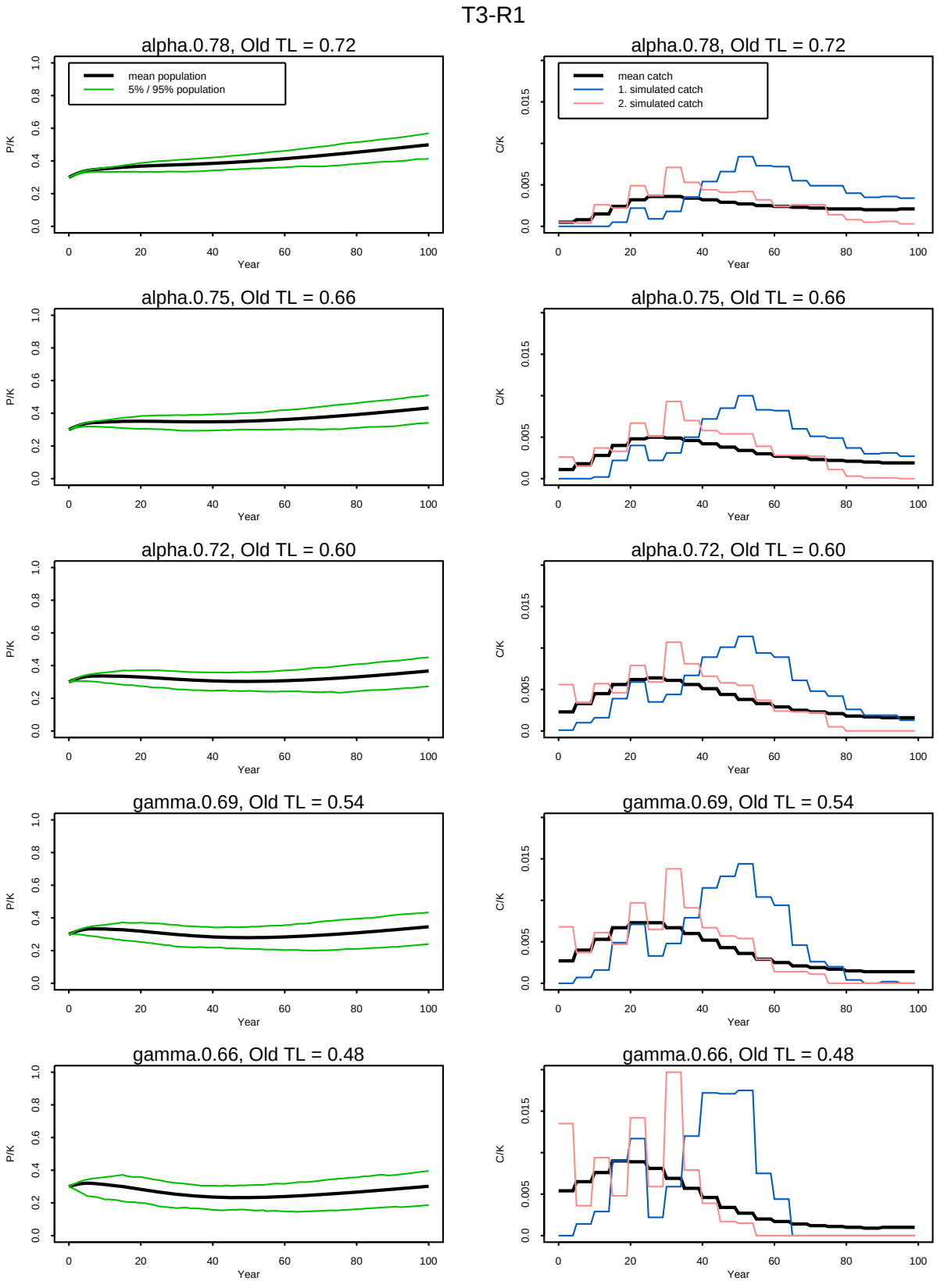


Figure 17. Trial T3-R1. 50% positive bias in abundance estimates.

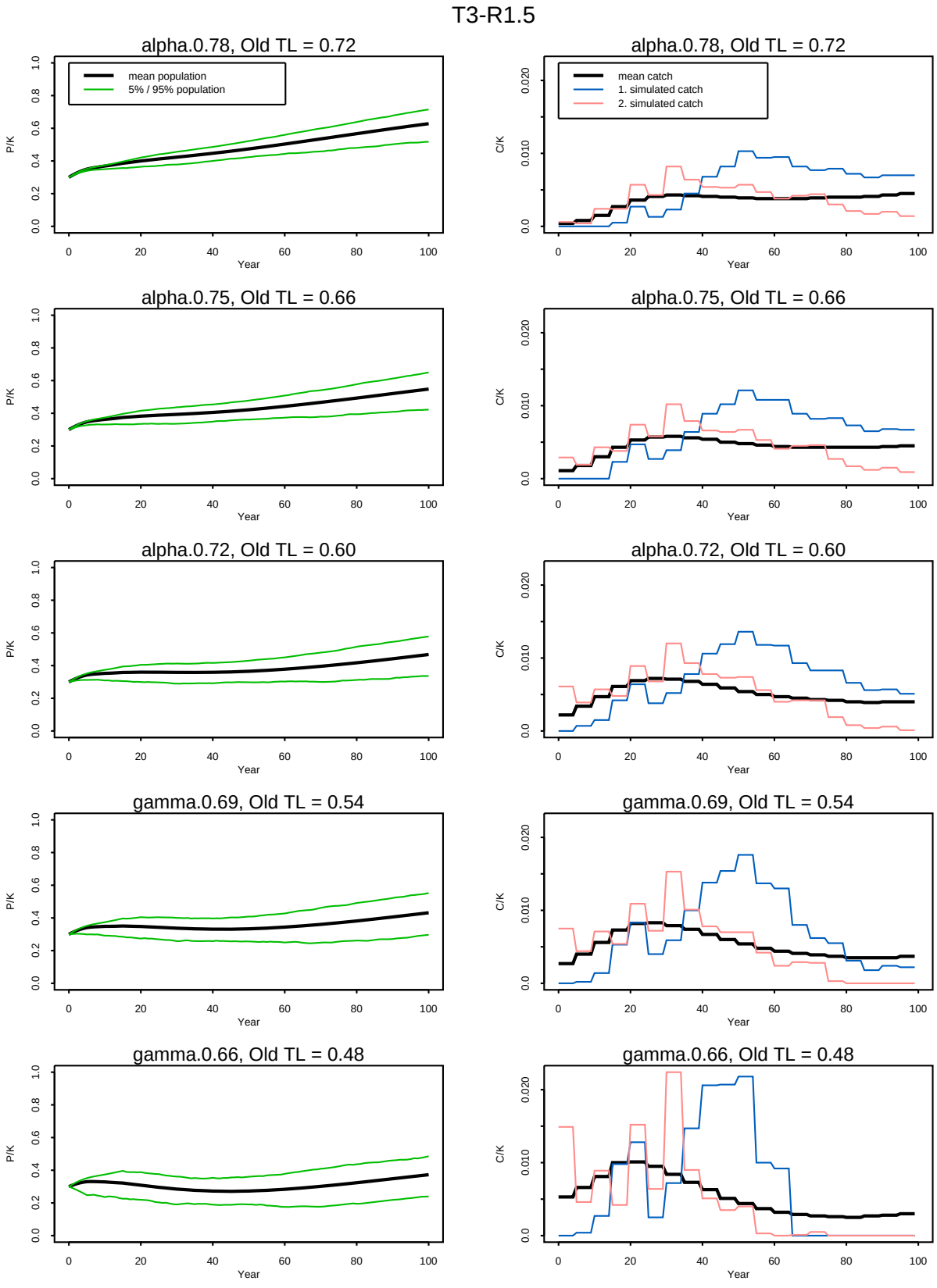


Figure 18. Trial T3-R1.5. 50% positive bias in abundance estimates.

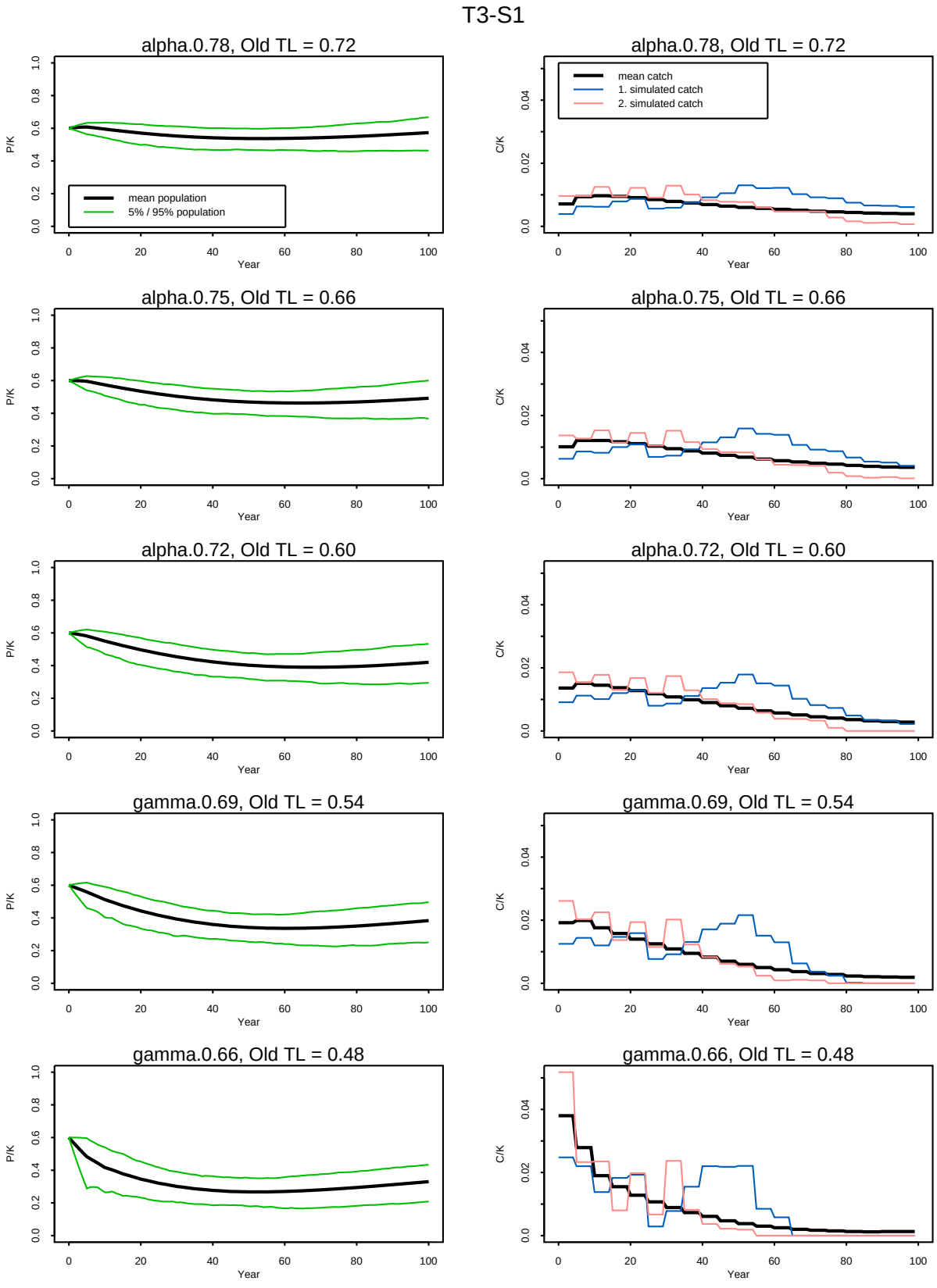


Figure 19. Trial T3-S1. 50% positive bias in abundance estimates.

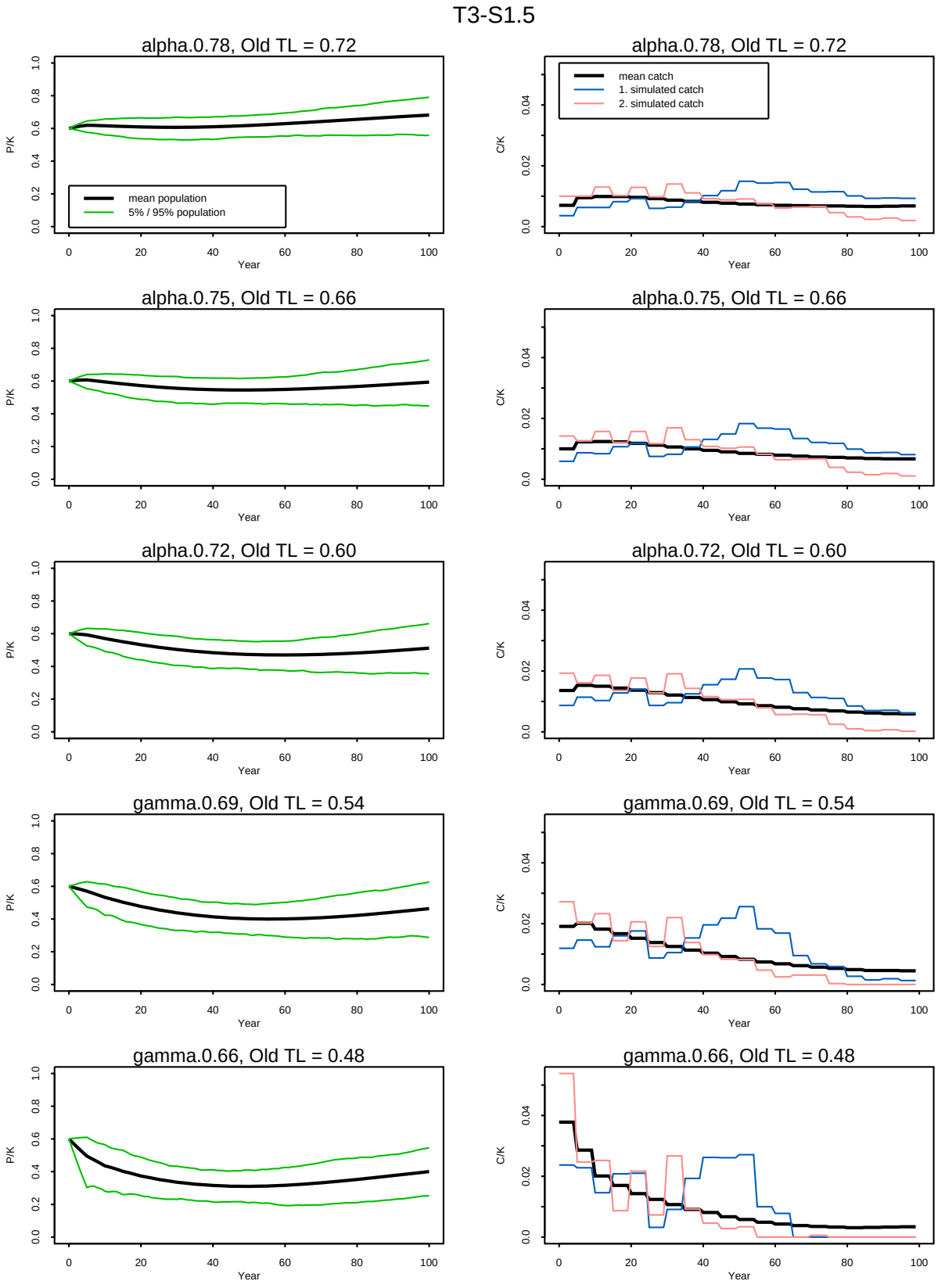


Figure 20. Trial T3-S1.5. 50% positive bias in abundance estimates.

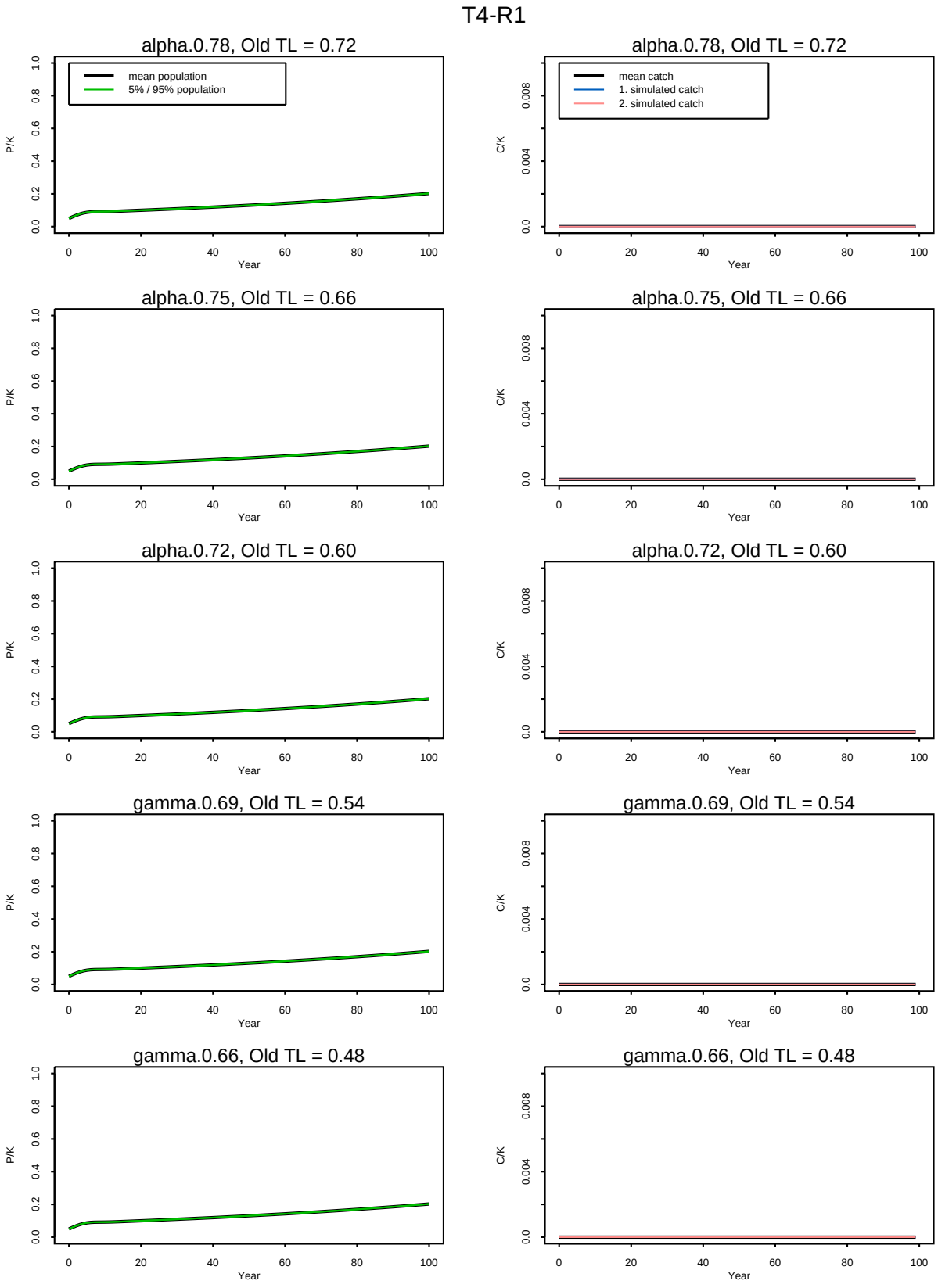


Figure 21. Trial T4-R1. Initial depletion 0.05K.

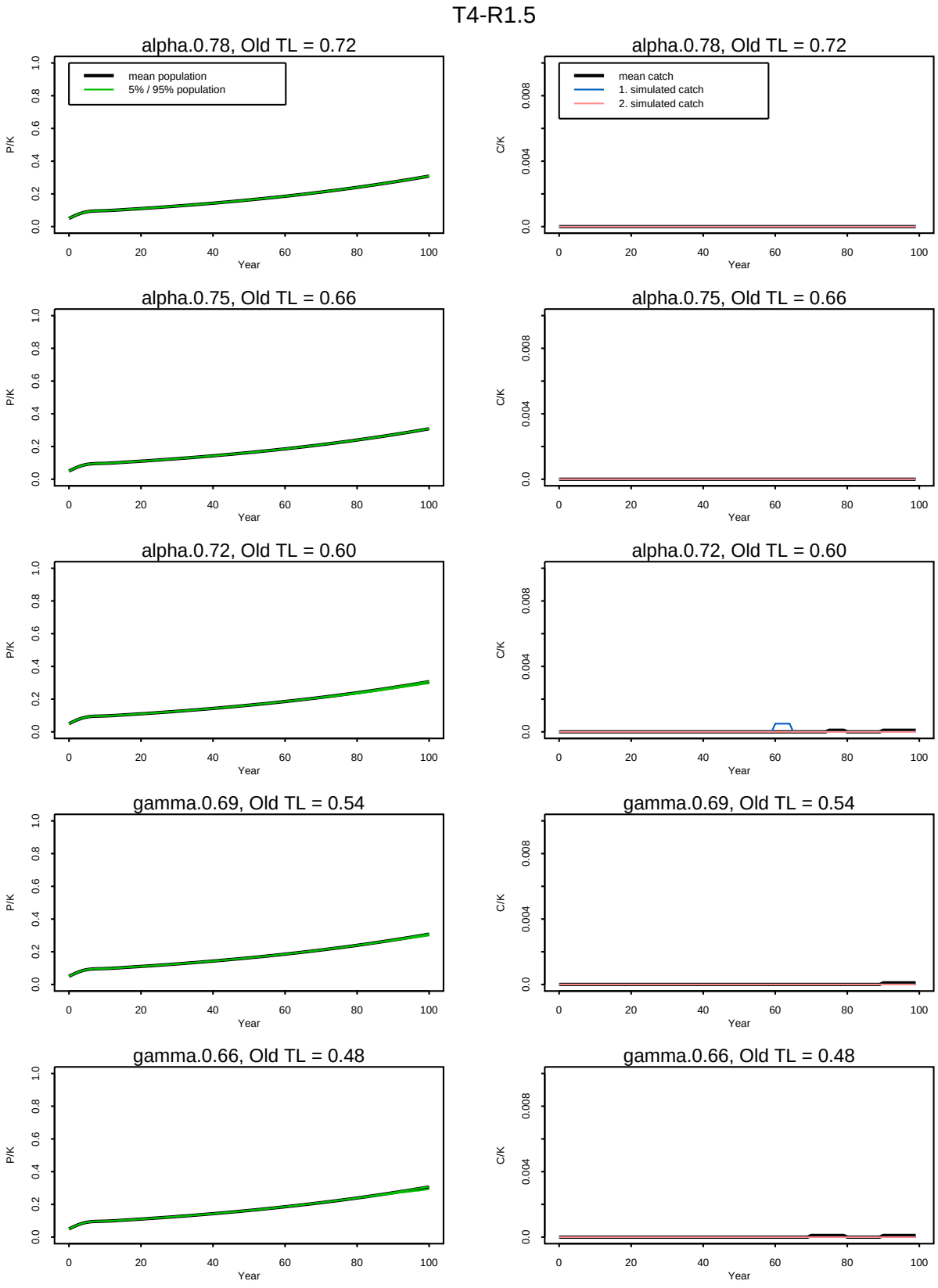


Figure 22. Trial T4-R1.5. Initial depletion 0.05K.

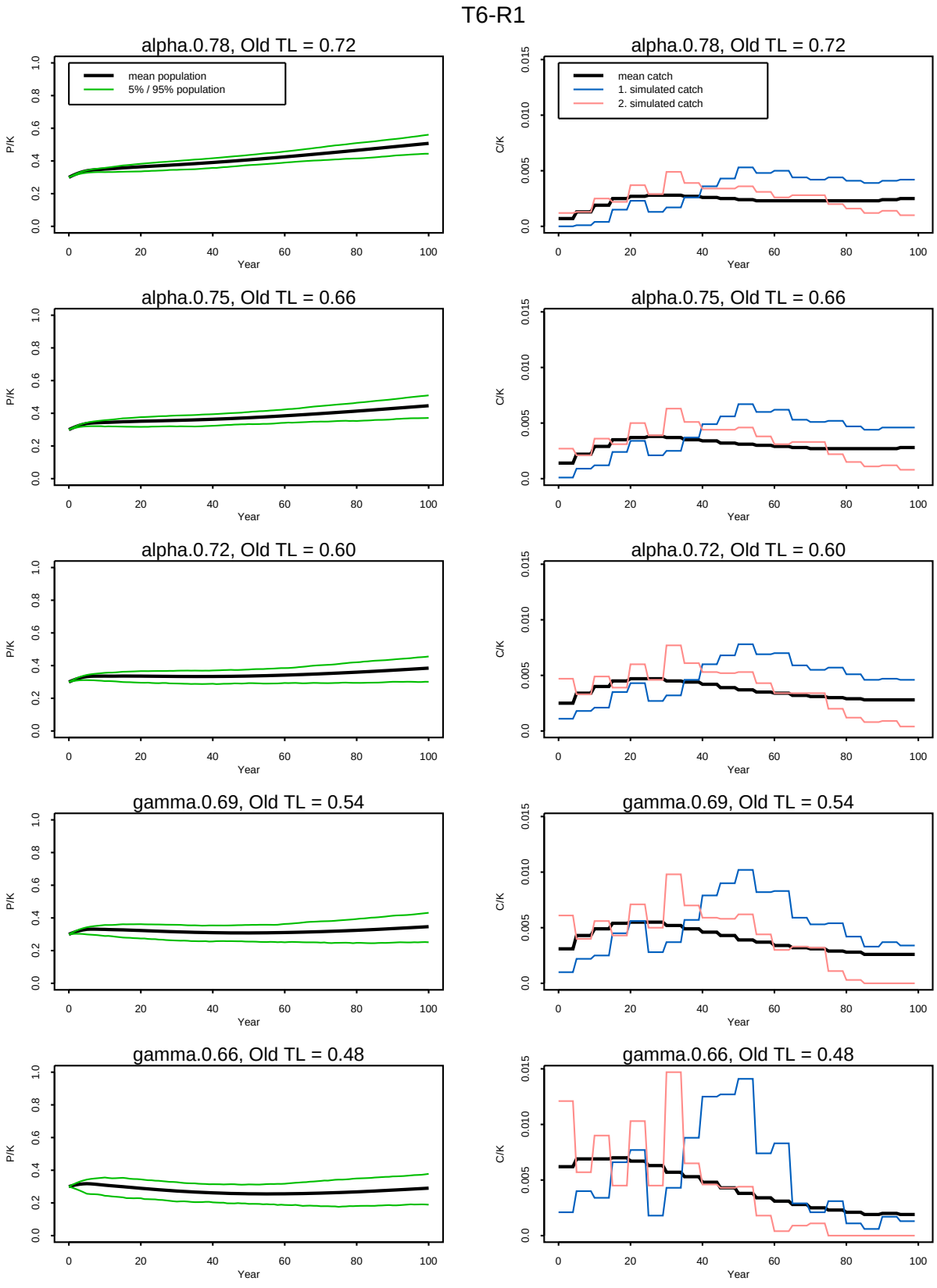


Figure 23. Trial T6-R1. Reported historic catch = 50% of the true catch.

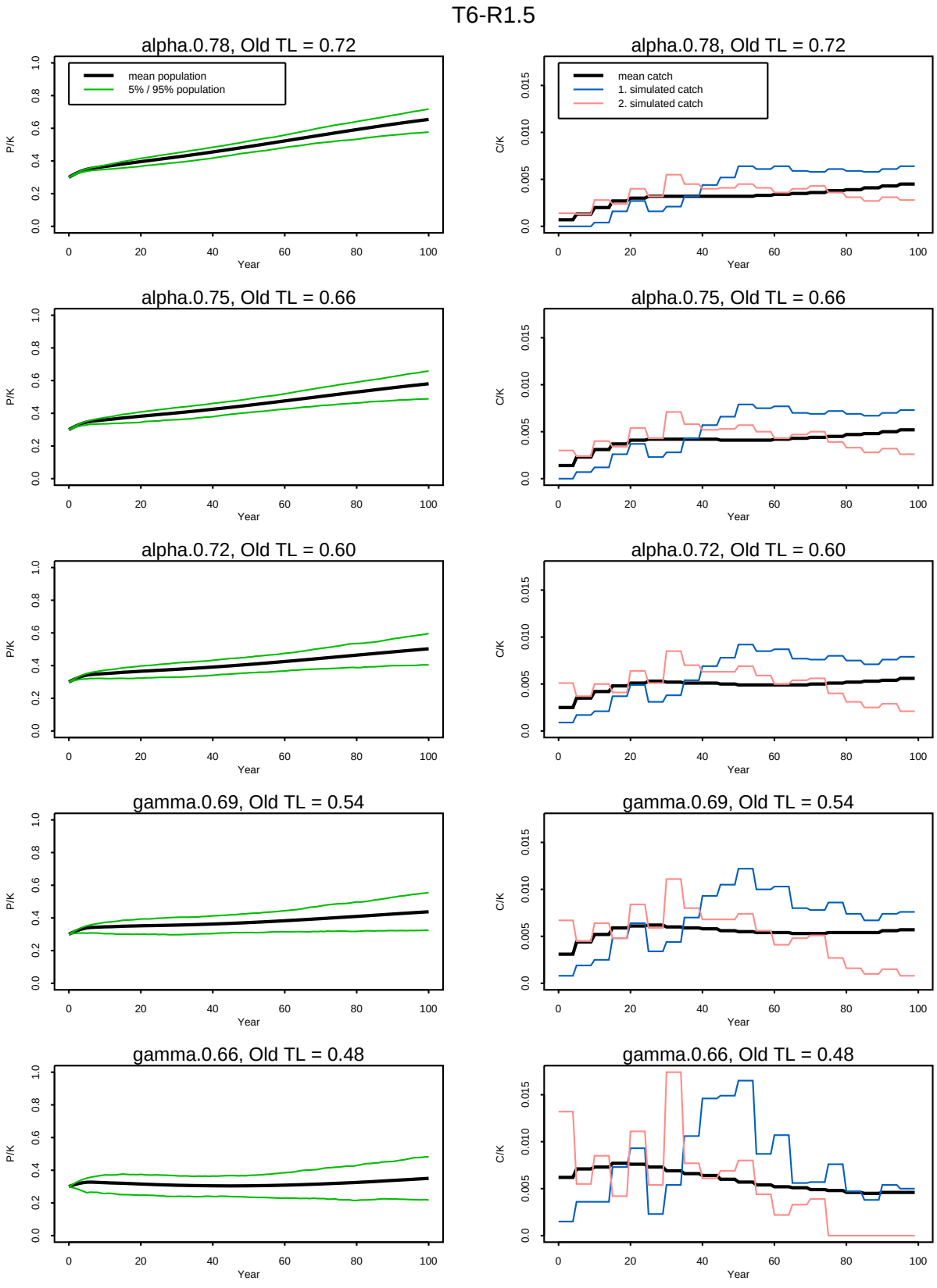


Figure 24. Trial T6-R1.5. Reported historic catch = 50% of the true catch.

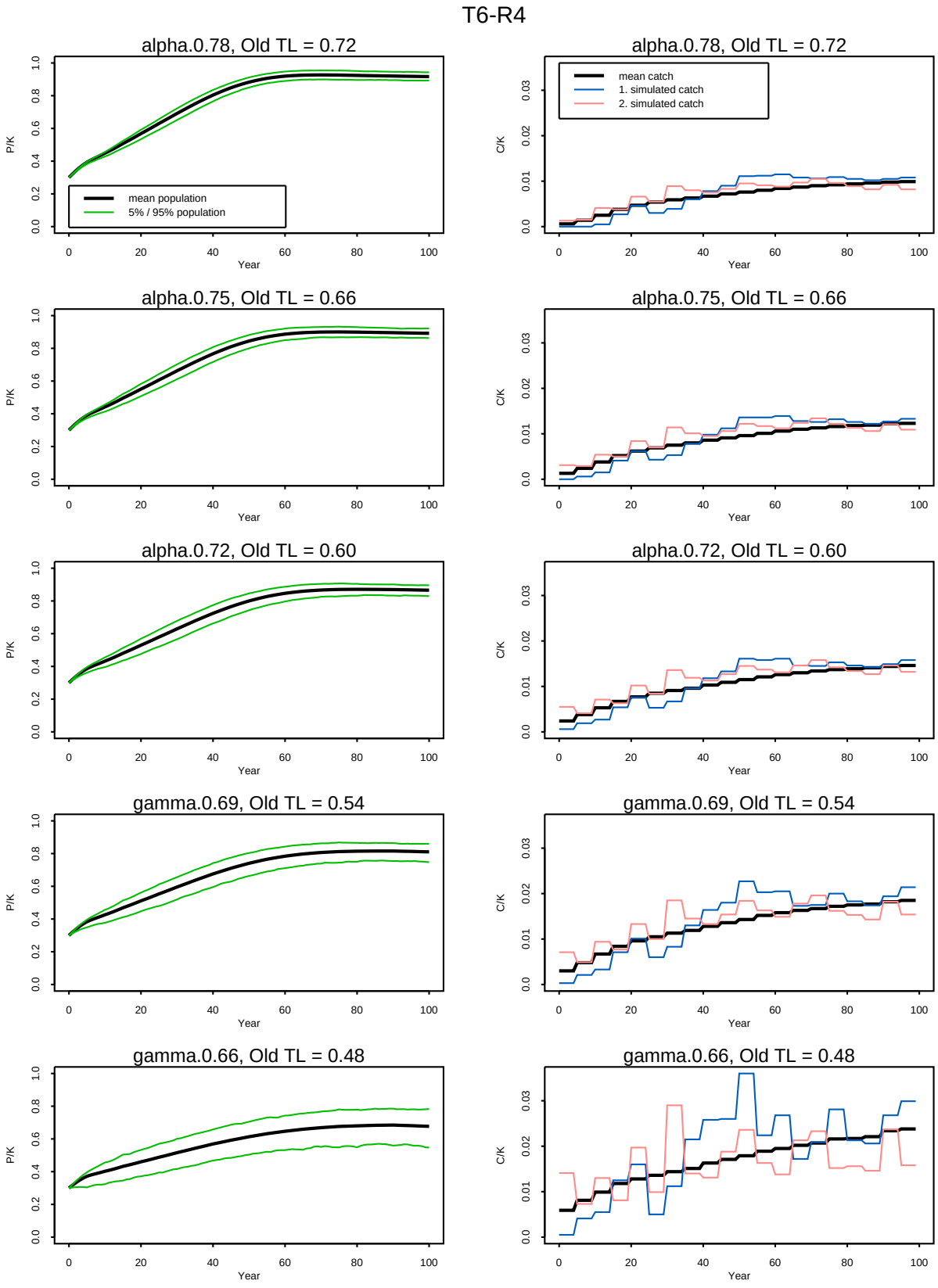


Figure 25. Trial T6-R4. Reported historic catch = 50% of the true catch.

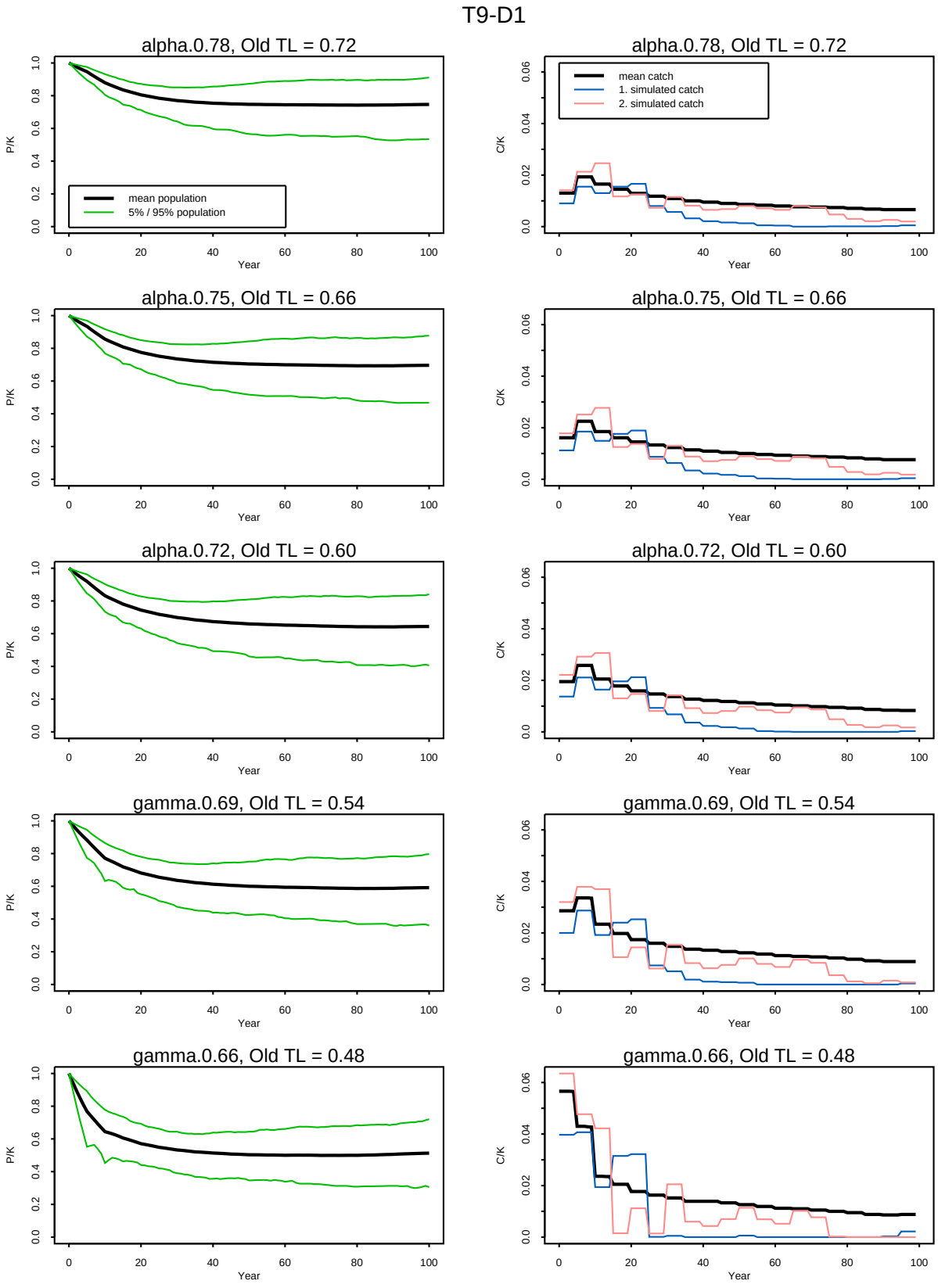


Figure 26. Trial T9-D1. Episodic events; (Rate = 0.02).

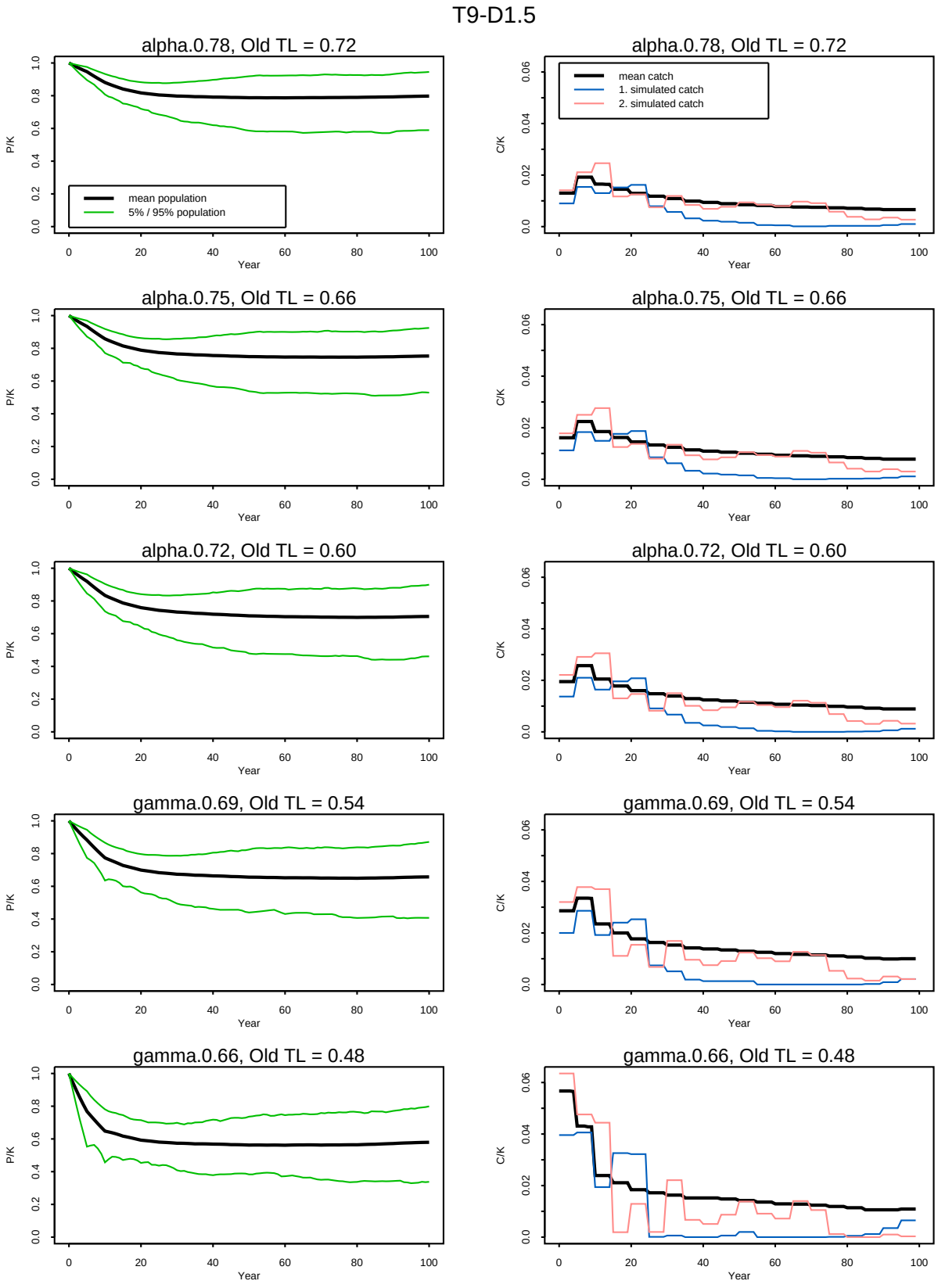


Figure 27. Trial T9-D1.5. Episodic events; (Rate = 0.02).

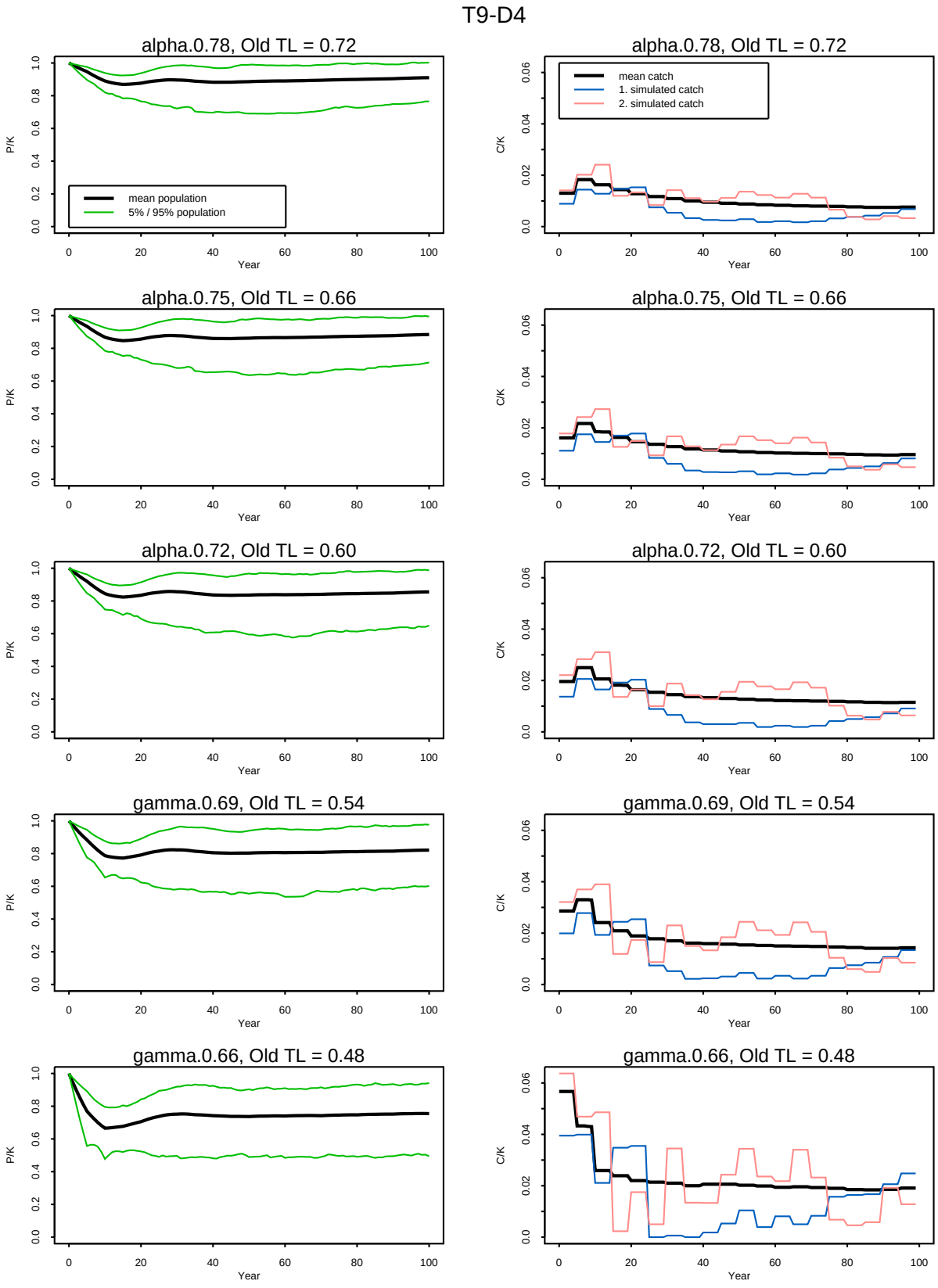


Figure 28. Trial T9-D4. Episodic events; (Rate = 0.02).

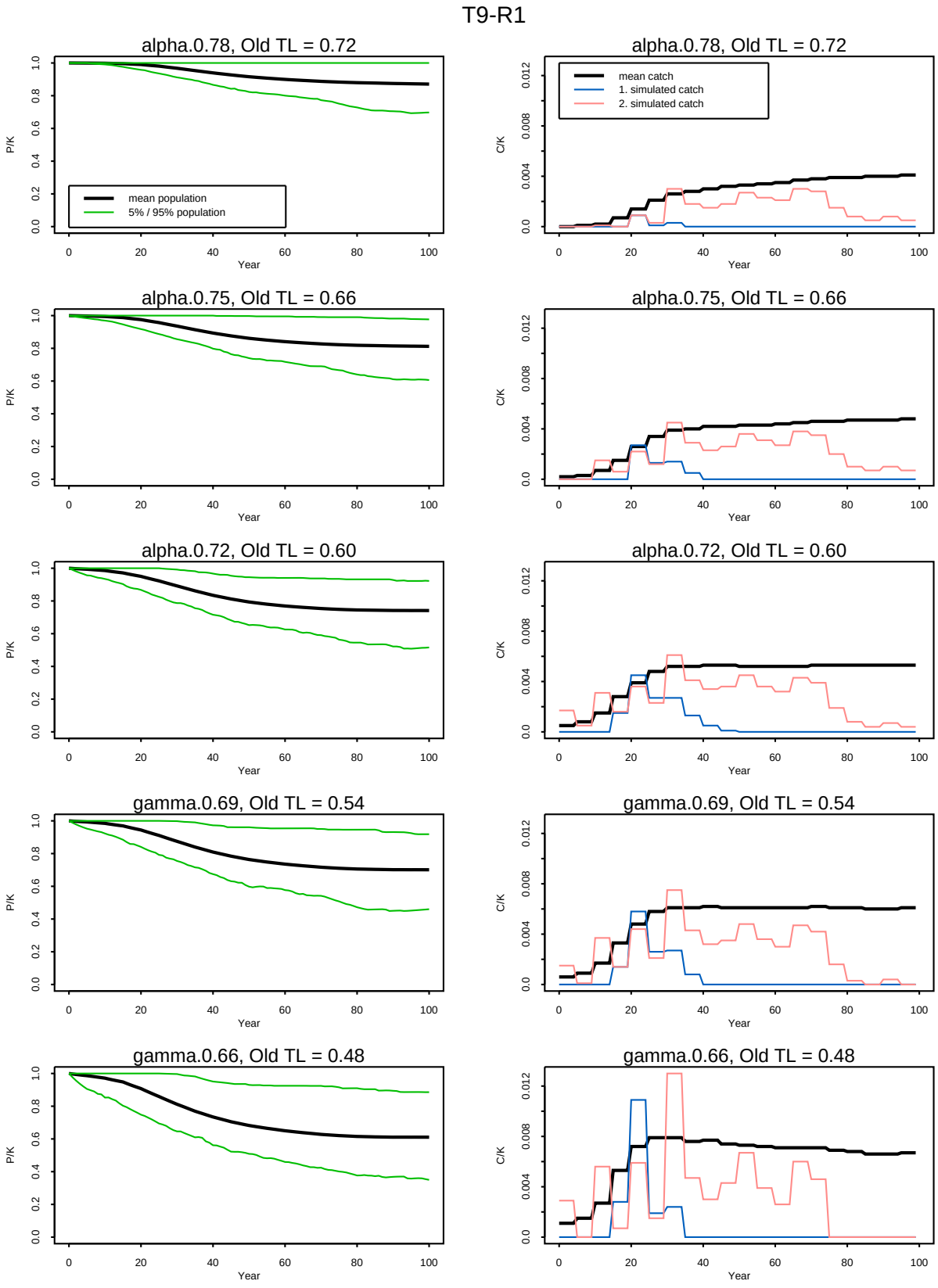


Figure 29. Trial T9-R1. Episodic events; (Rate = 0.02).

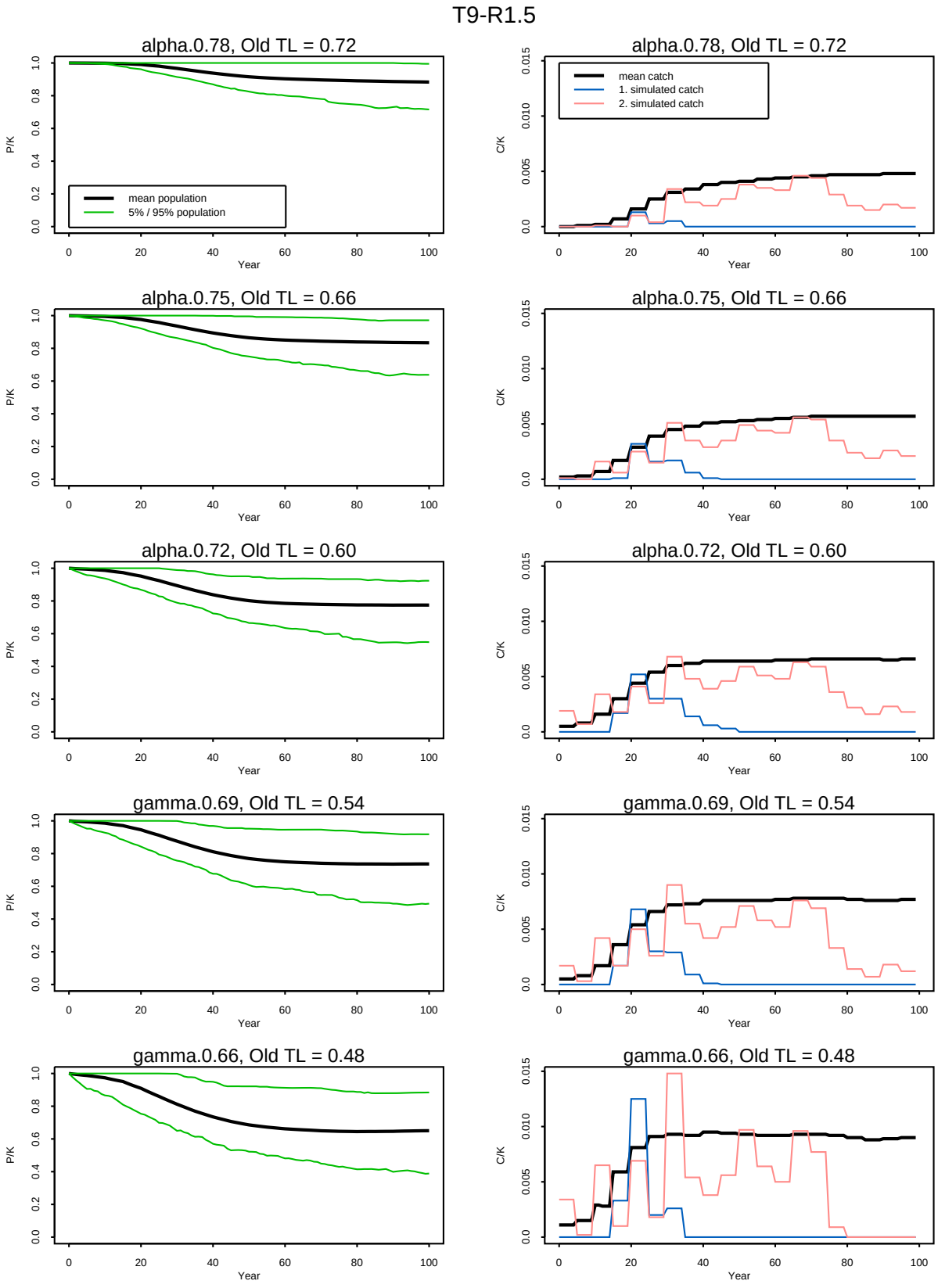


Figure 30. Trial T9-R1.5. Episodic events; (Rate = 0.02).

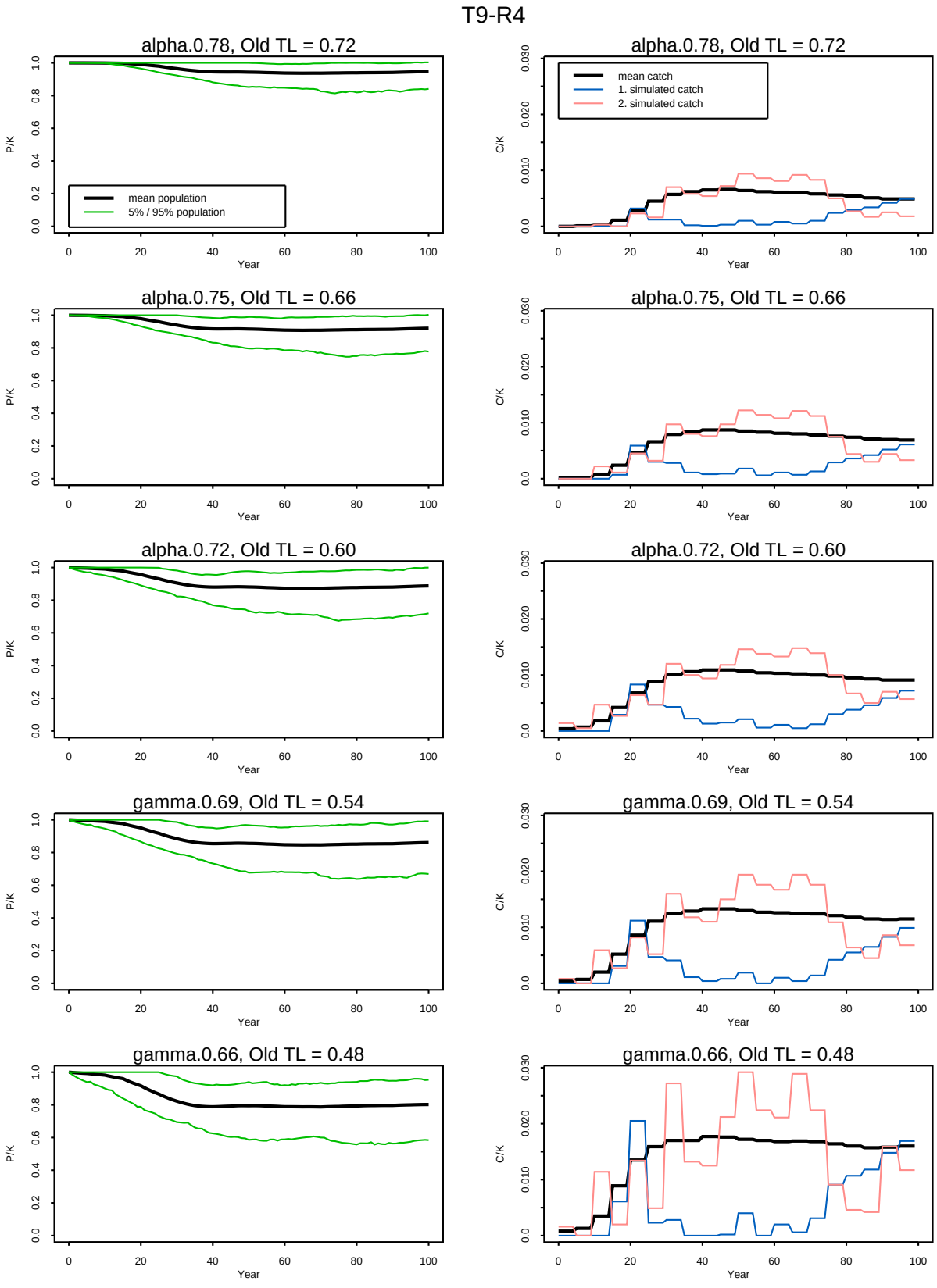


Figure 31. Trial T9-R4. Episodic events; (Rate = 0.02).

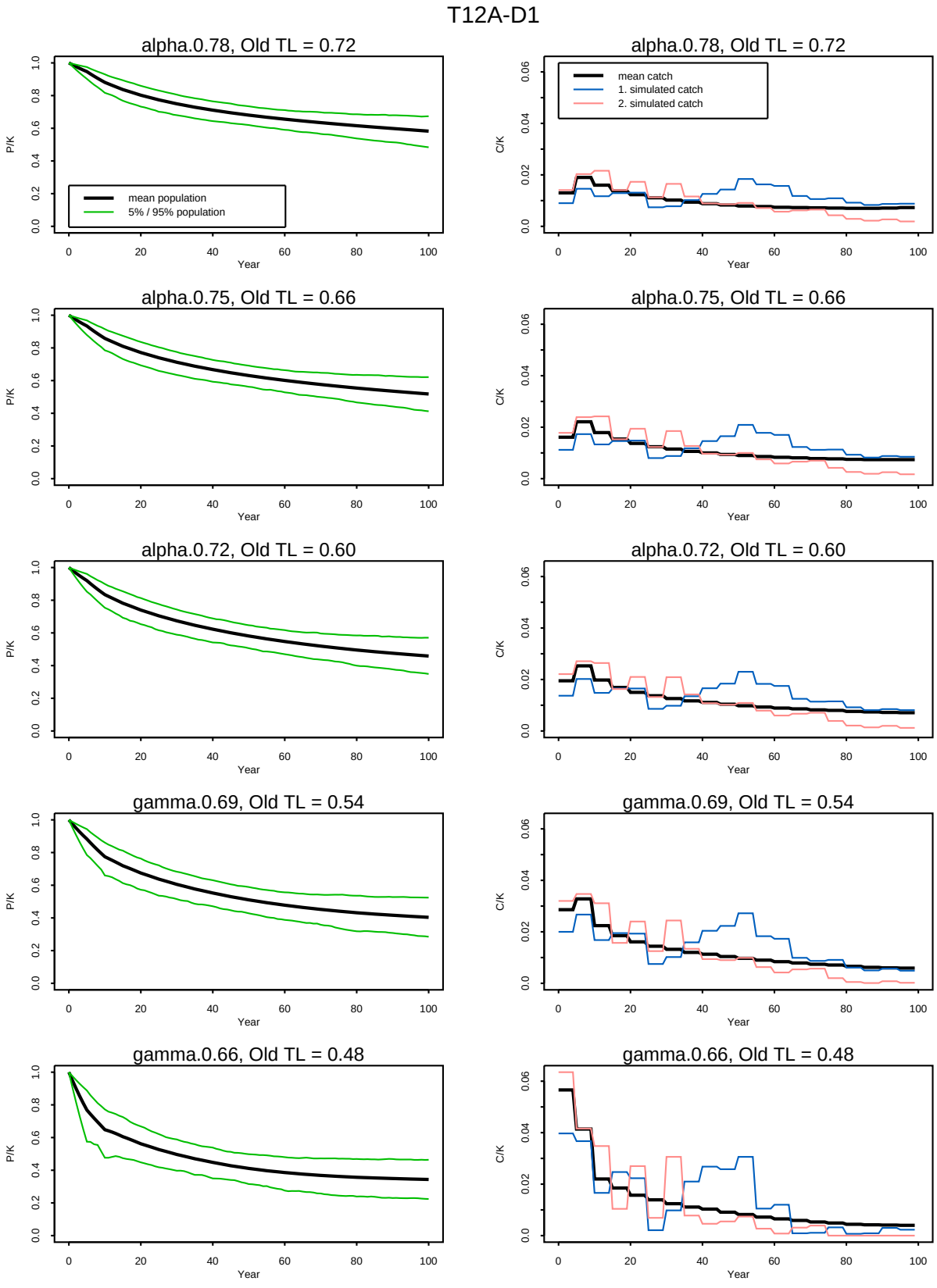


Figure 32. Trial T12A-D1. Linear increase in K from K_0 to $2 \cdot K_0$ after 100 years.

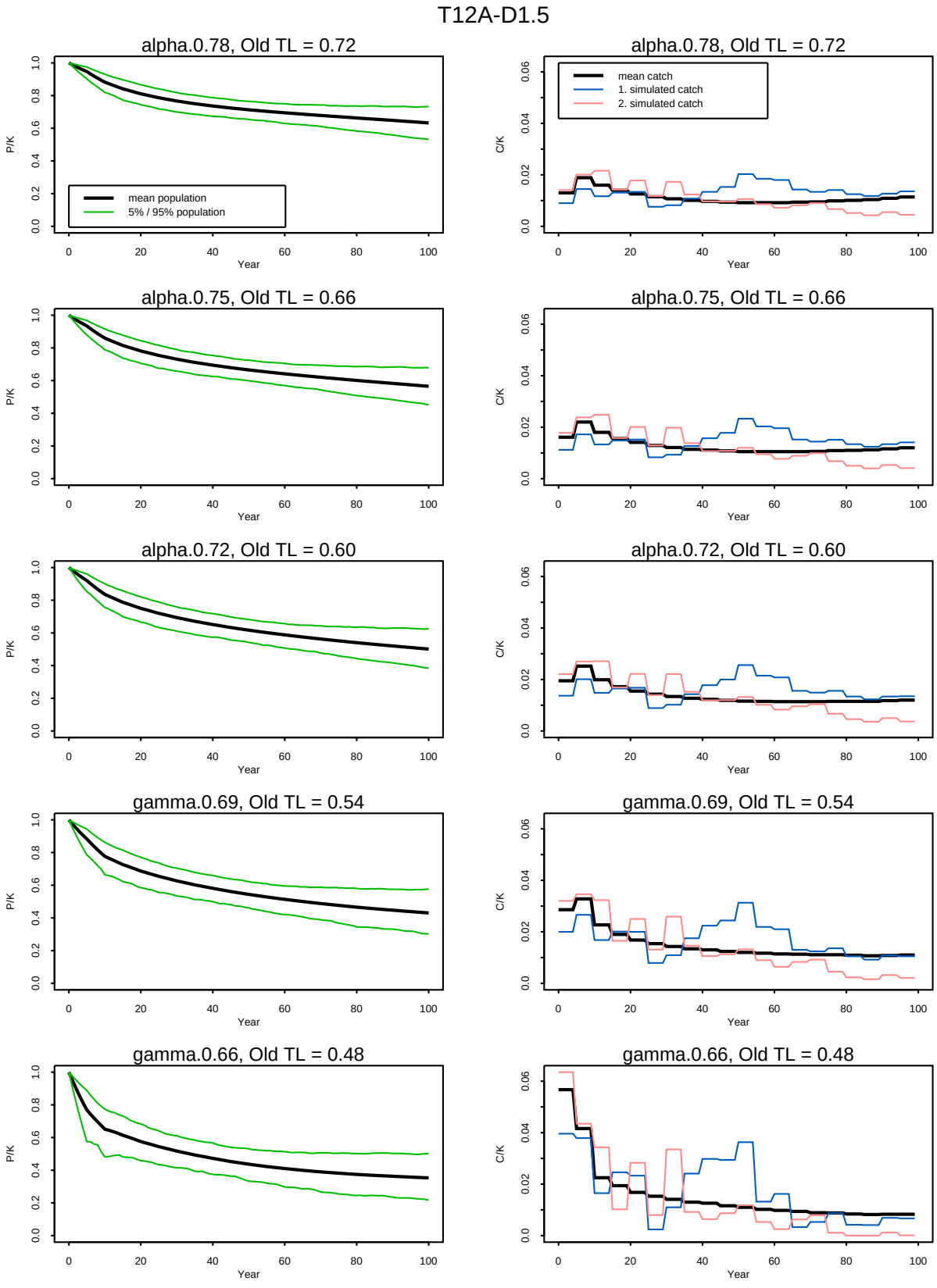


Figure 33. Trial T12A-D1.5. Linear increase in K from K_0 to $2 \cdot K_0$ after 100 years.

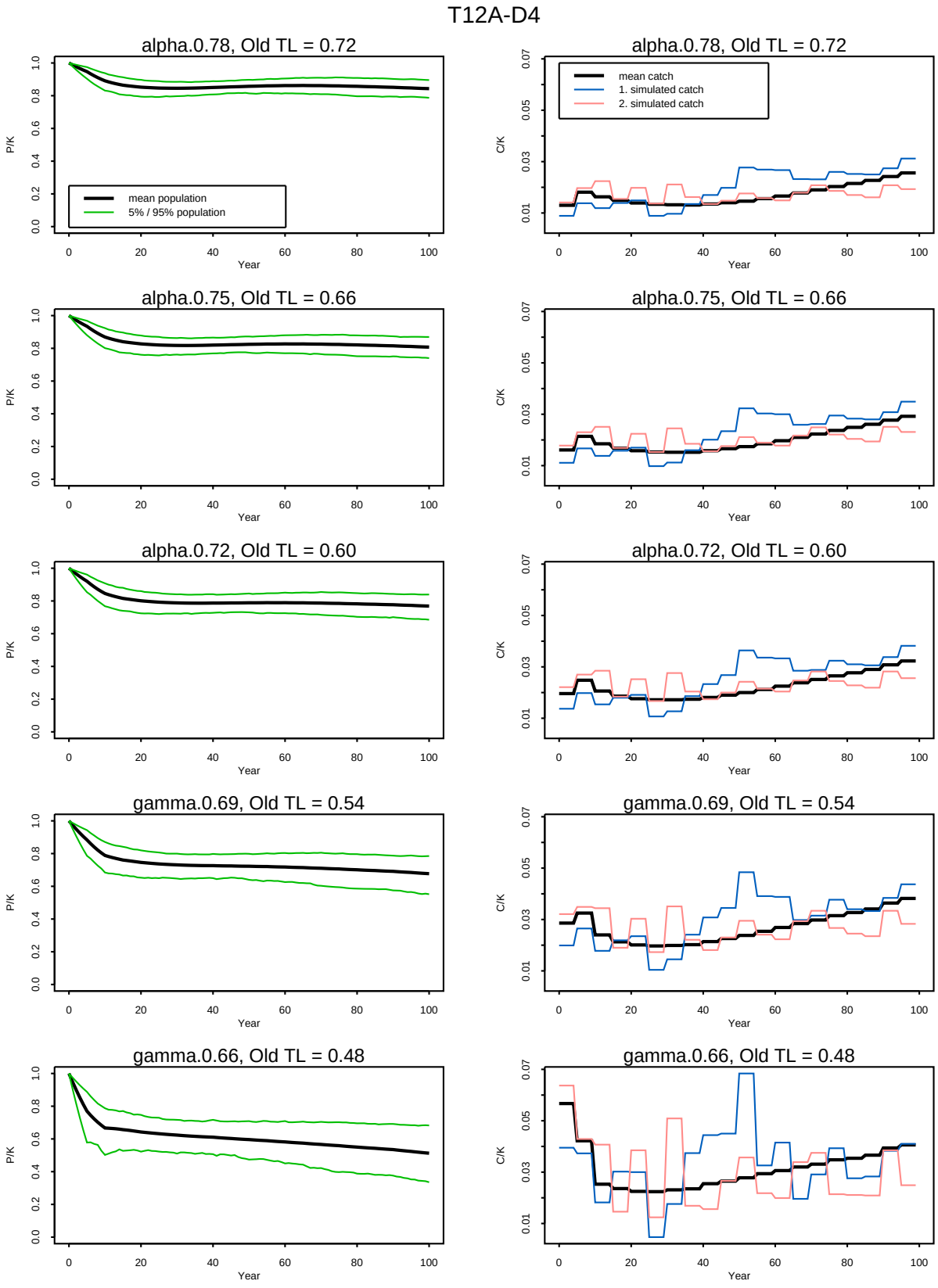


Figure 34. Trial T12A-D4. Linear increase in K from K_0 to $2 \cdot K_0$ after 100 years.

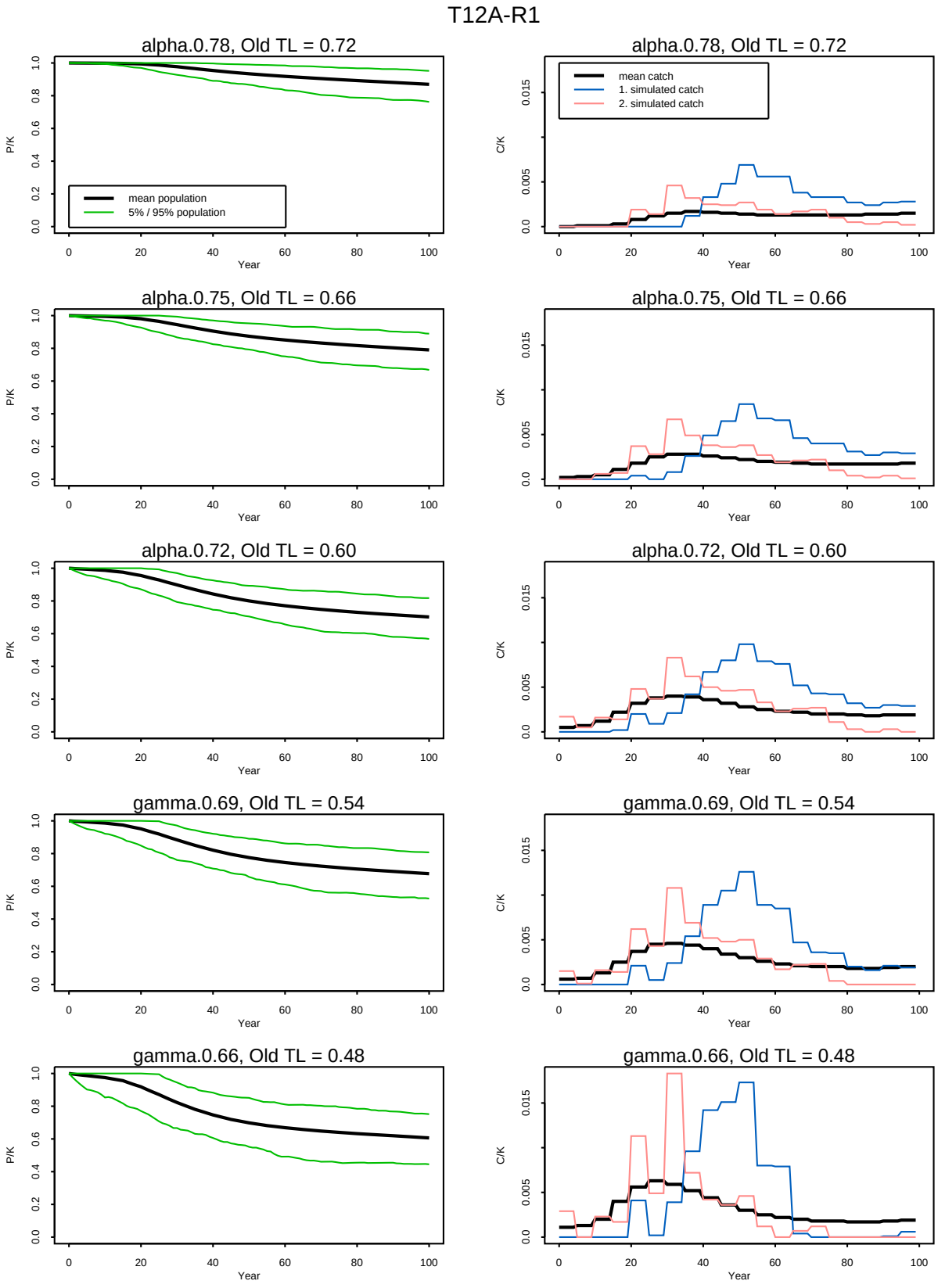


Figure 35. Trial T12A-R1. Linear increase in K from K_0 to $2 \cdot K_0$ after 100 years.

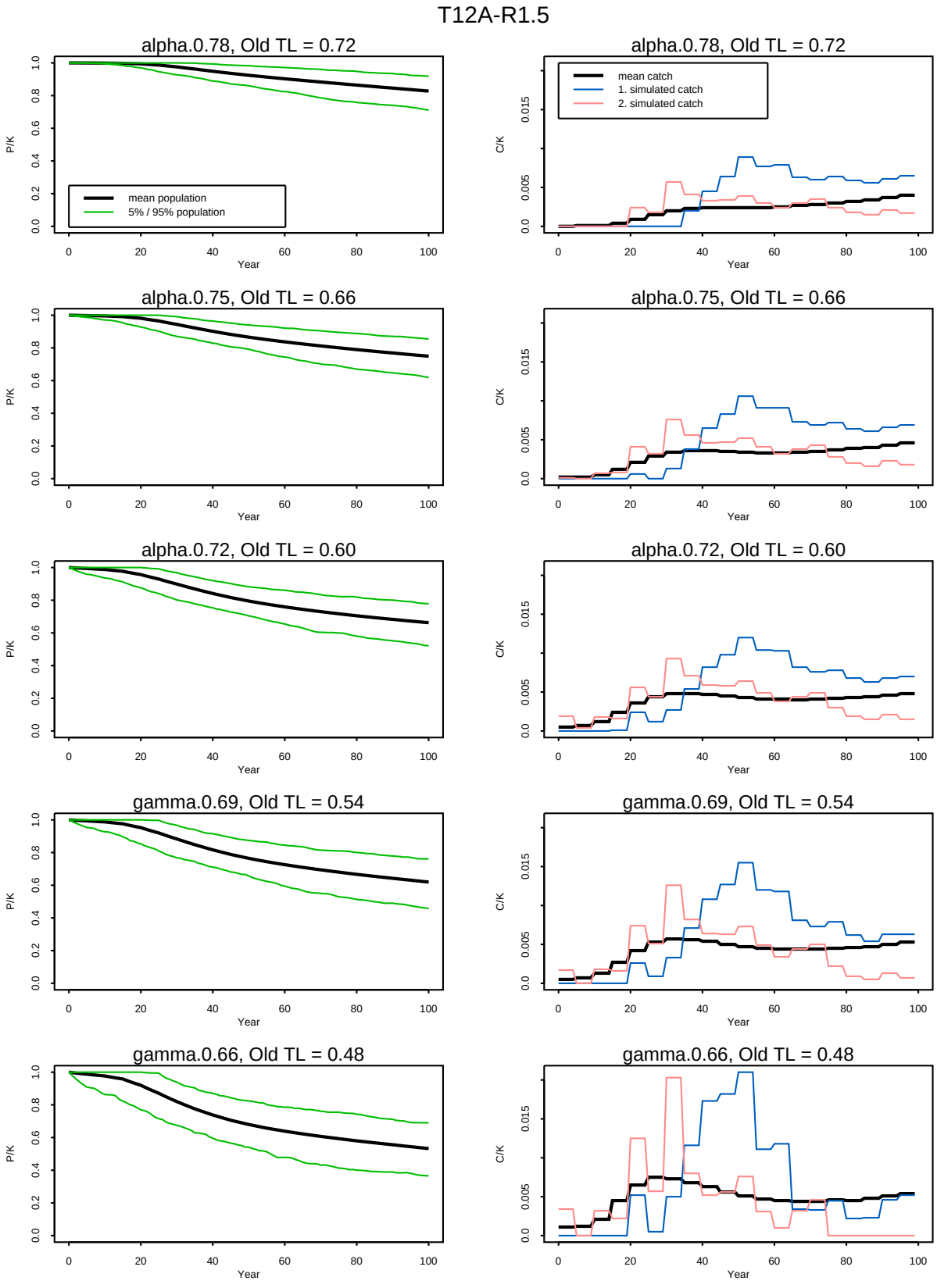


Figure 36. Trial T12A-R1.5. Linear increase in K from K_0 to $2 \cdot K_0$ after 100 years.

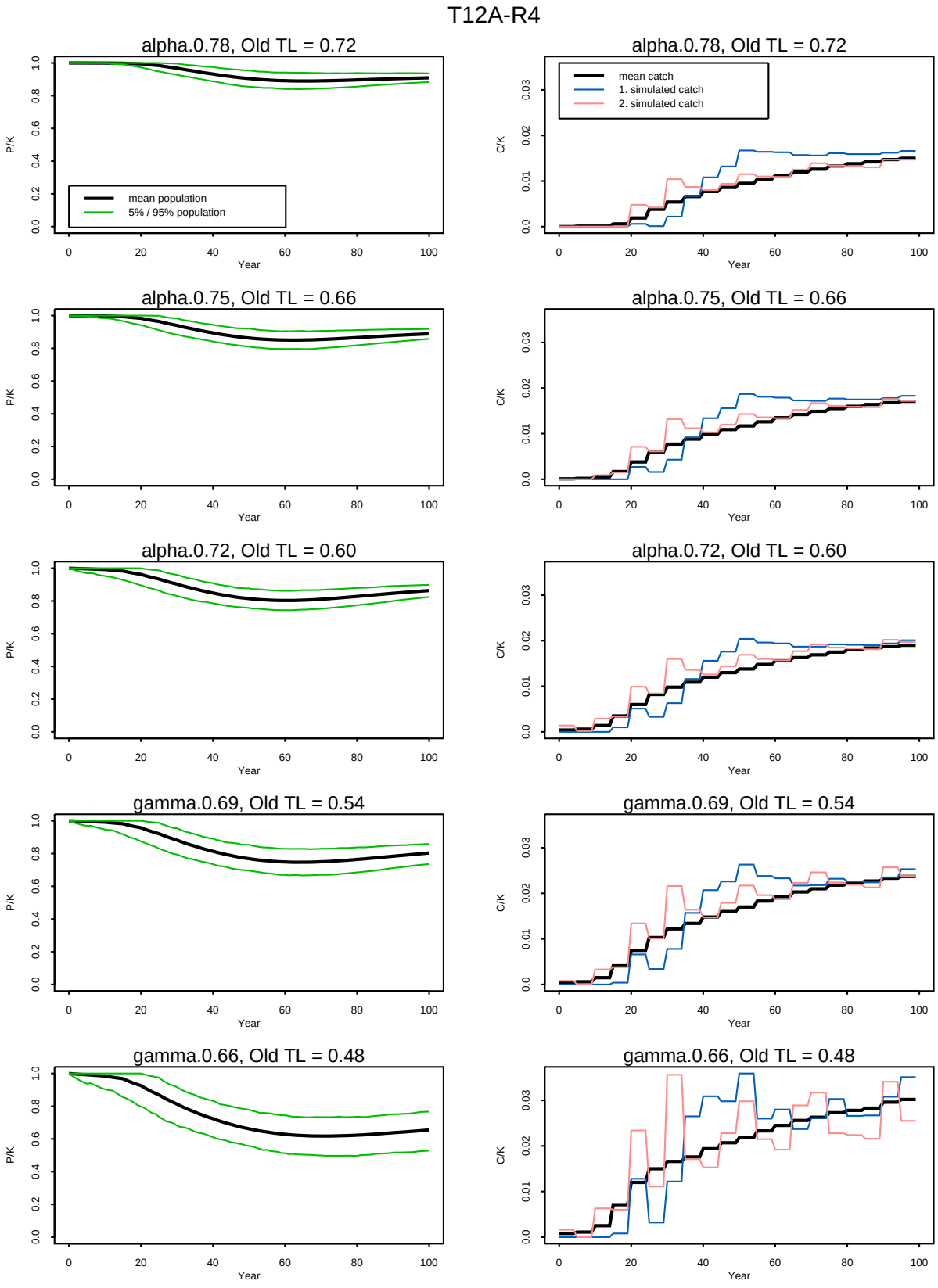


Figure 37. Trial T12A-R4. Linear increase in K from K_0 to $2 \cdot K_0$ after 100 years.

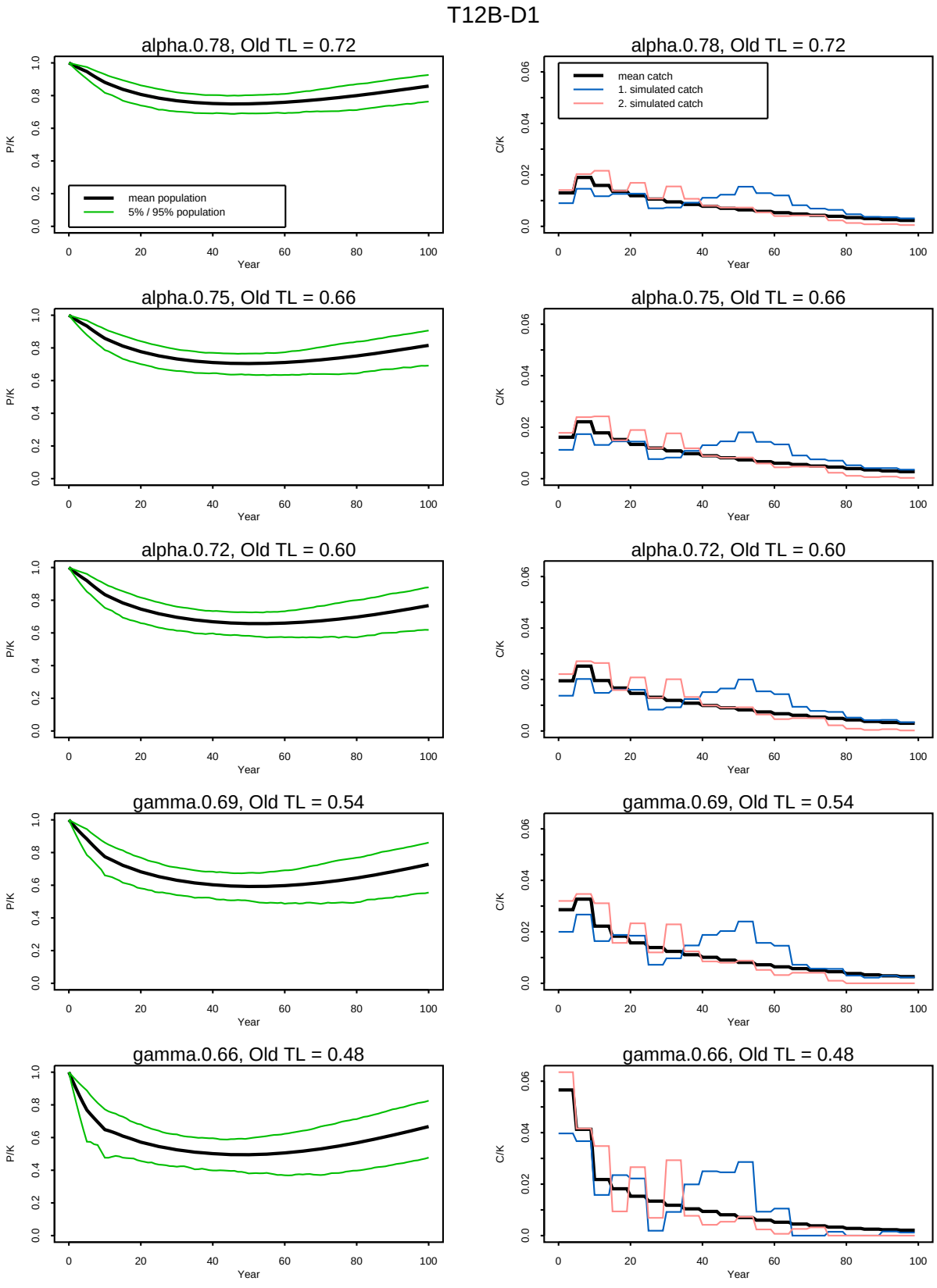


Figure 38. Trial T12B-D1. Linear decrease in K from K_0 to $0.5 \cdot K_0$ after 100 years.

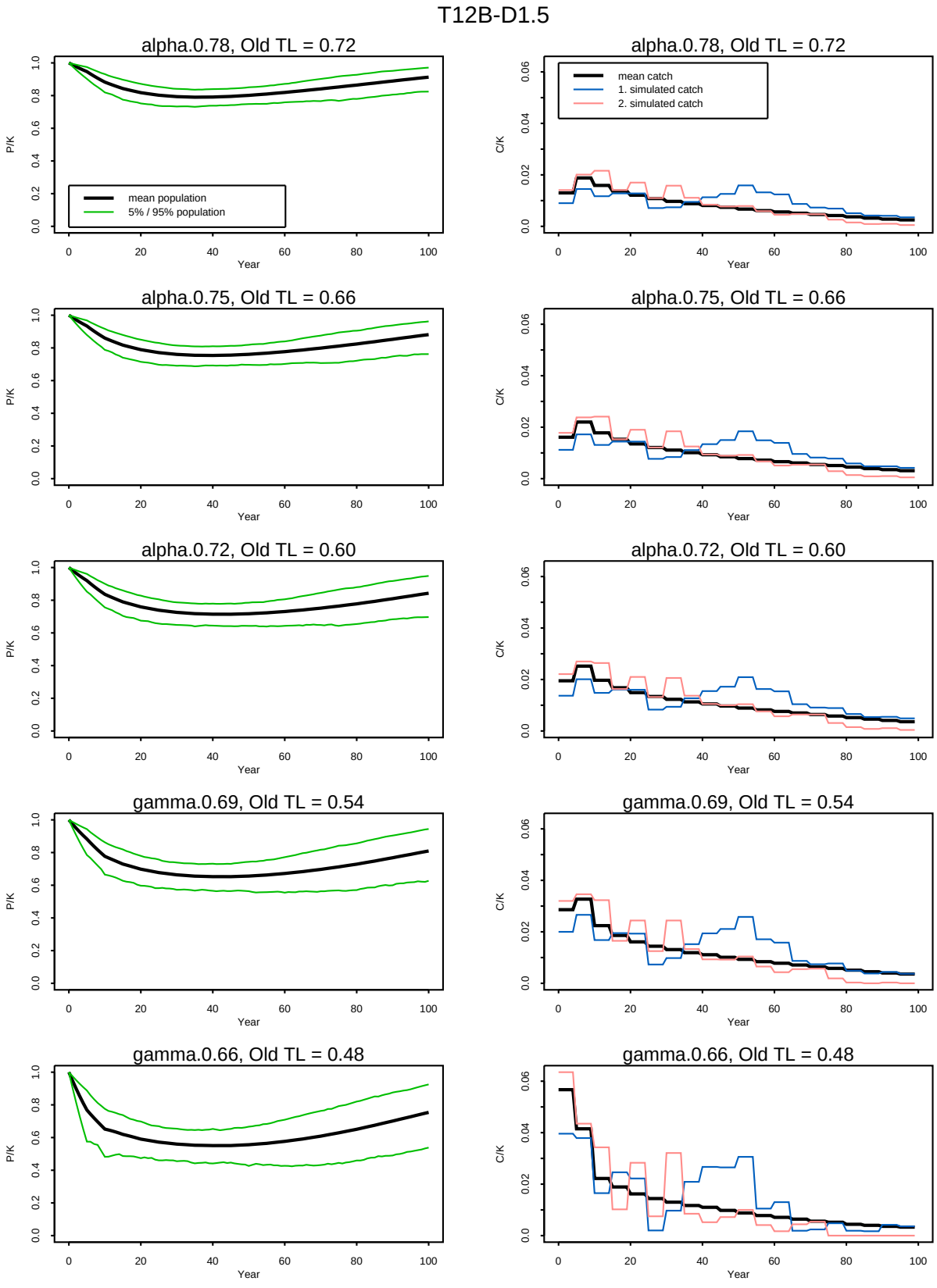


Figure 39. Trial T12B-D1.5. Linear decrease in K from K_0 to $0.5 \cdot K_0$ after 100 years.

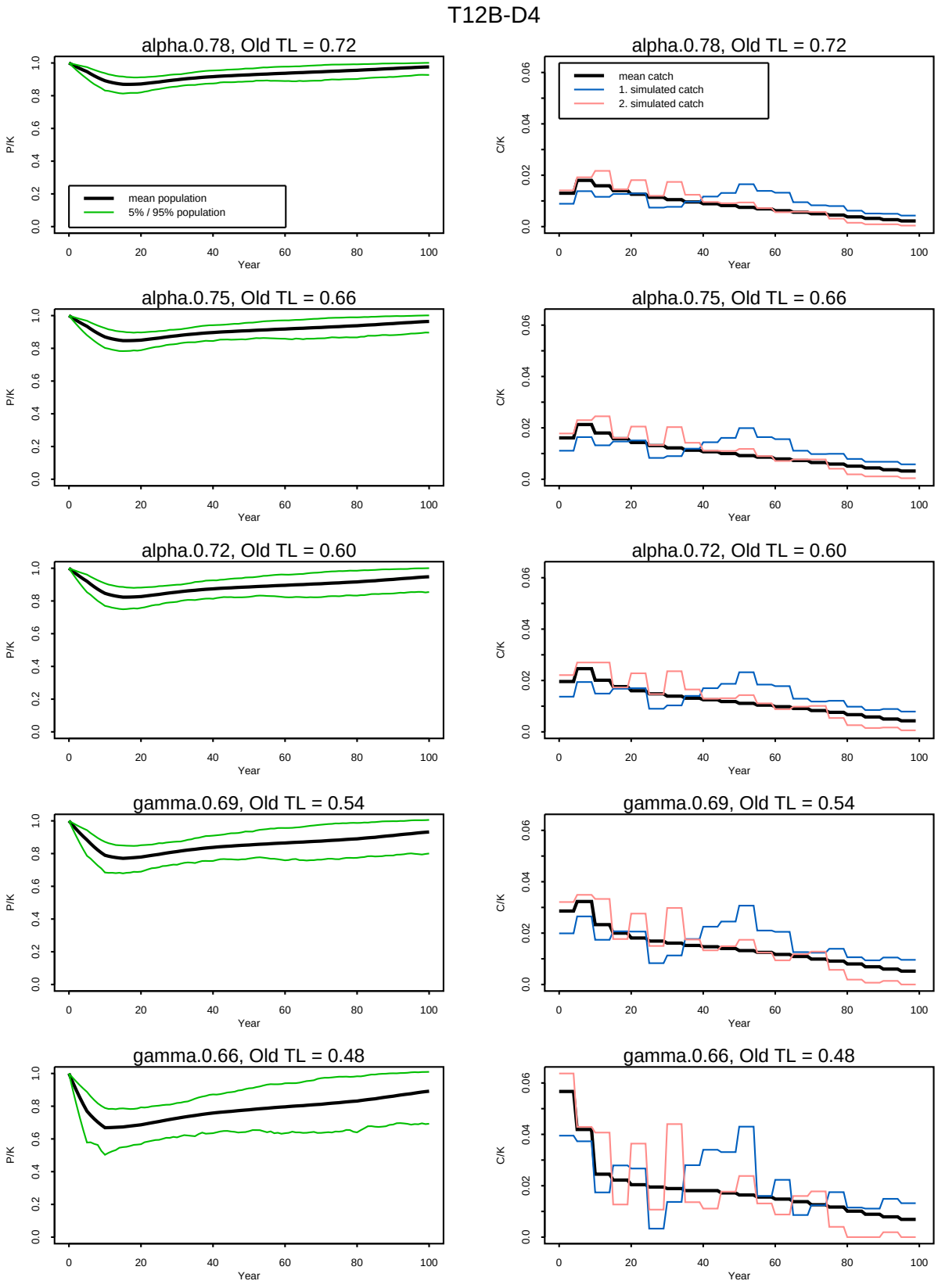


Figure 40. Trial T12B-D4. Linear decrease in K from K_0 to $0.5 \cdot K_0$ after 100 years.

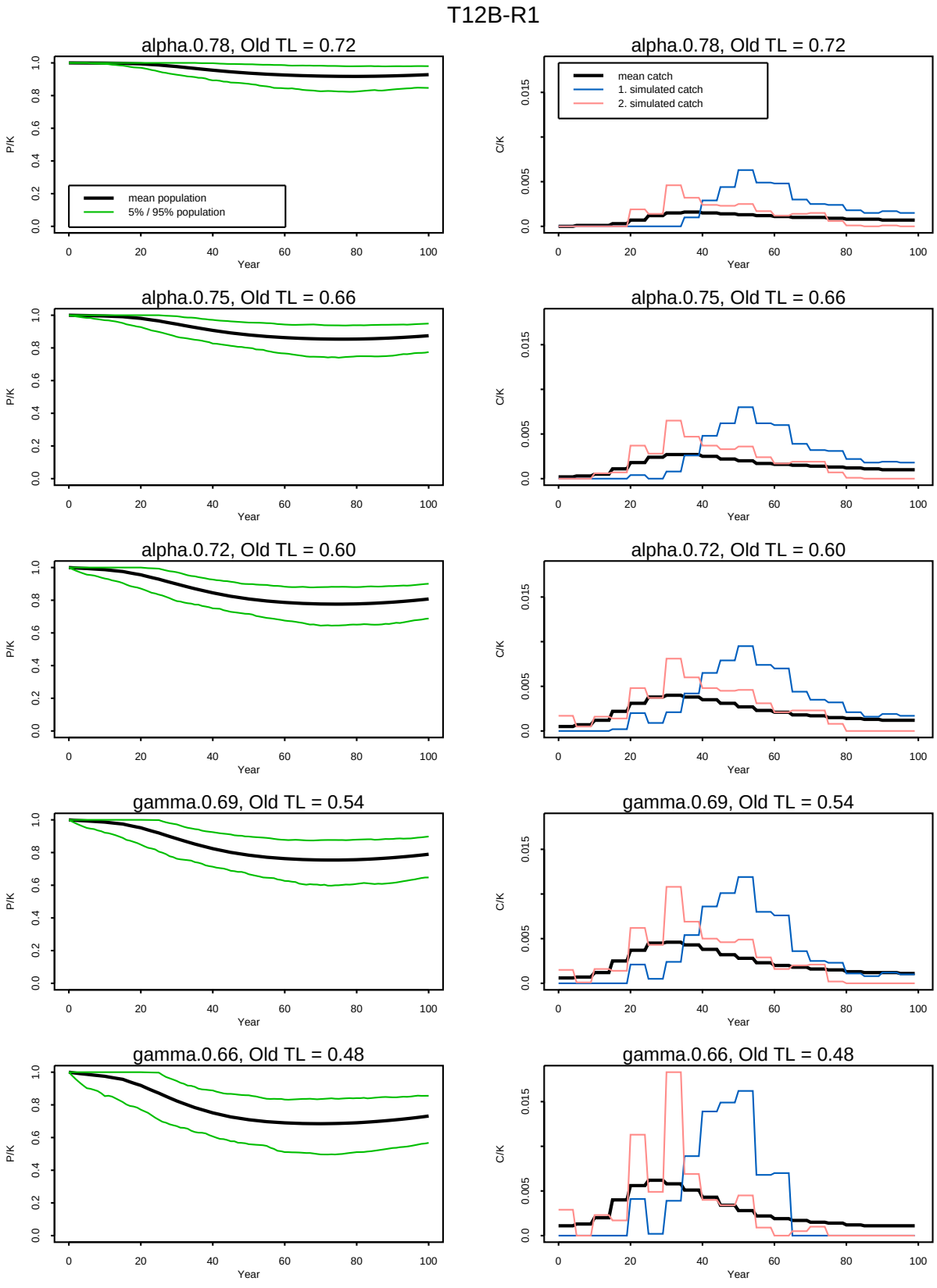


Figure 41. Trial T12B-R1. Linear decrease in K from K_0 to $0.5 \cdot K_0$ after 100 years.

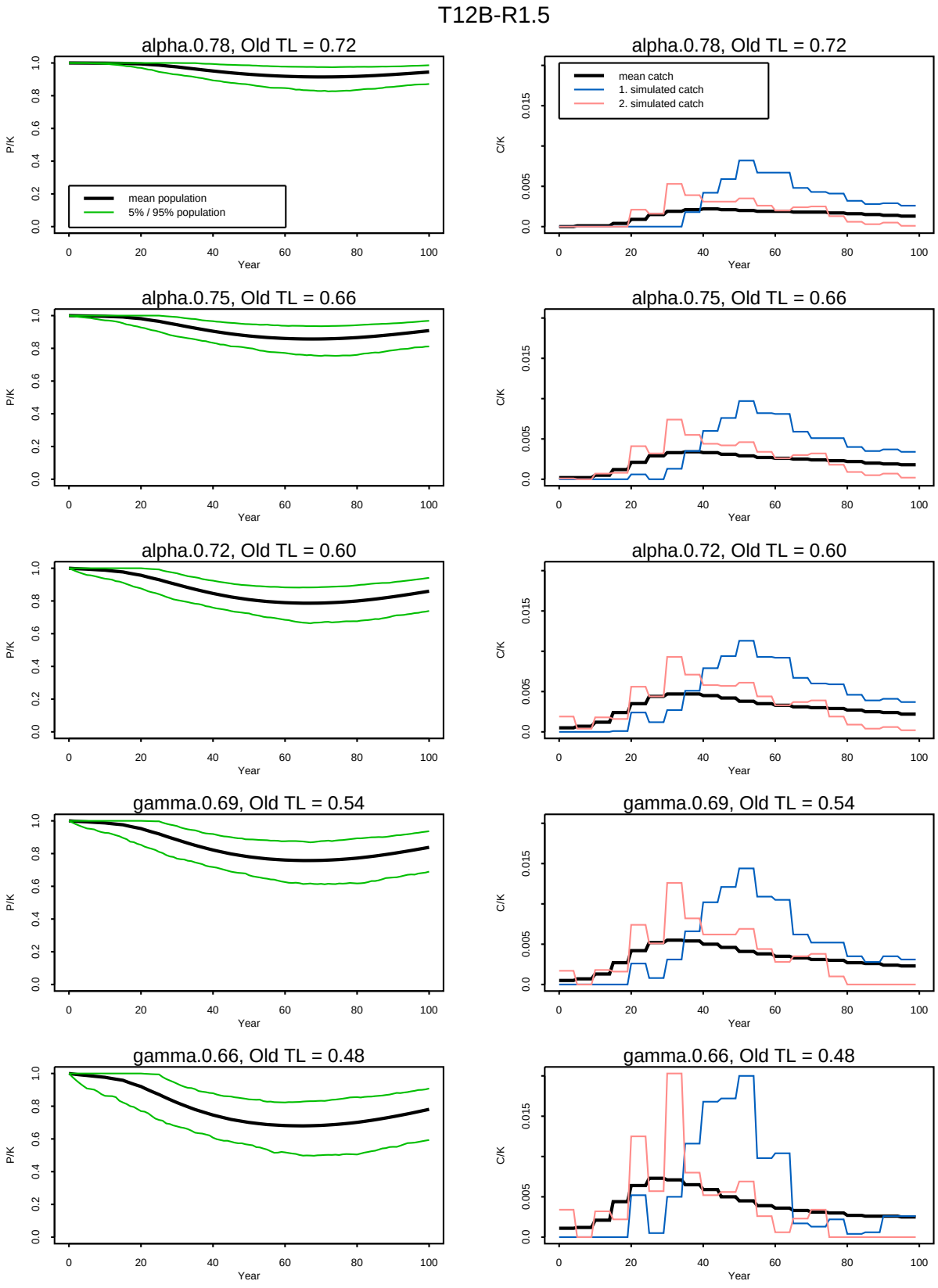


Figure 42. Trial T12B-R1.5. Linear decrease in K from K_0 to $0.5 \cdot K_0$ after 100 years.

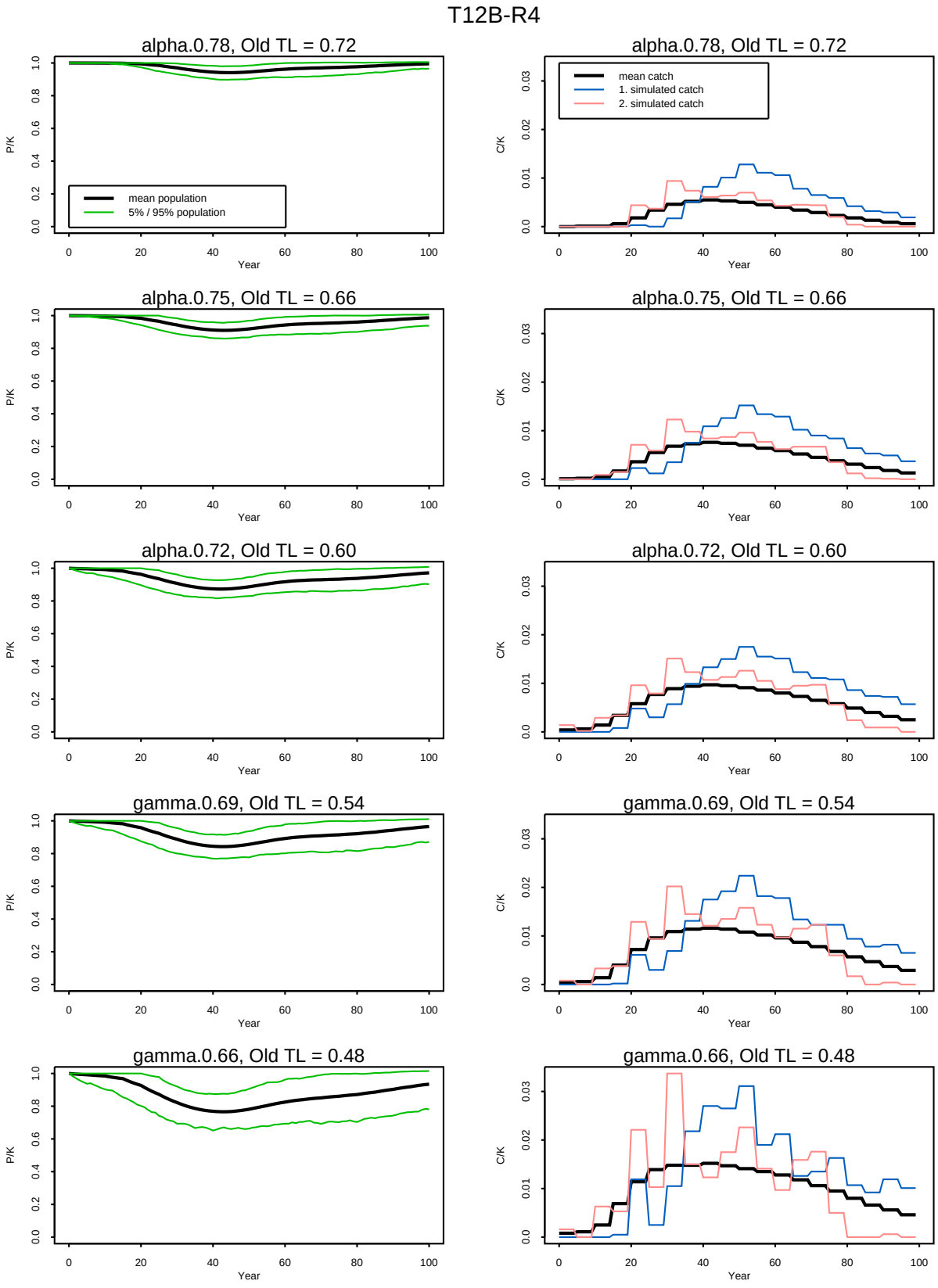


Figure 43. Trial T12B-R4. Linear decrease in K from K_0 to $0.5 \cdot K_0$ after 100 years.

3.2 Results of response curve trials in Tables 3-6

In this Section, the results of the trials specified in Tables 3-6 are shown as response curves plots in Figures 44-67, as requested in CLA06. In addition, the results may be downloaded in tabular form from
`http://www.nr.no/~aldrin/whales/ResponseCurveTrialsResults2007.pdf`.

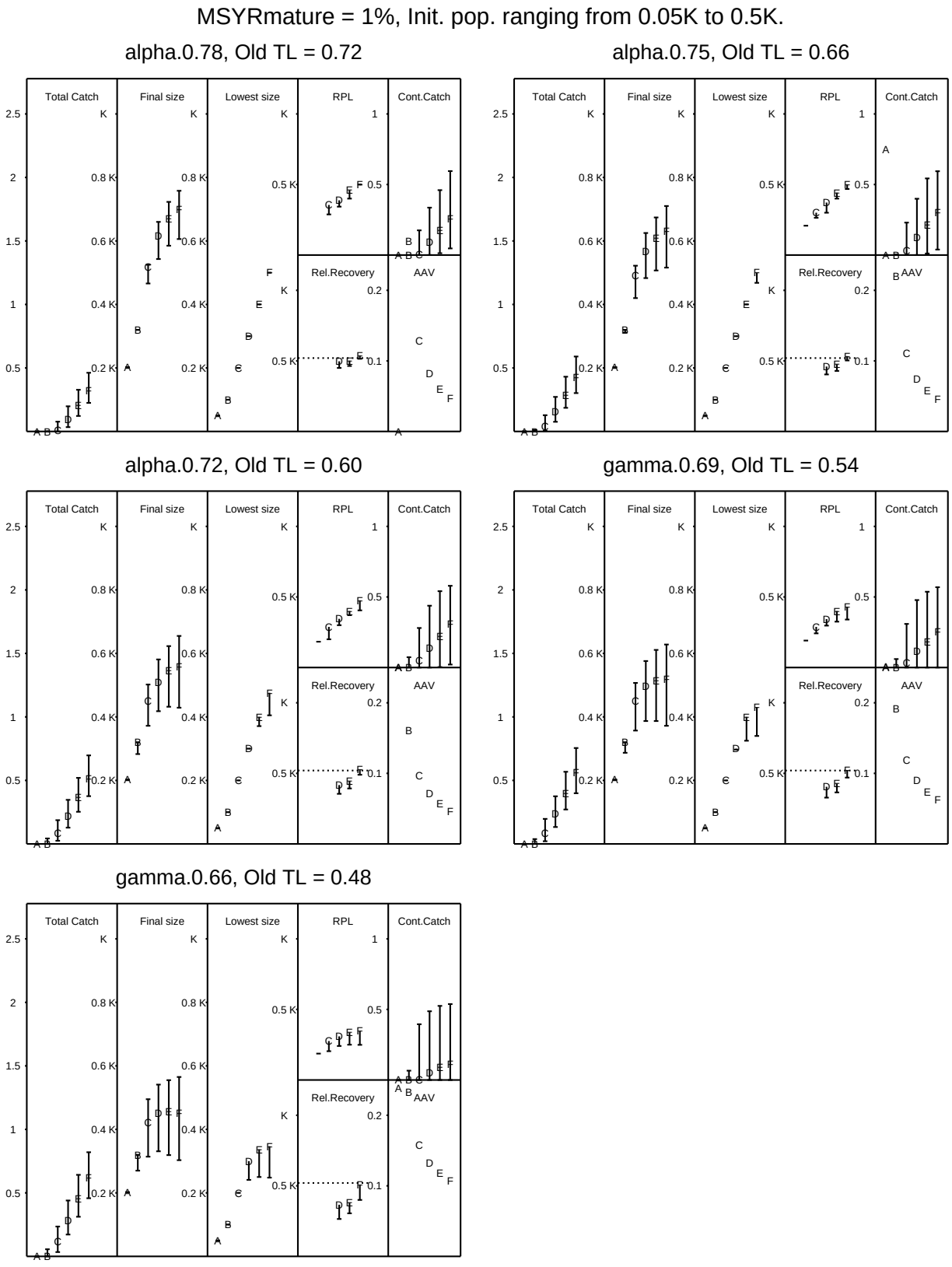


Figure 44. Sample response curves. The horizontal dashed line in the Relative Recovery panel denotes the 0.54 K level.

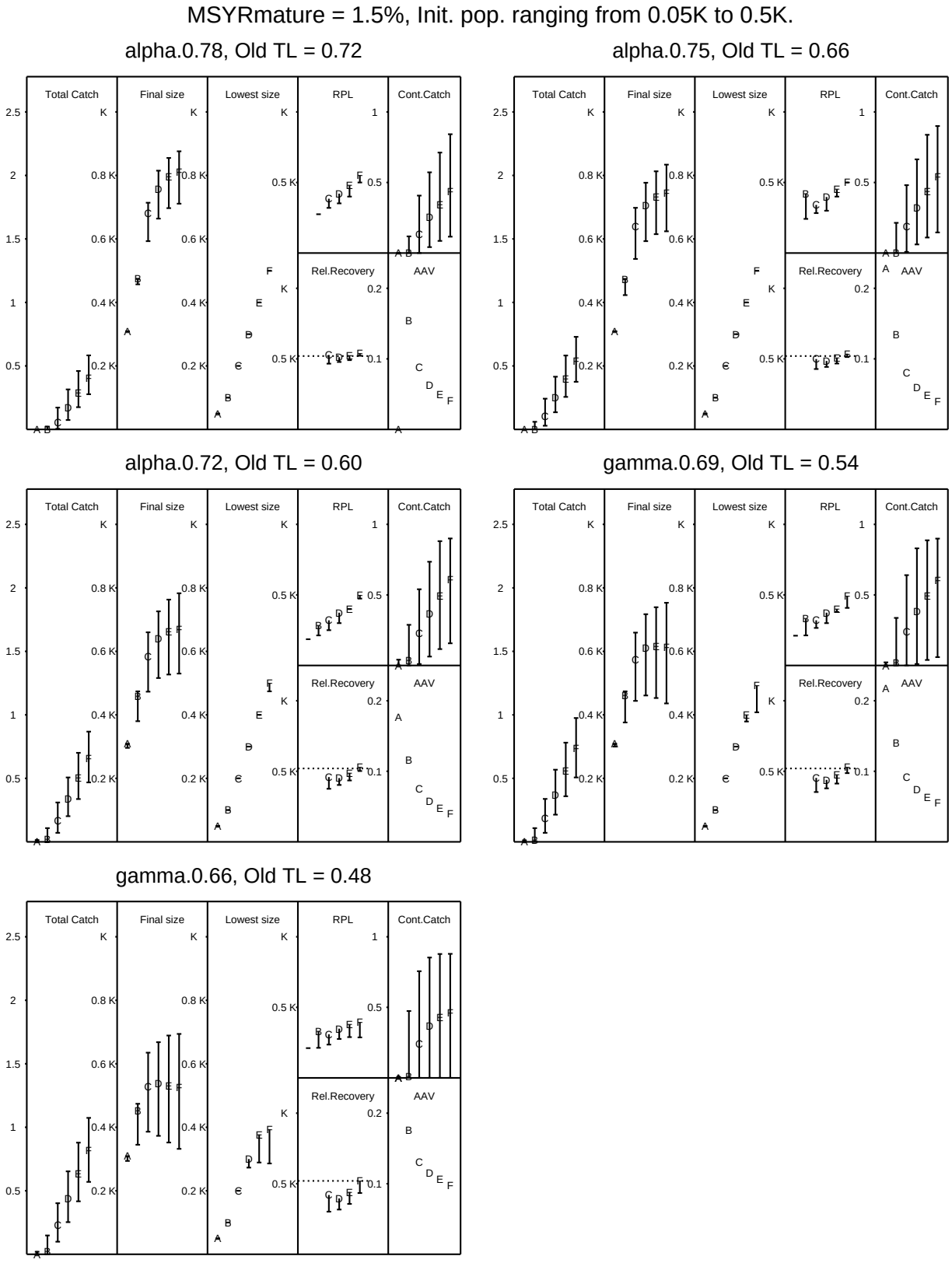


Figure 45. Sample response curves.

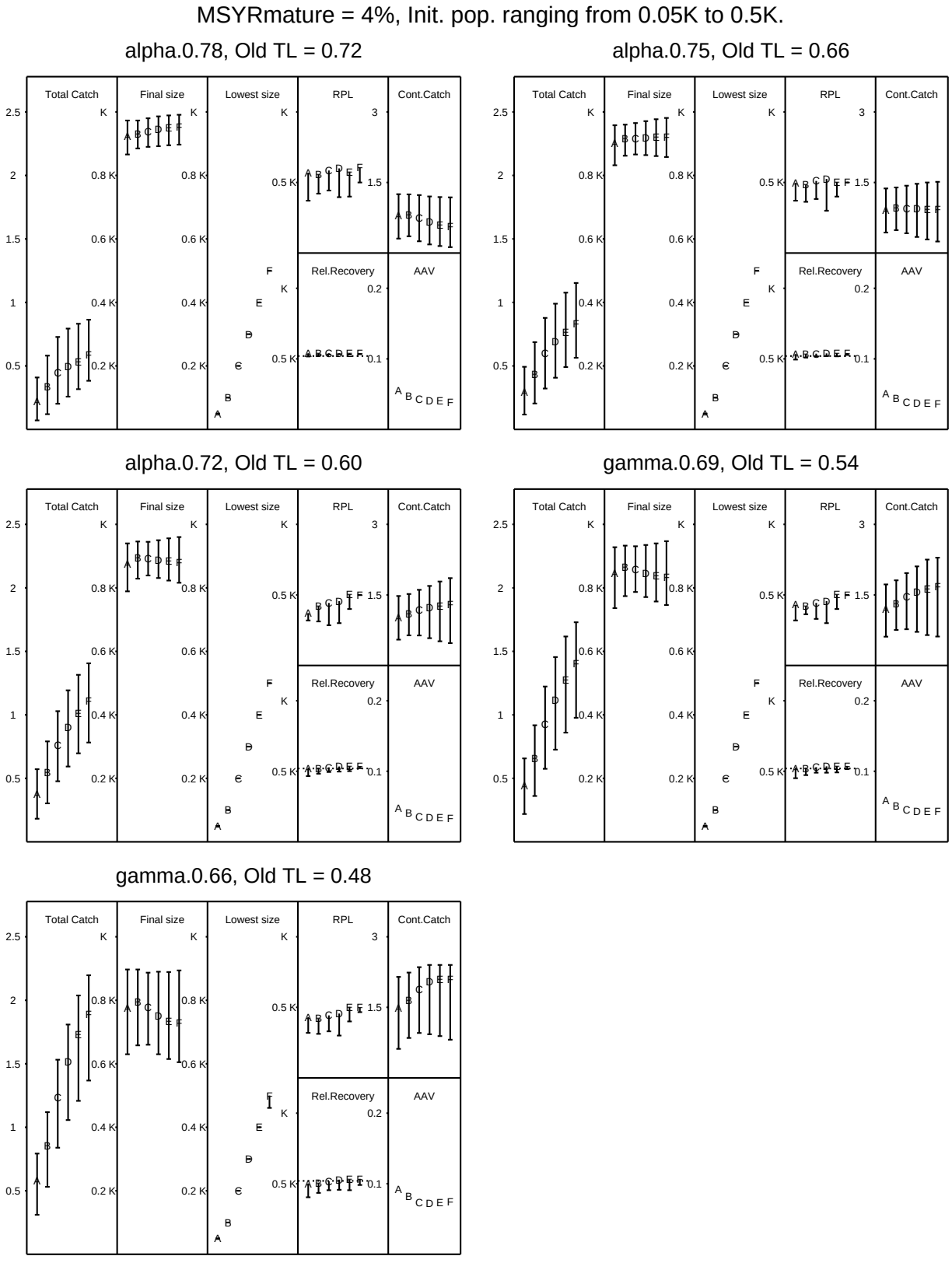


Figure 46. Sample response curves.

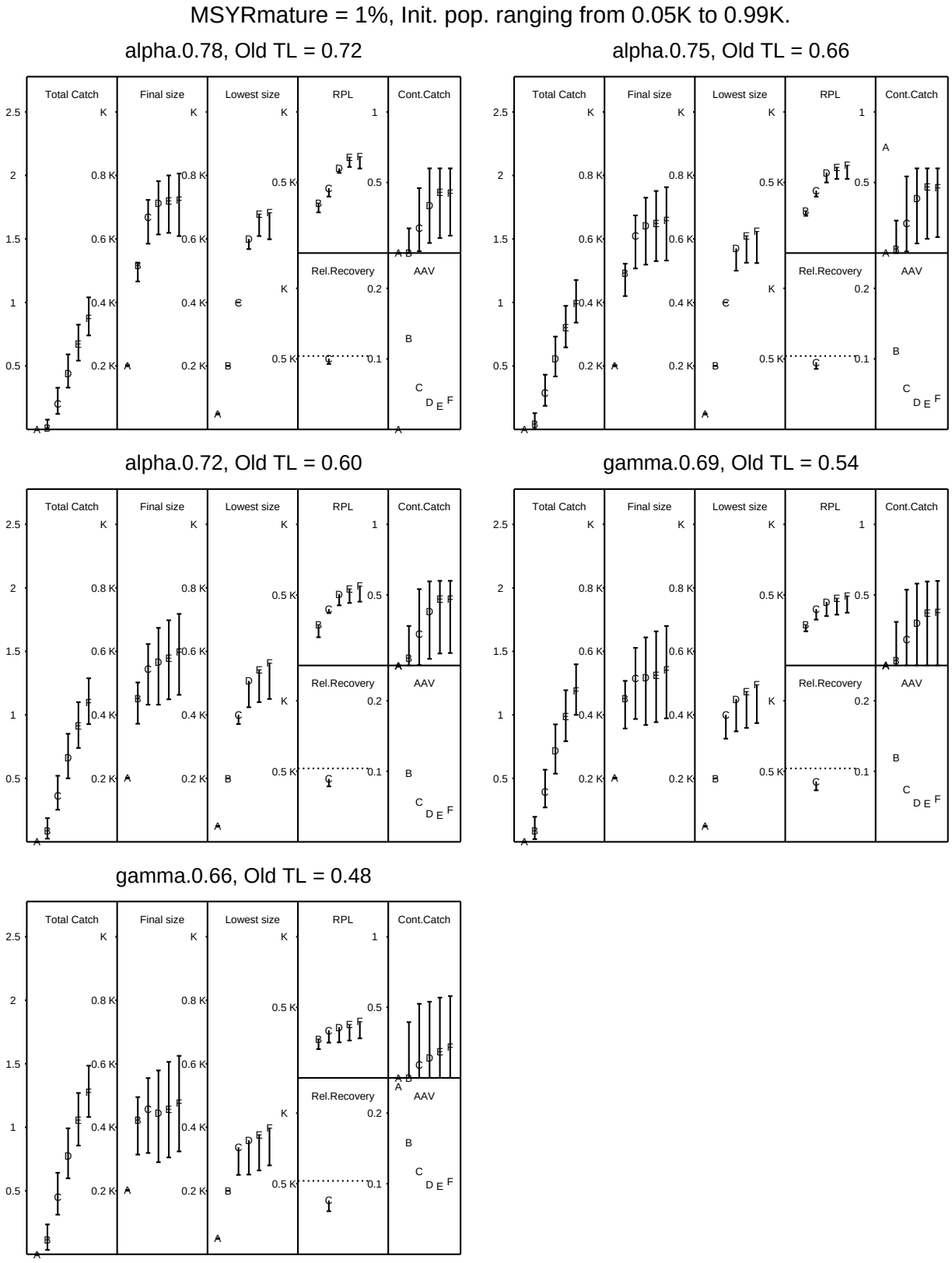


Figure 47. Sample response curves.

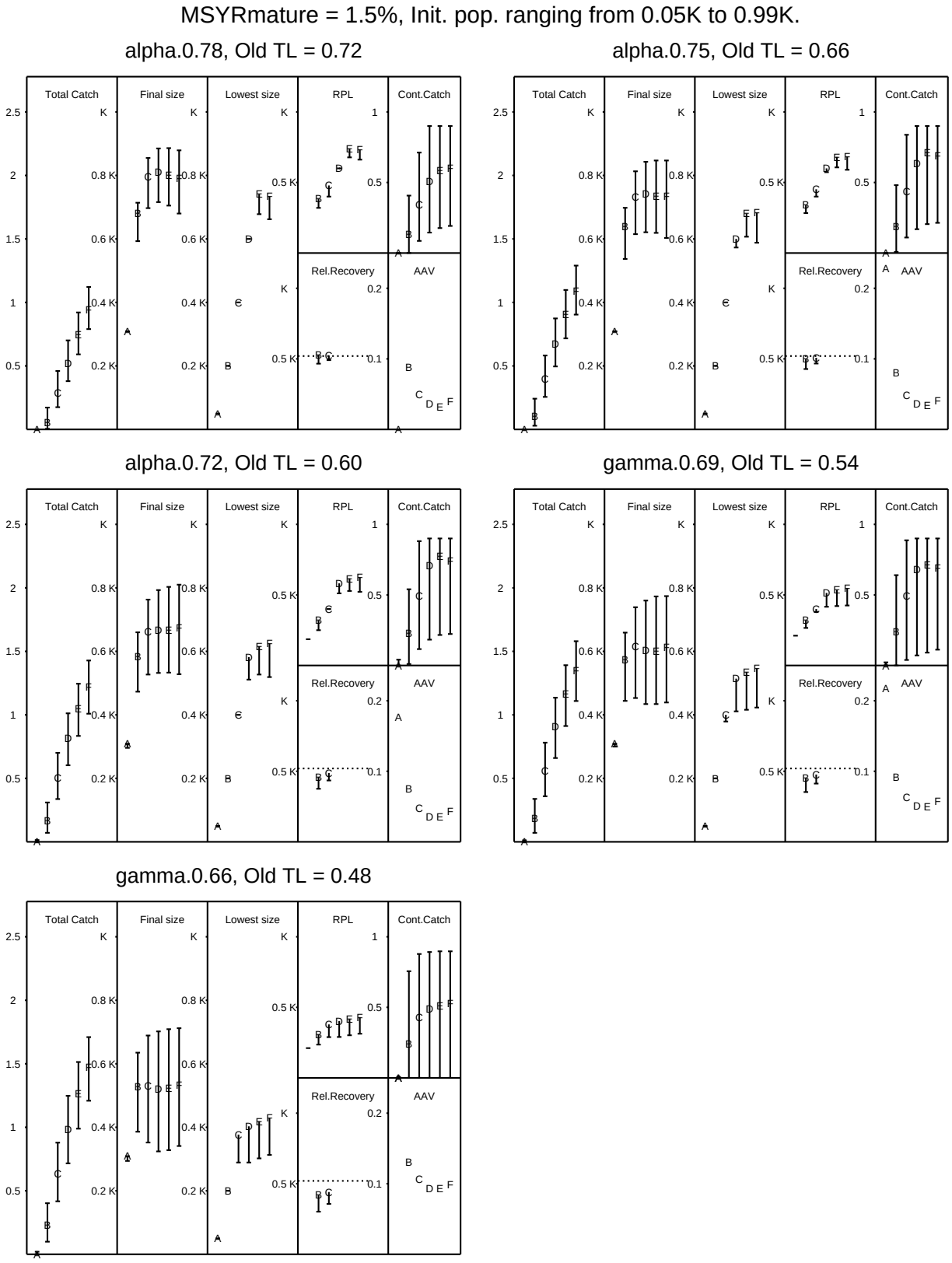


Figure 48. Sample response curves.

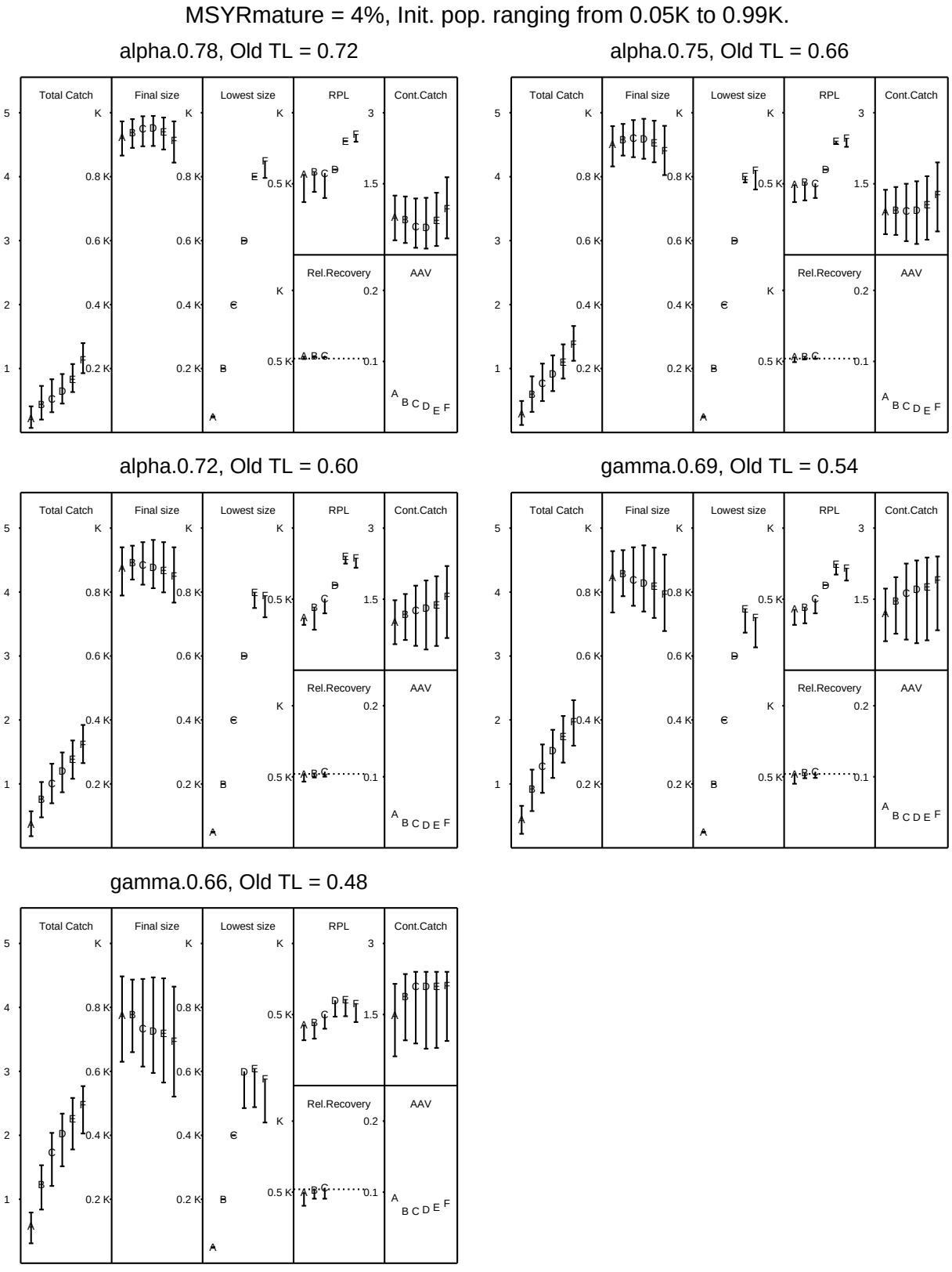


Figure 49. Sample response curves.

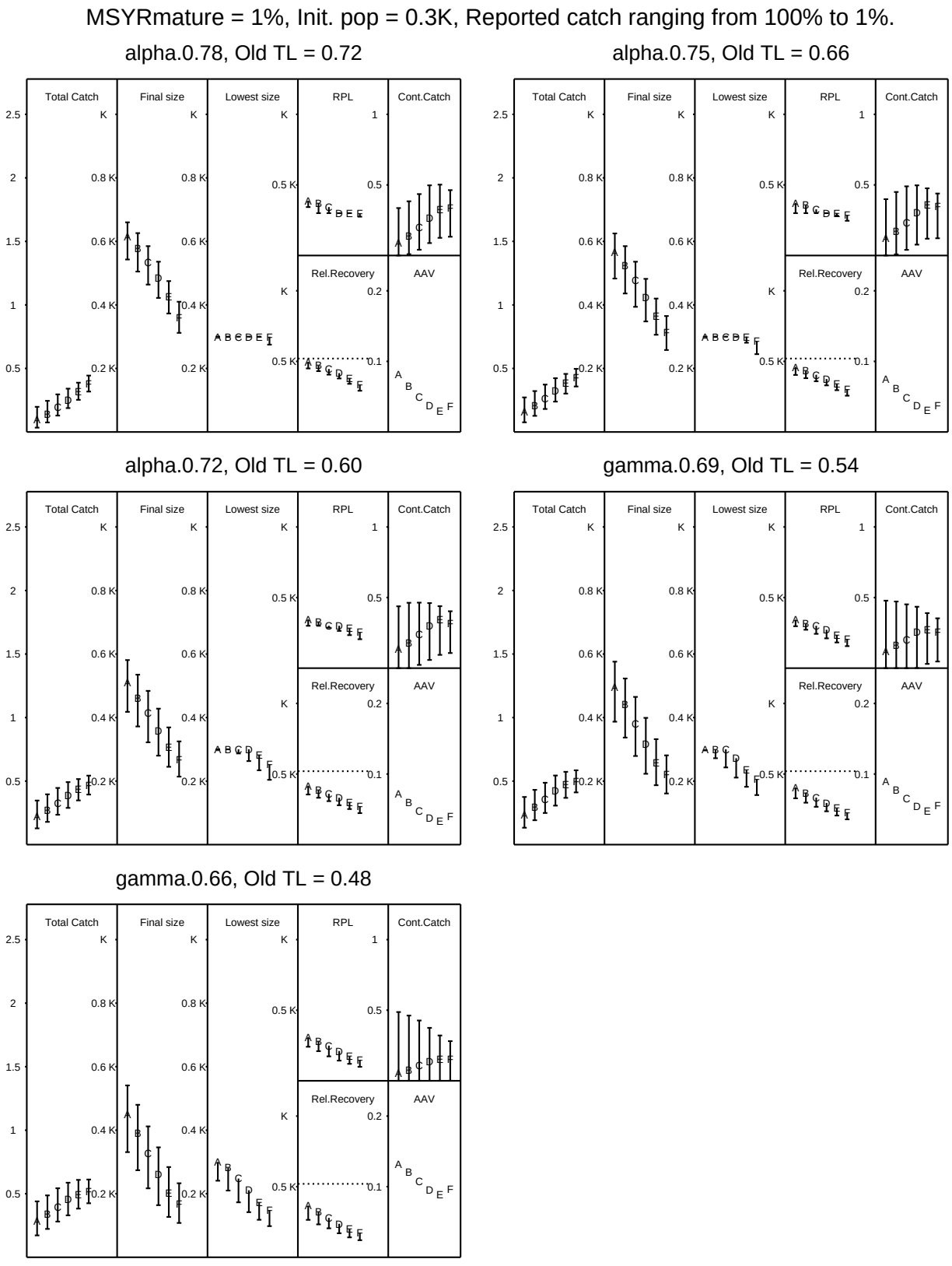


Figure 50. Sample response curves.

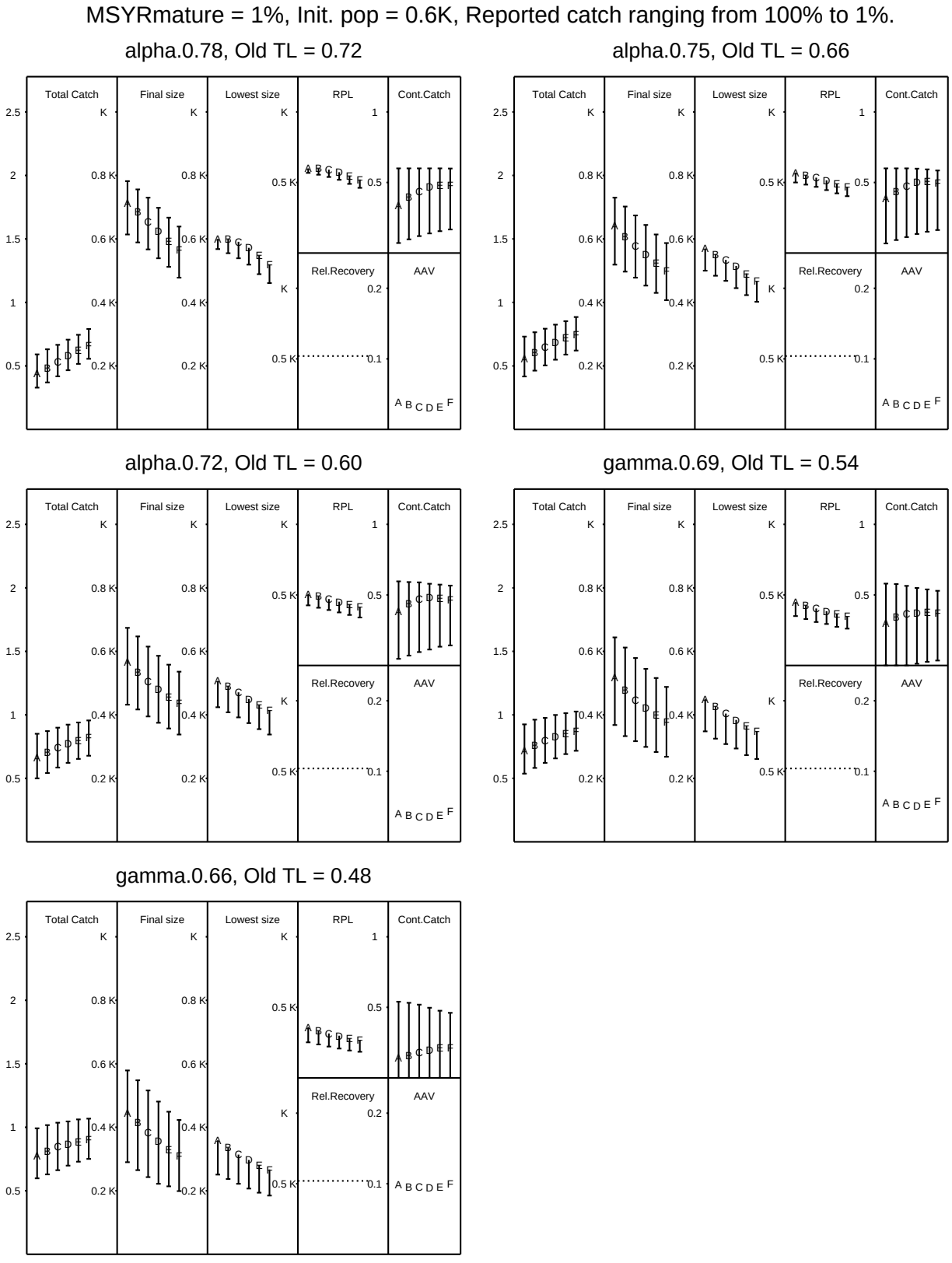


Figure 51. Sample response curves.

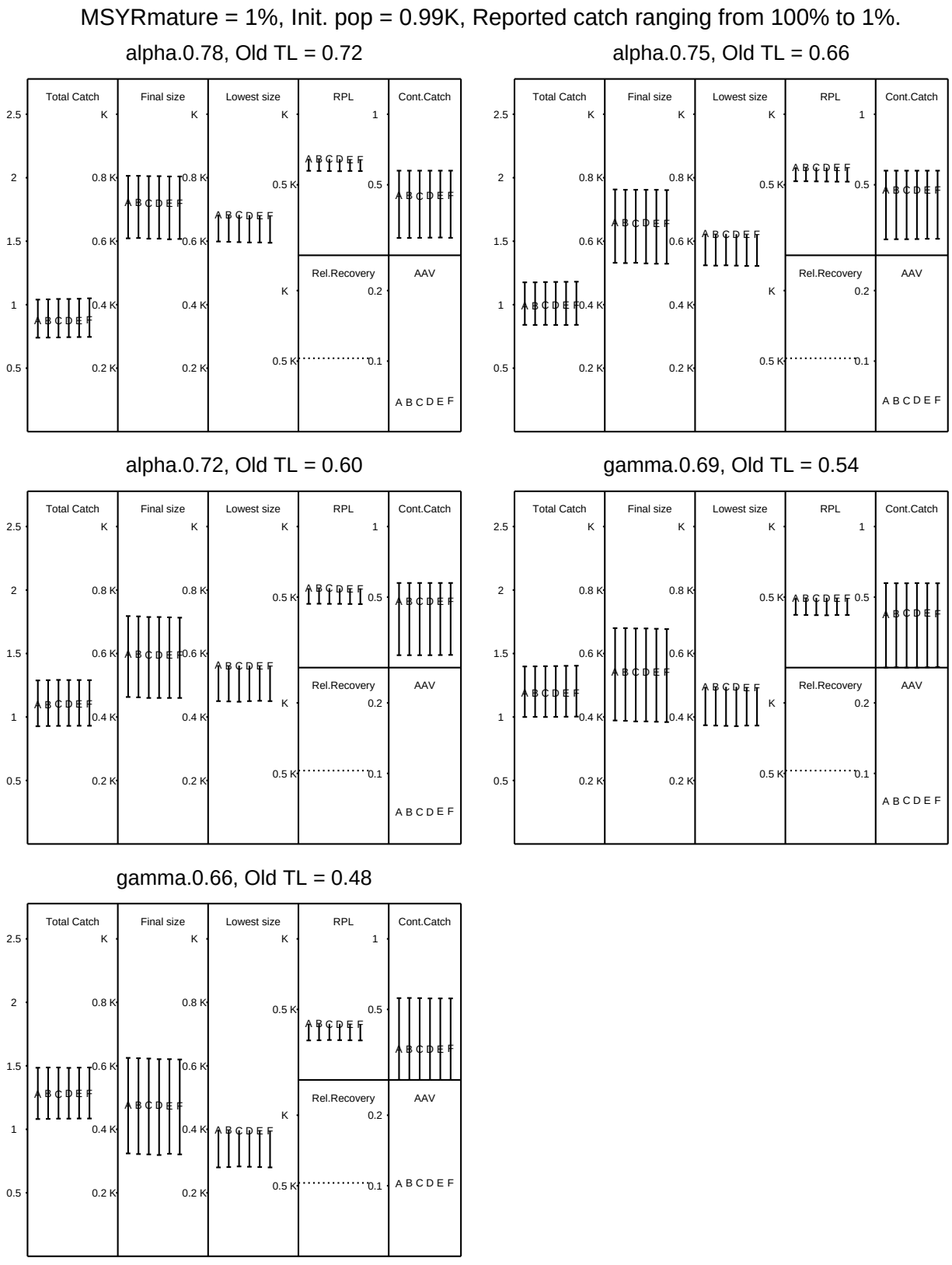


Figure 52. Sample response curves.

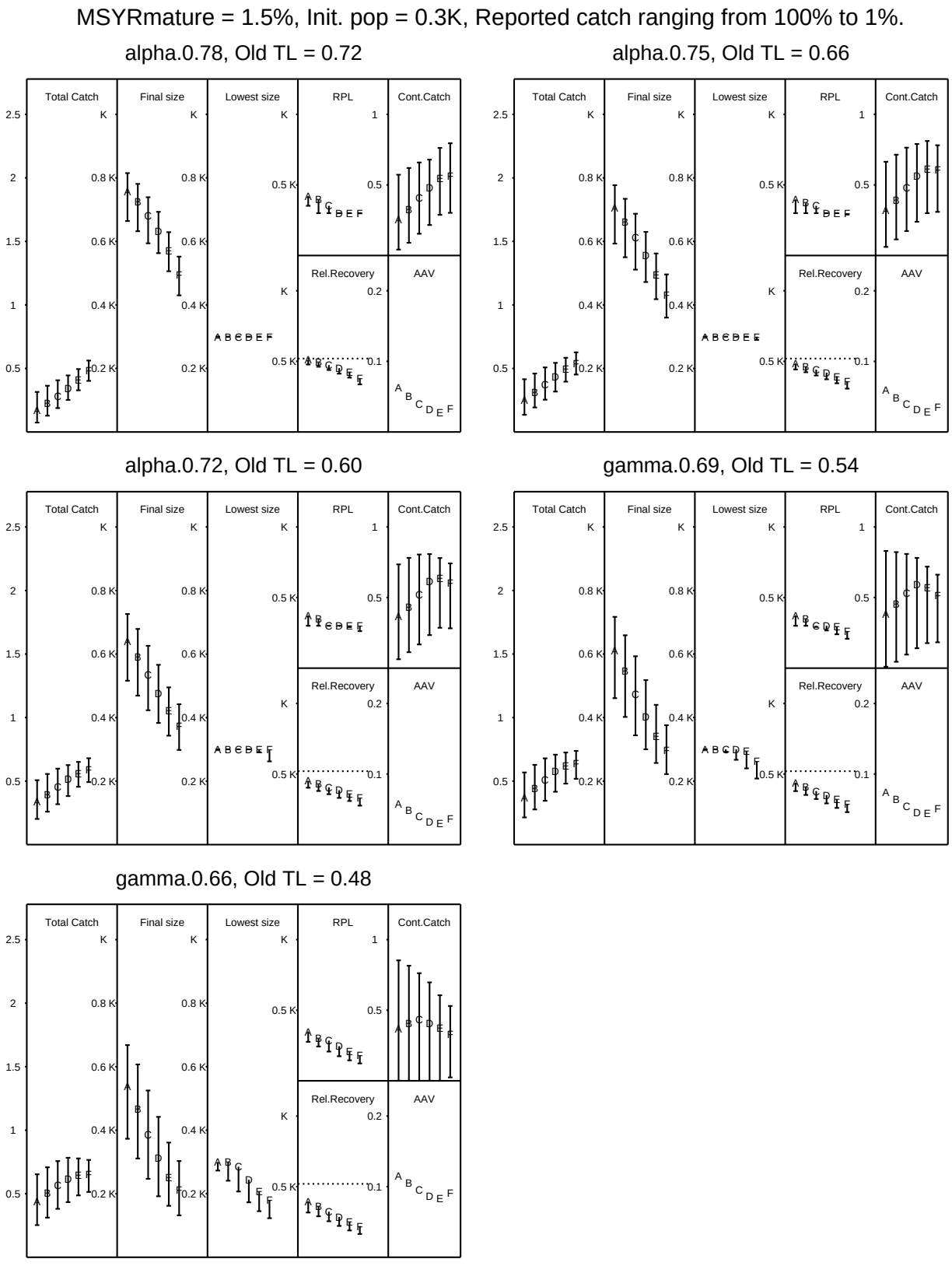


Figure 53. Sample response curves.

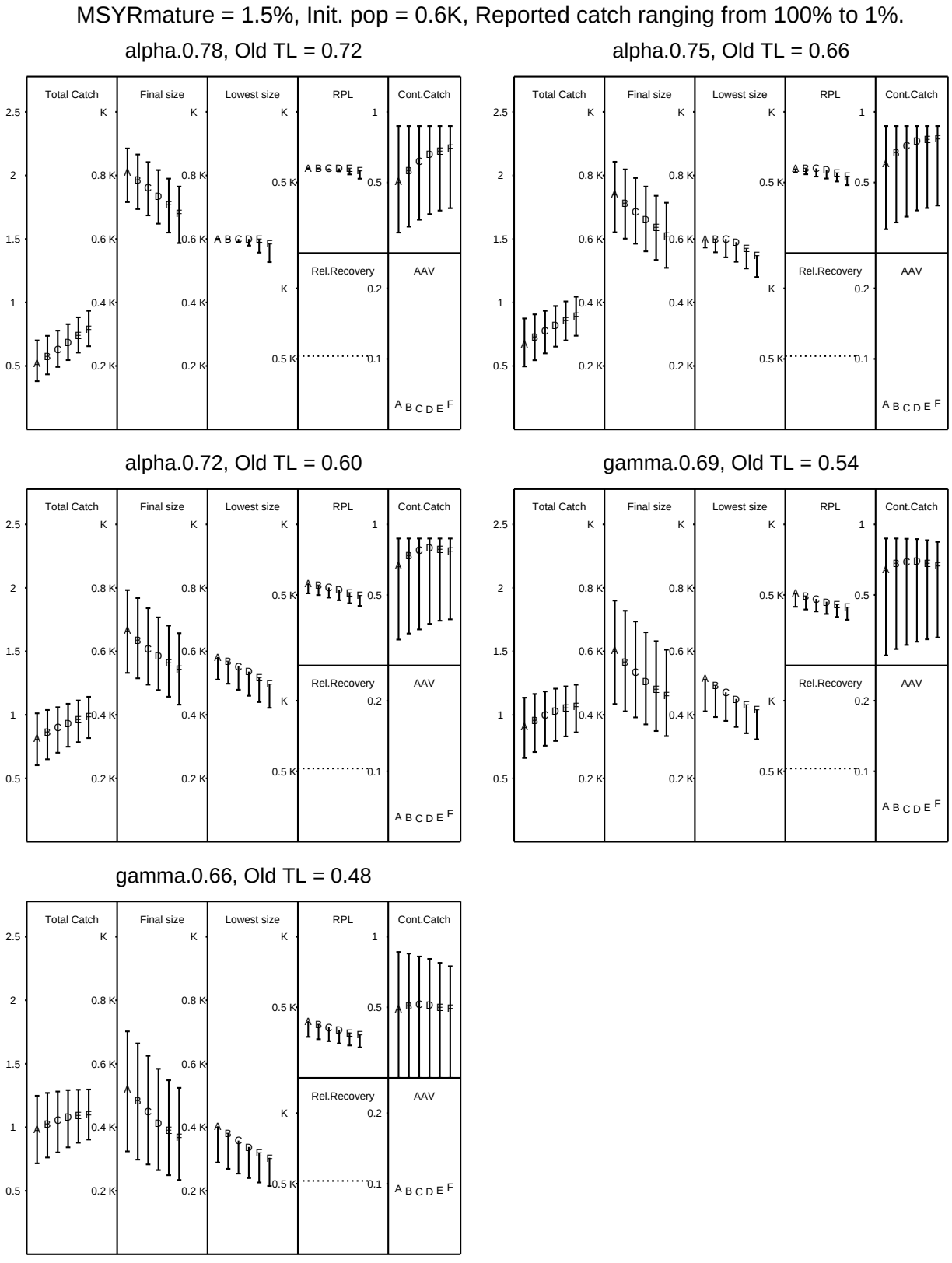


Figure 54. Sample response curves.

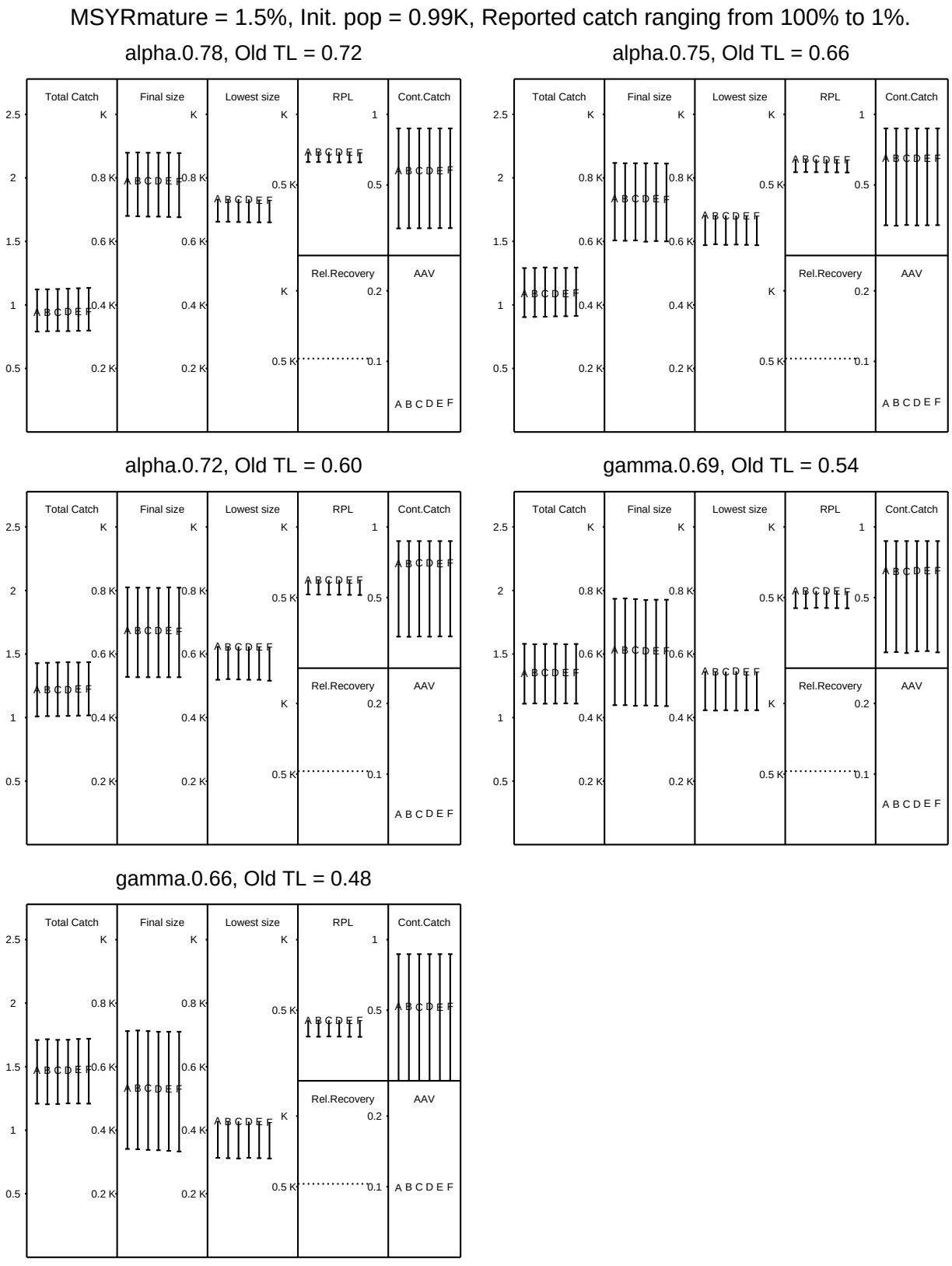


Figure 55. Sample response curves.

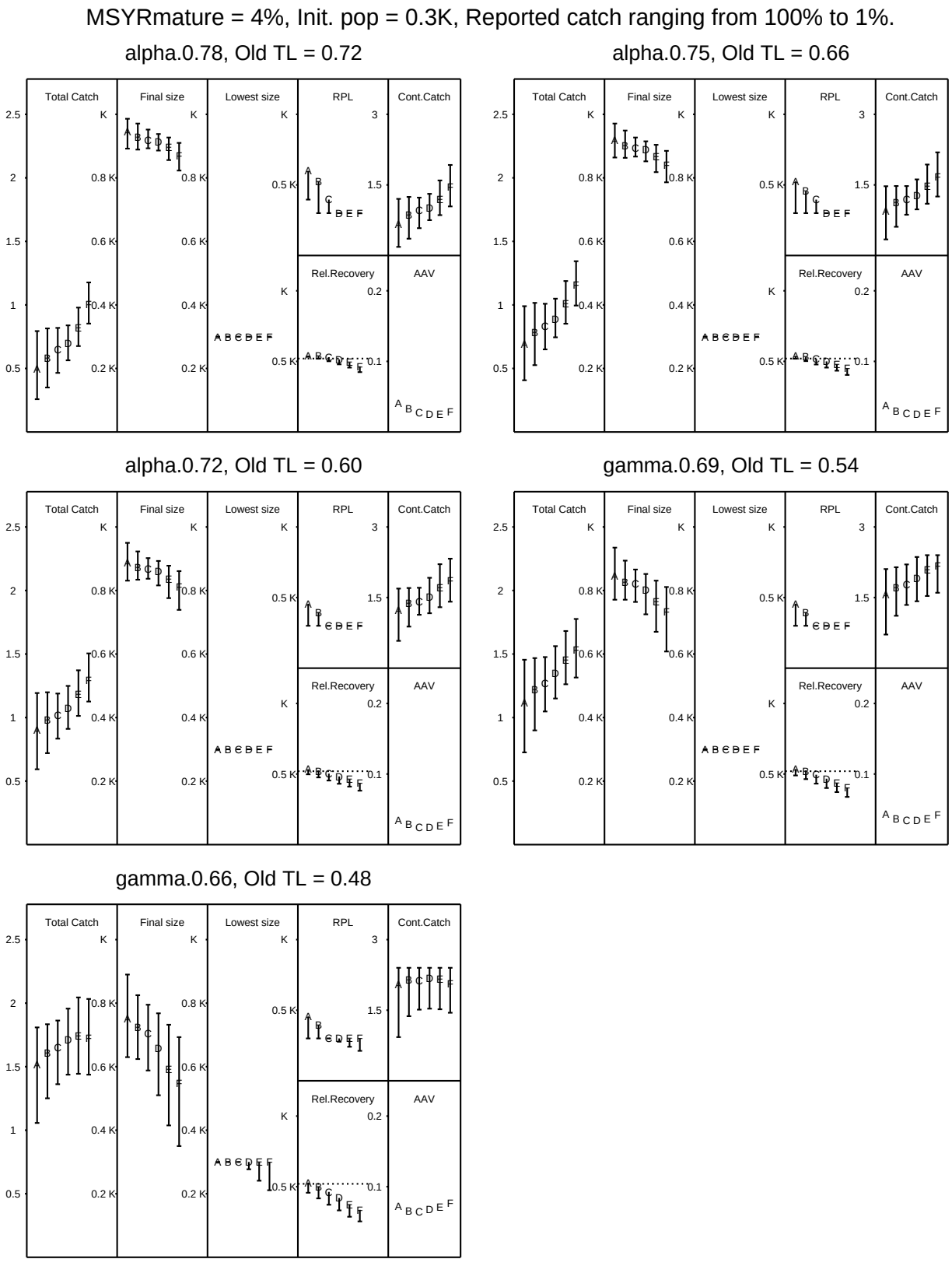


Figure 56. Sample response curves.

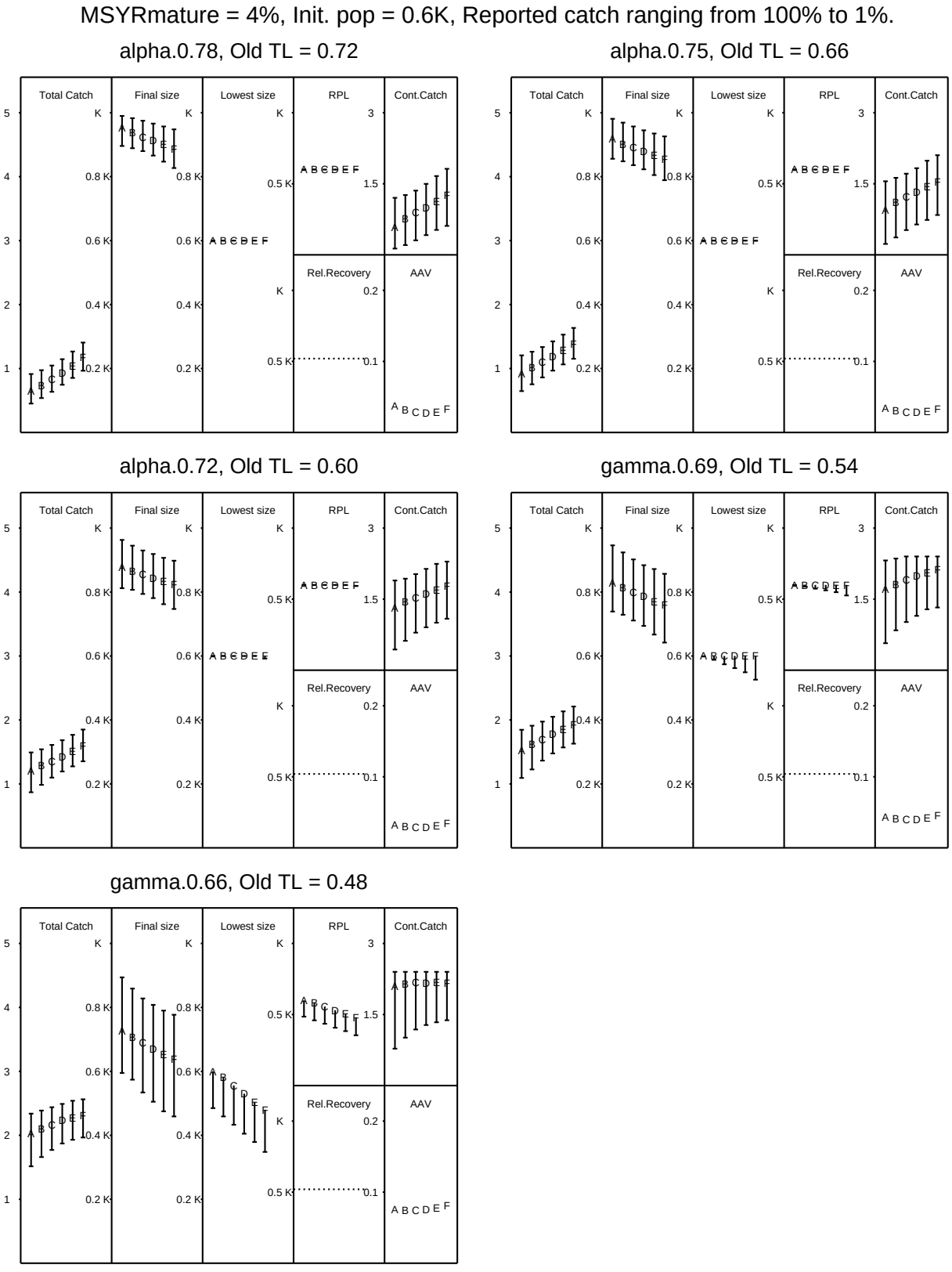


Figure 57. Sample response curves.

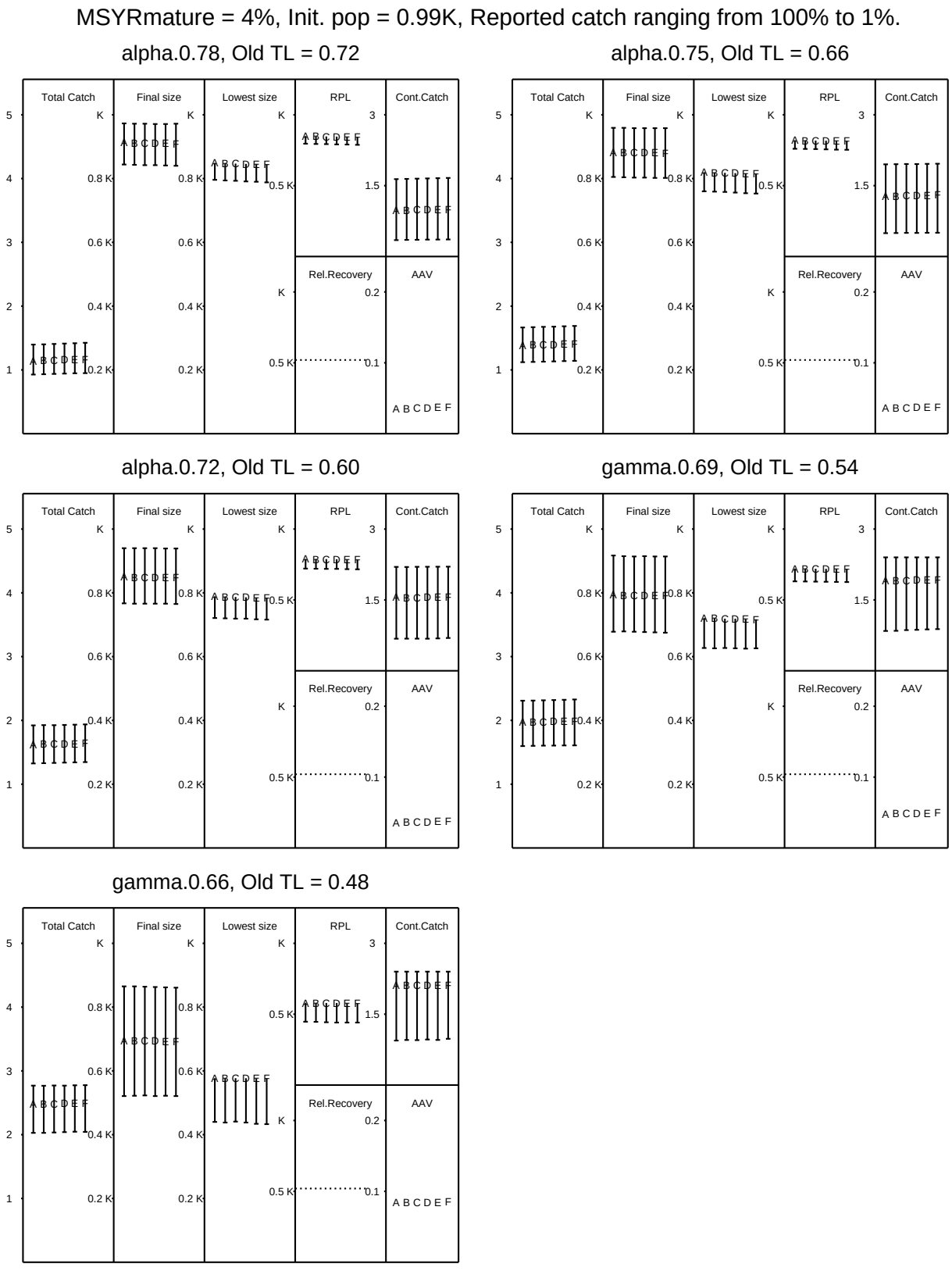


Figure 58. Sample response curves.

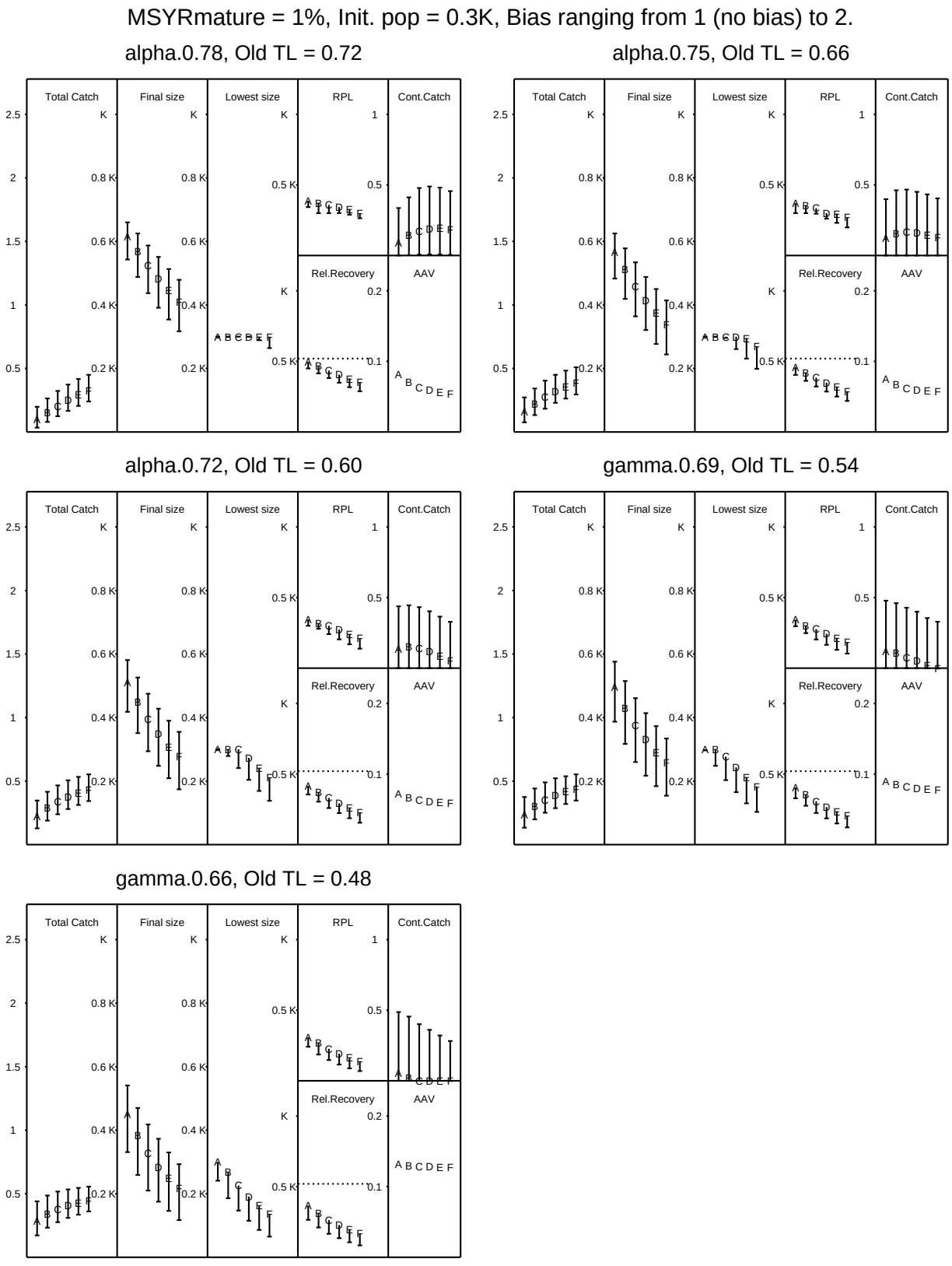
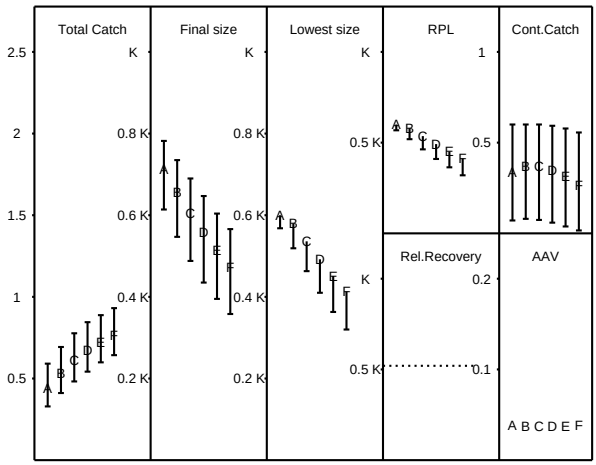


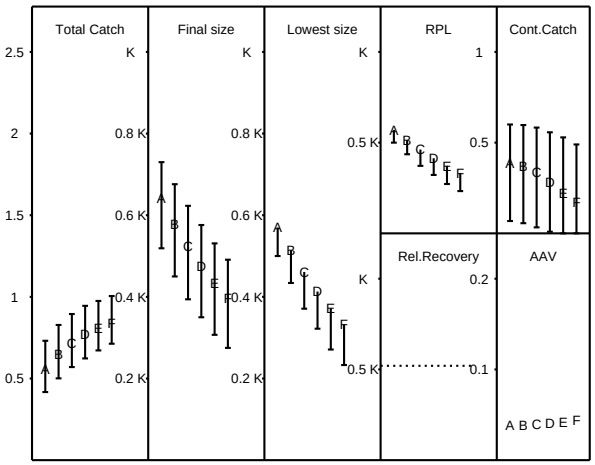
Figure 59. Sample response curves.

MSYRmature = 1%, Init. pop = 0.6K, Bias ranging from 1 (no bias) to 2.

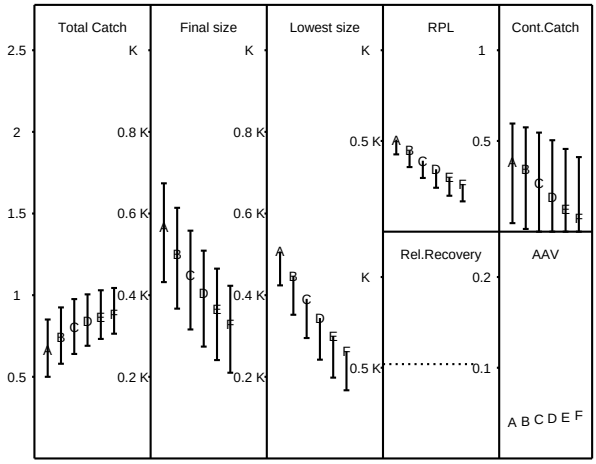
alpha.0.78, Old TL = 0.72



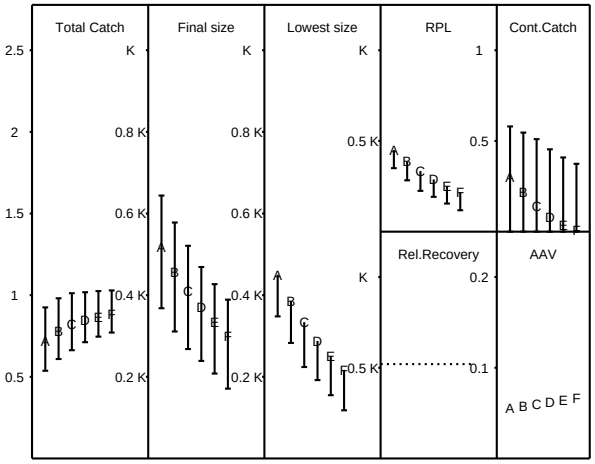
alpha.0.75, Old TL = 0.66



alpha.0.72, Old TL = 0.60



gamma.0.69, Old TL = 0.54



gamma.0.66, Old TL = 0.48

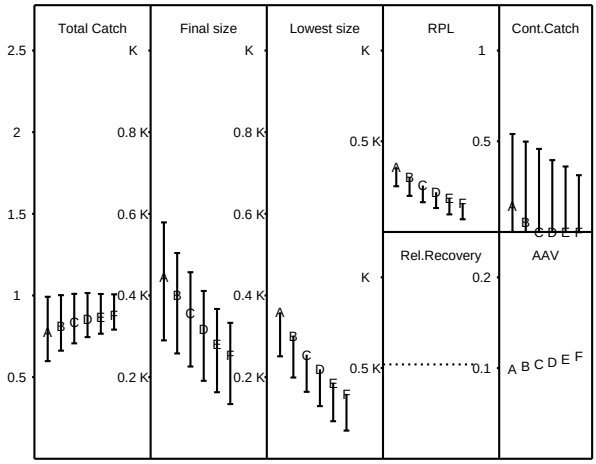


Figure 60. Sample response curves.

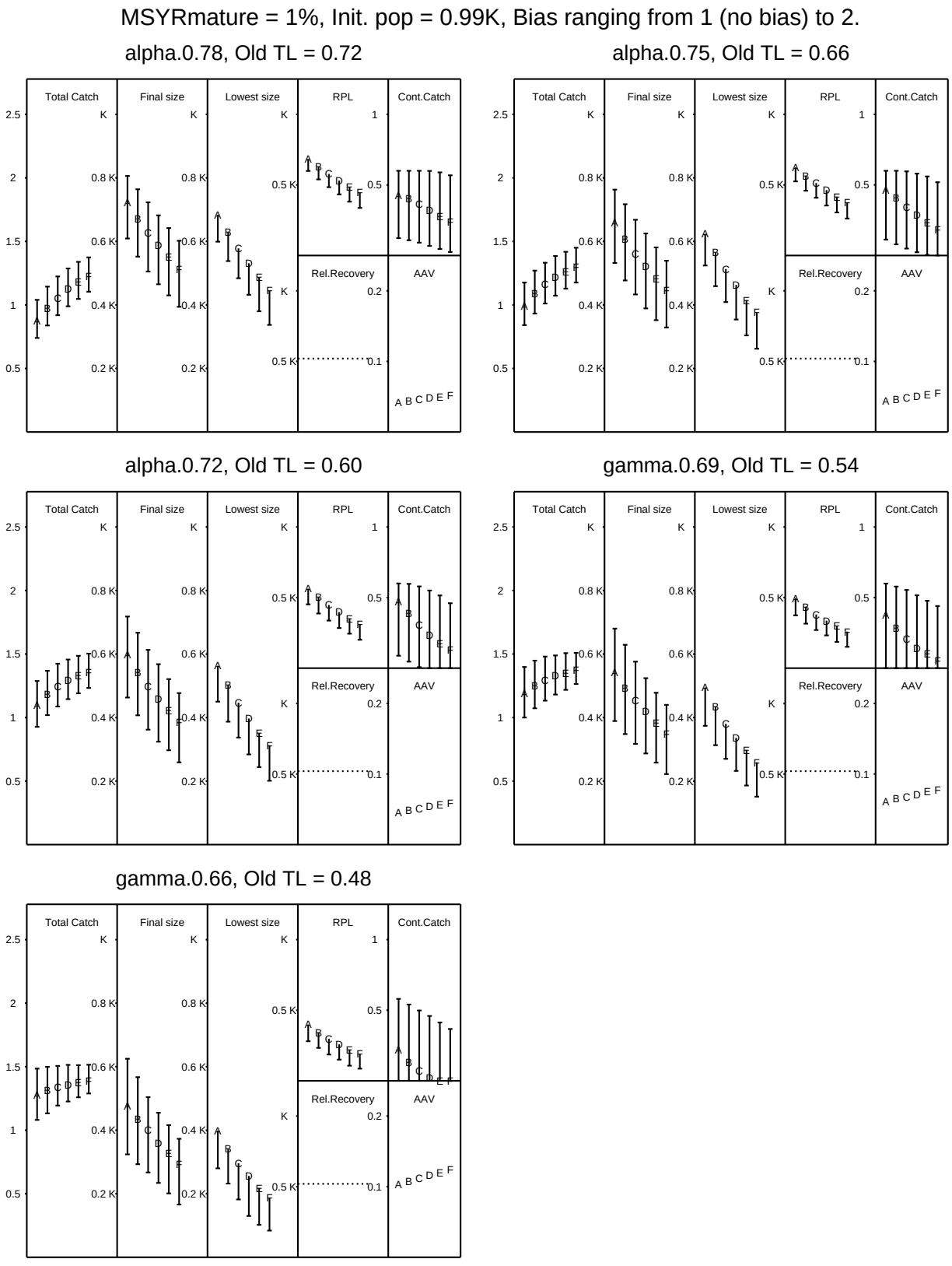


Figure 61. Sample response curves.

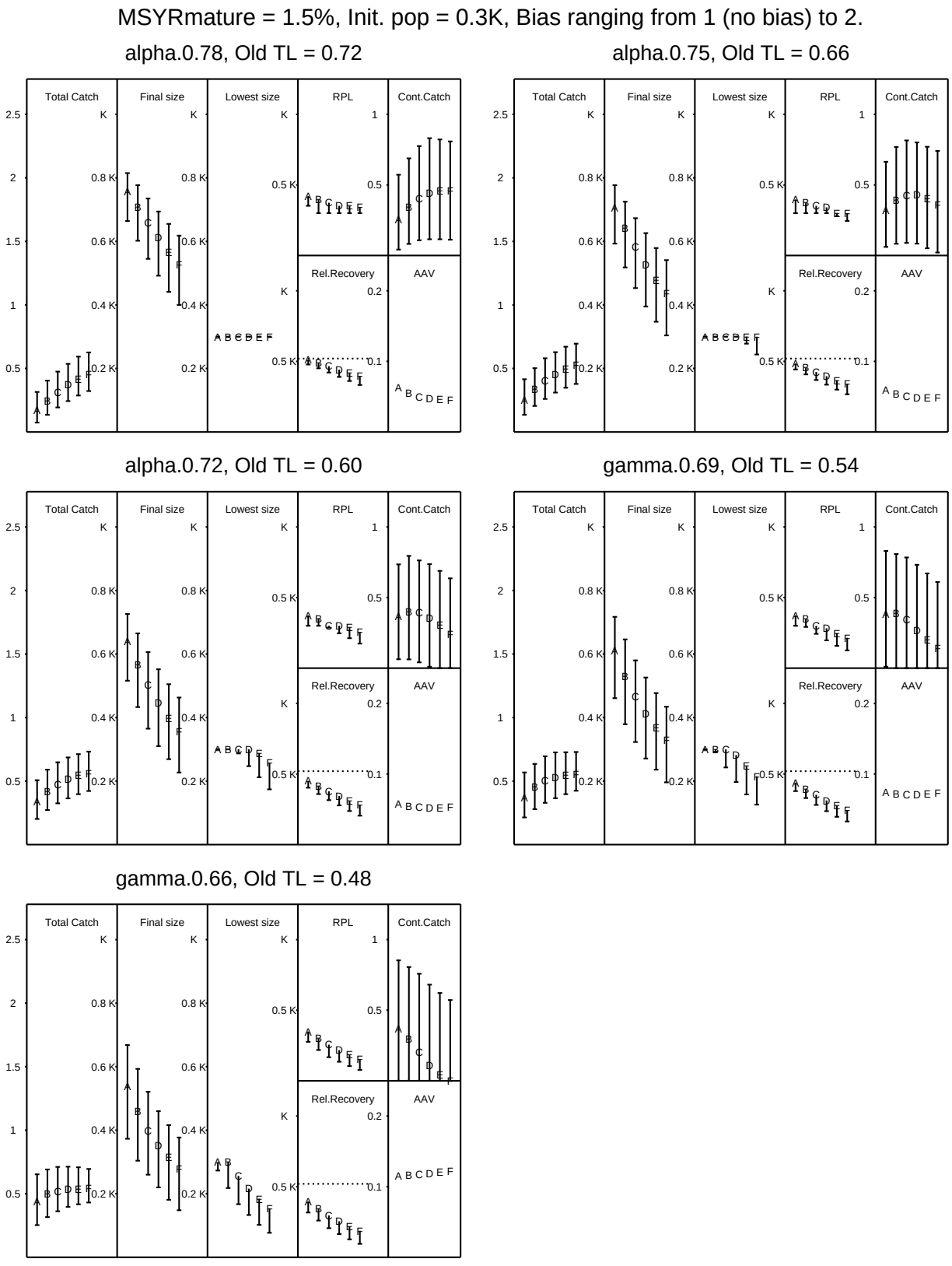


Figure 62. Sample response curves.

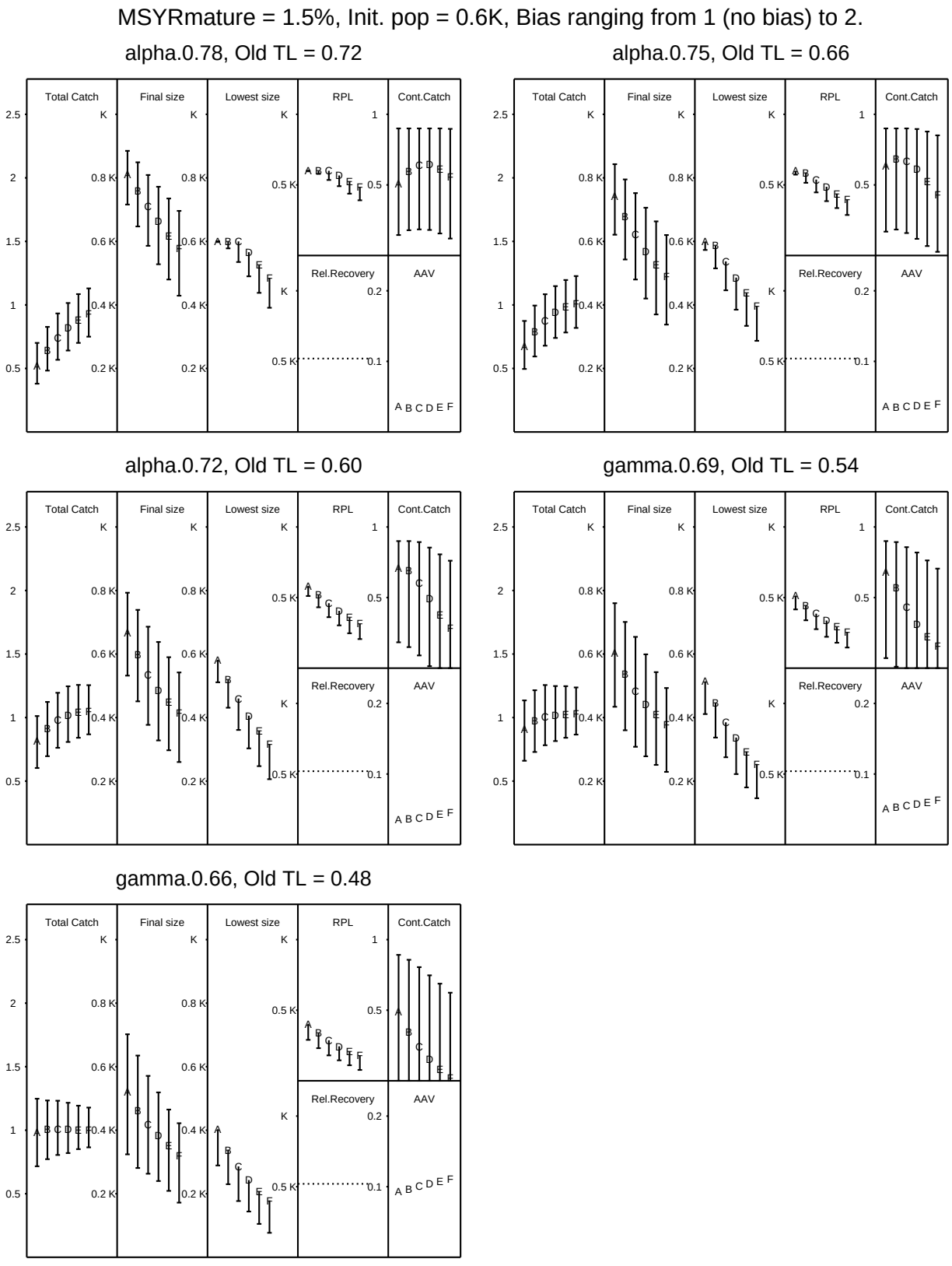


Figure 63. Sample response curves.

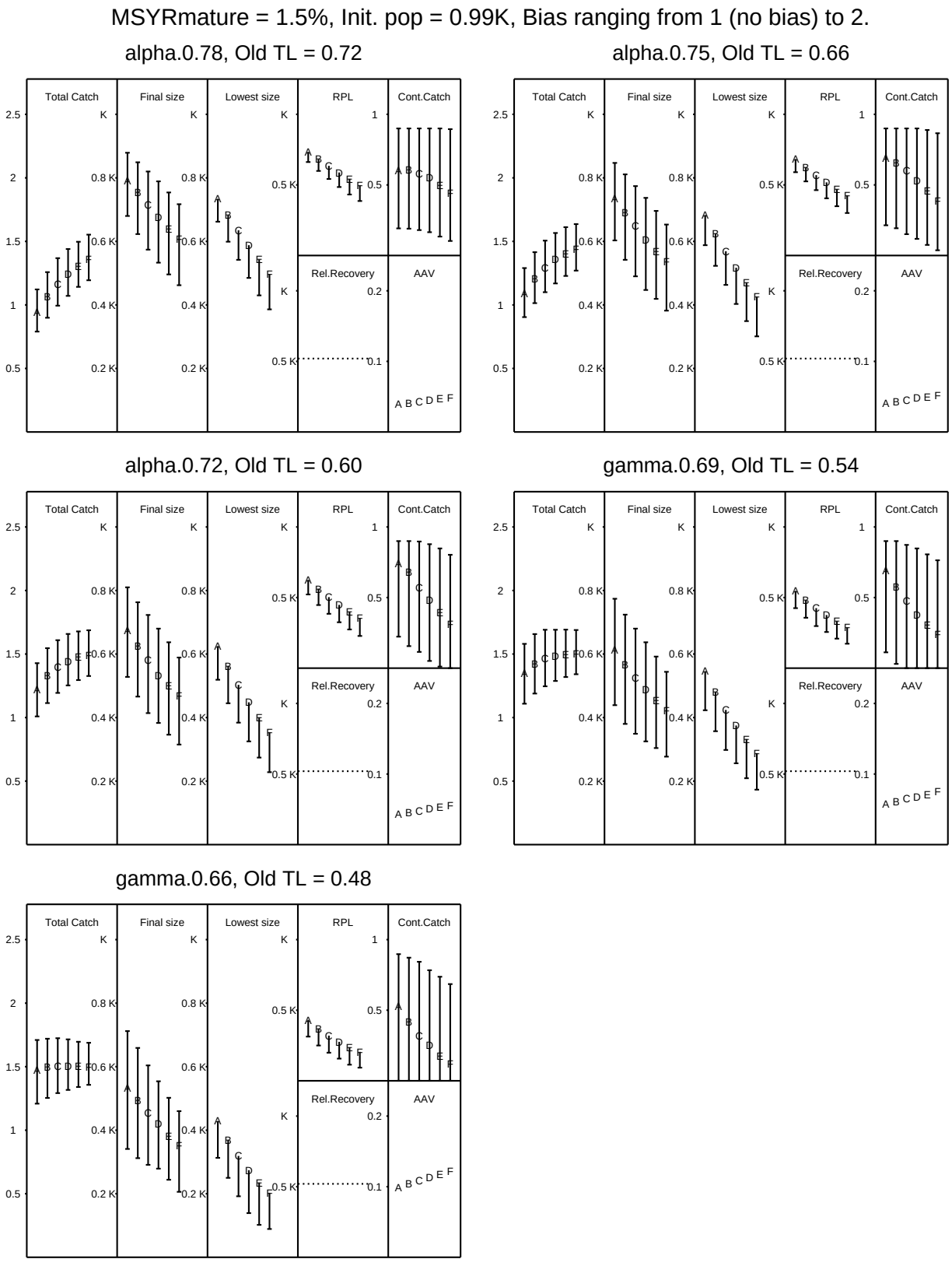


Figure 64. Sample response curves.

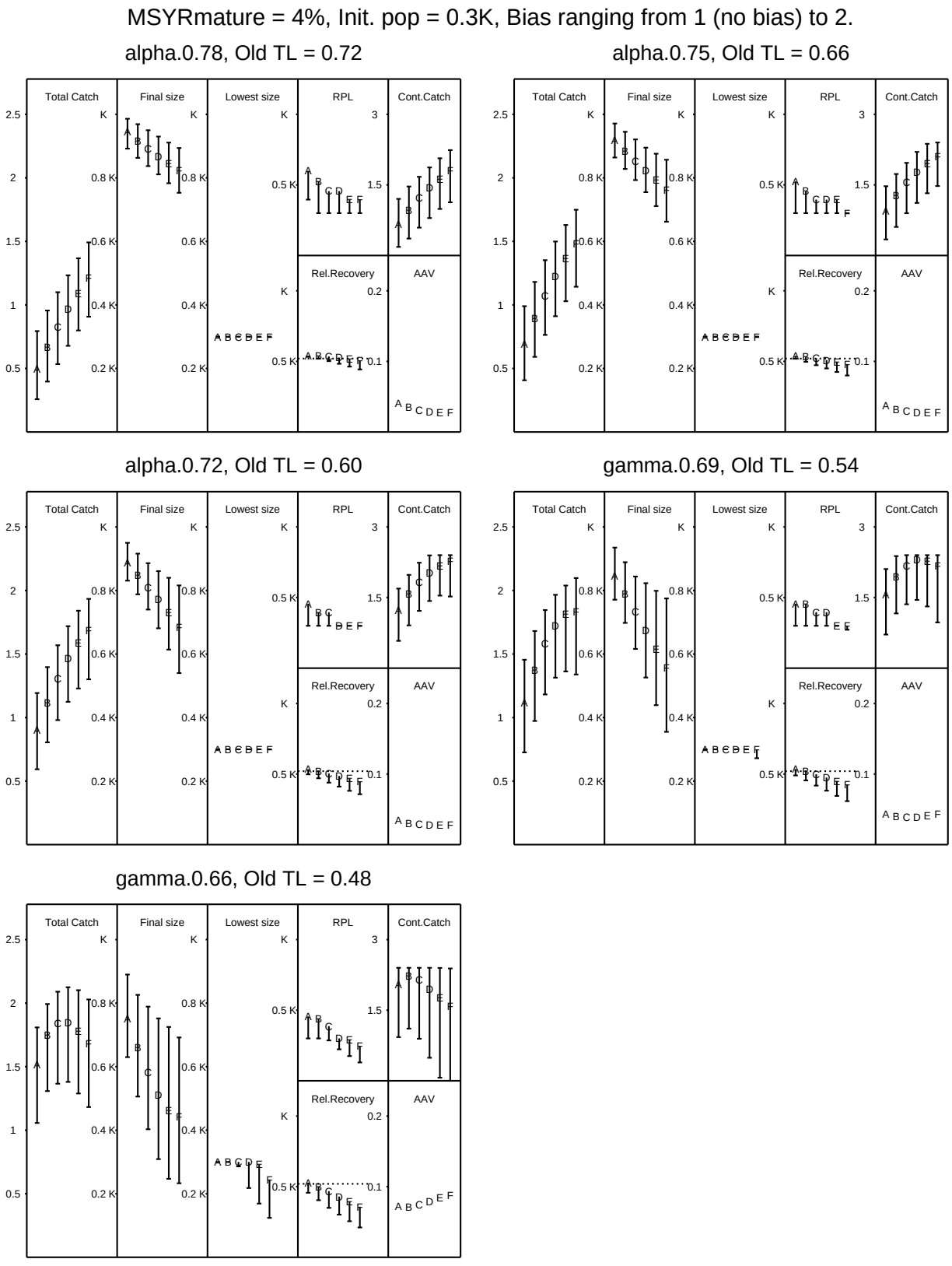


Figure 65. Sample response curves.

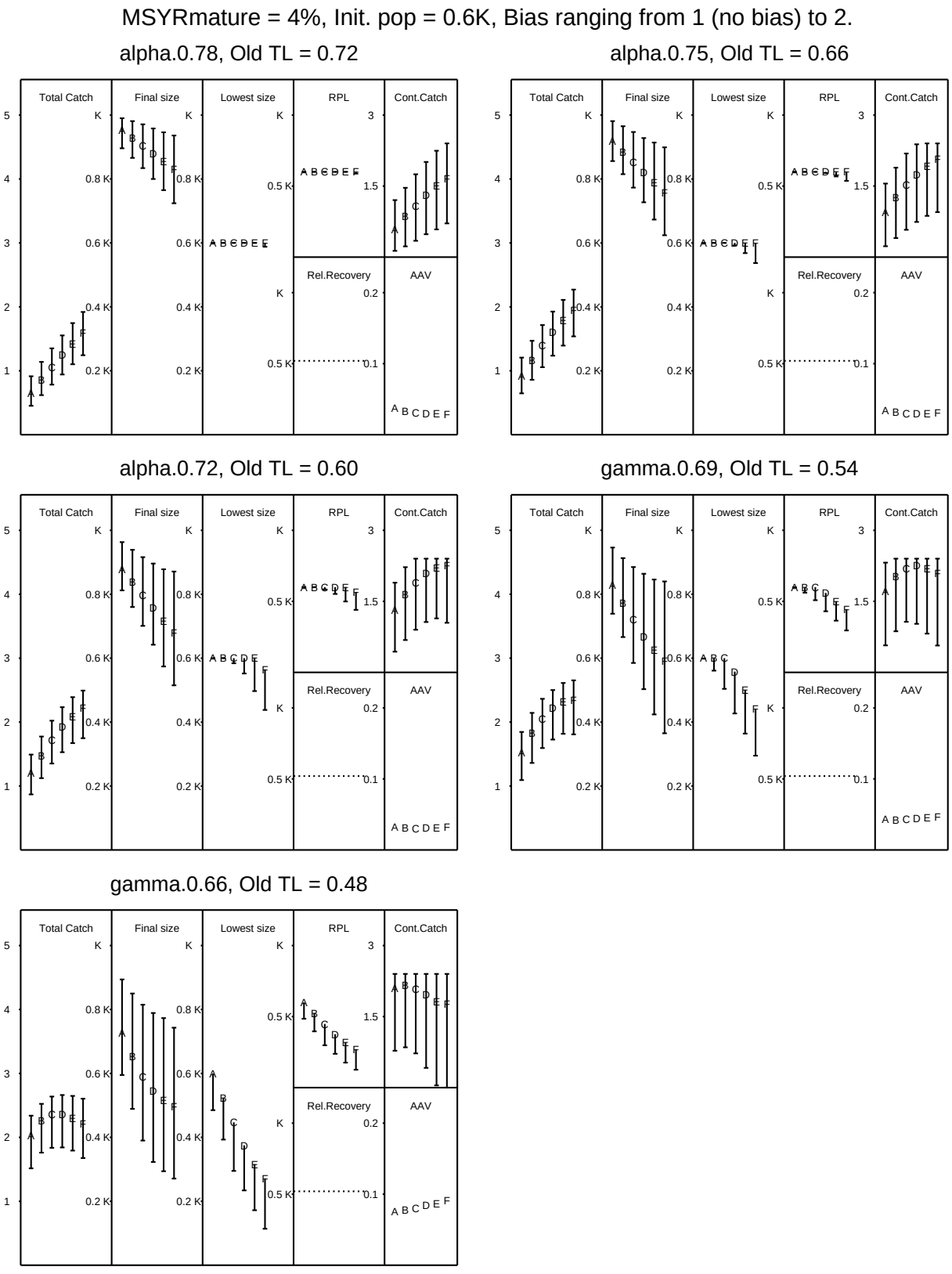


Figure 66. Sample response curves.

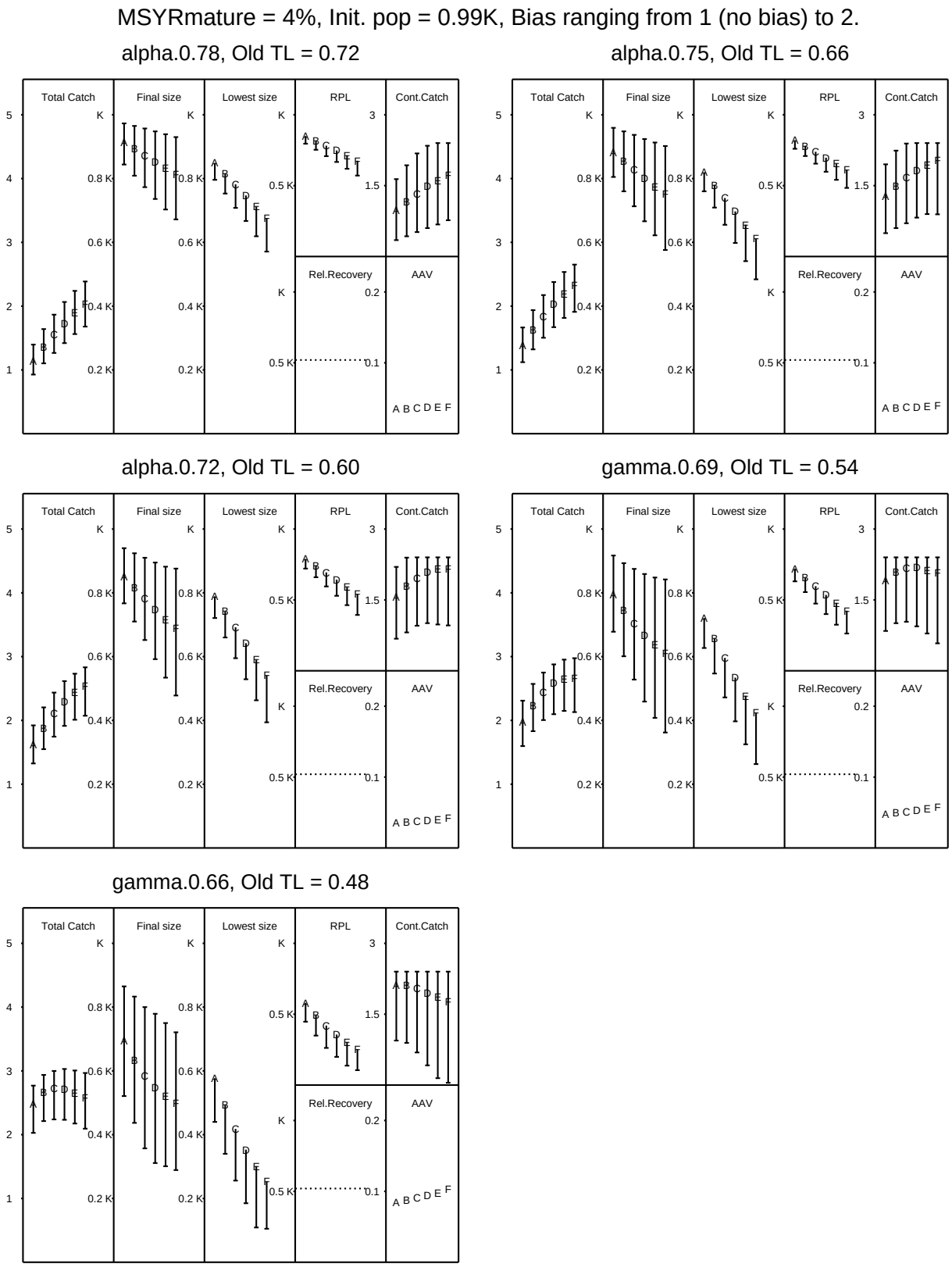


Figure 67. Sample response curves.

3.3 Additional results of trials in Table 2 with horizon 300 years

So far, we have only reported results for the first 100 years of simulation, as requested in CLA06. However, we have in fact run the simulations for 300 years. Here, we will report the results for all trials in Table 2 by figures similar to those presented by AHS. There are some important differences from the way the results were presented in Section 3.1:

- All quantities are calculated based on the first 100 and the next 200 years of each simulation.
- We report results for the final population size (final depletion), average catch, lowest population and average annual catch variation.
- Note that we report the average (per year) catch instead of the total catch, such that the catch in the last 200 years more easily can be compared to the catch the first 100 years.
- The definition of the average annual catch variation is slightly different from Equation (7), with a specific value for each simulation given by

$$AAV_i^a = \{\sum_{t=0}^{98} |C_{i,t+1} - C_{i,t}|\}/\{\sum_{t=0}^{98} C_{i,t}\} \quad (8)$$

  for the first 100 years, and by

$$AAV_i^a = \{\sum_{t=100}^{298} |C_{i,t+1} - C_{i,t}|\}/\{\sum_{t=100}^{298} C_{i,t}\} \quad (9)$$

  for the next 200 years. Then the median, 5% value and 95% value over the 400 simulations are calculated.
- Population sizes are always scaled by the initial carrying capacity. Note that this also applies to the T-9 and T-12 trials, because this scaling may be of interest in addition to the scaling by the no-catch population used in previous sections (at least for the T-12 trials), and because this is the scaling used in the corresponding figures in AHS.
- For the lowest population we calculate the lowest, 5%, 10%, 25%, median and 95% values.

The results presented here are computed by a computer program we have made ourselves. It gives answers identical to the ones from the MANRES program for all quantities that are calculated in both programs.

The results from each trial are shown separately in the upper four panels of Figures 68 to 110. In each panel of the figures, the results for the first 100 and the

next 200 years are presented pairwise for each version of CLA, with the former to the left and the latter to the right. The various summary statistics are represented by the following symbols:

- The median is shown as a diamond.
- The 90% interval between the 5% and 95% values is represented by a vertical line.
- The lowest, 10% and 25% values for the lowest population are marked by three short horizontal lines.

The next three panels in each figure show time series of year-specific summary statistics for each version of CLA. The three statistics are the average population, 5% population level, and average catch. The final panel in each figure shows catch trajectories for three individual simulations with catch quotas set by the gamma0.69 version, from the first three of the standard common sets of seeds.

Note that the scale on the y-axis for the population panels is usually between 0 and 1, except for the T12A trials, where the upper limits is 2. In the figures for the T12A and T12B trials, the year-specific K is marked by a separate line. The scale for AAV is the same in all figures. The scale on the y-axes for the catch panels may vary within and between figures.

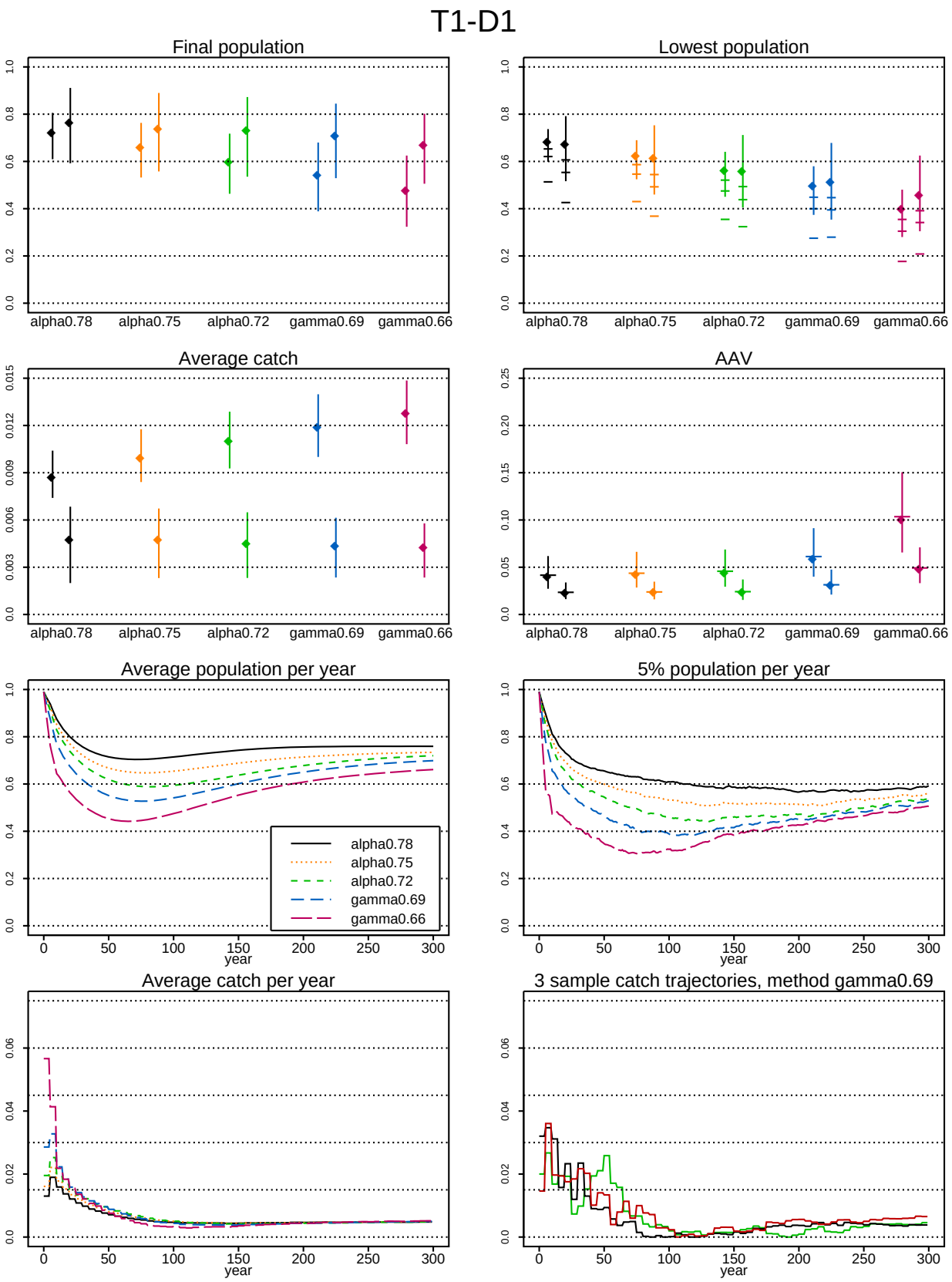


Figure 68. Trial T1-D1. Base case. The pairs of results from the CLA version in the upper four panels represent the first 100 years (left) and the last 200 years (right).

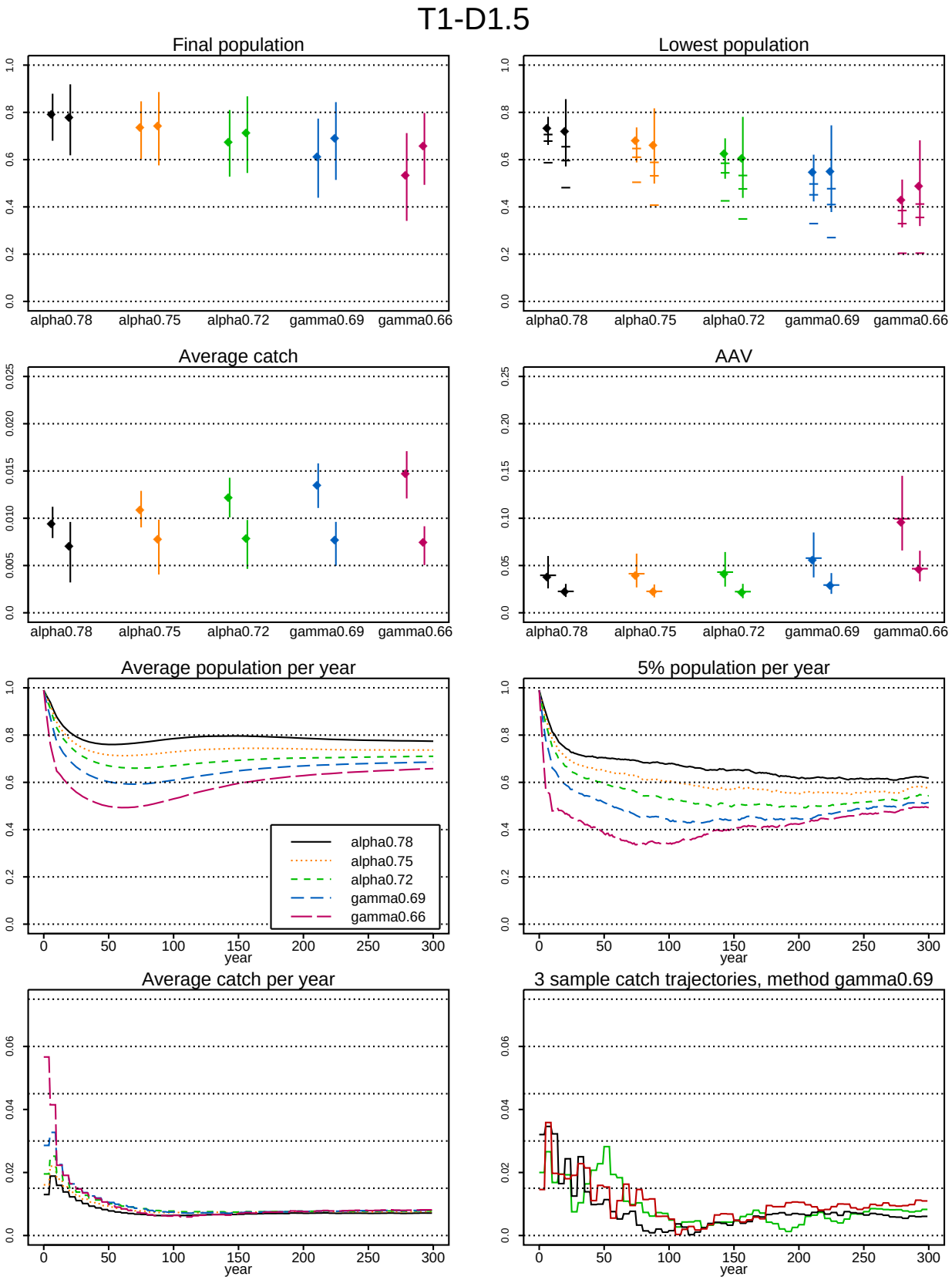


Figure 69. Trial T1-D1.5. Base case.

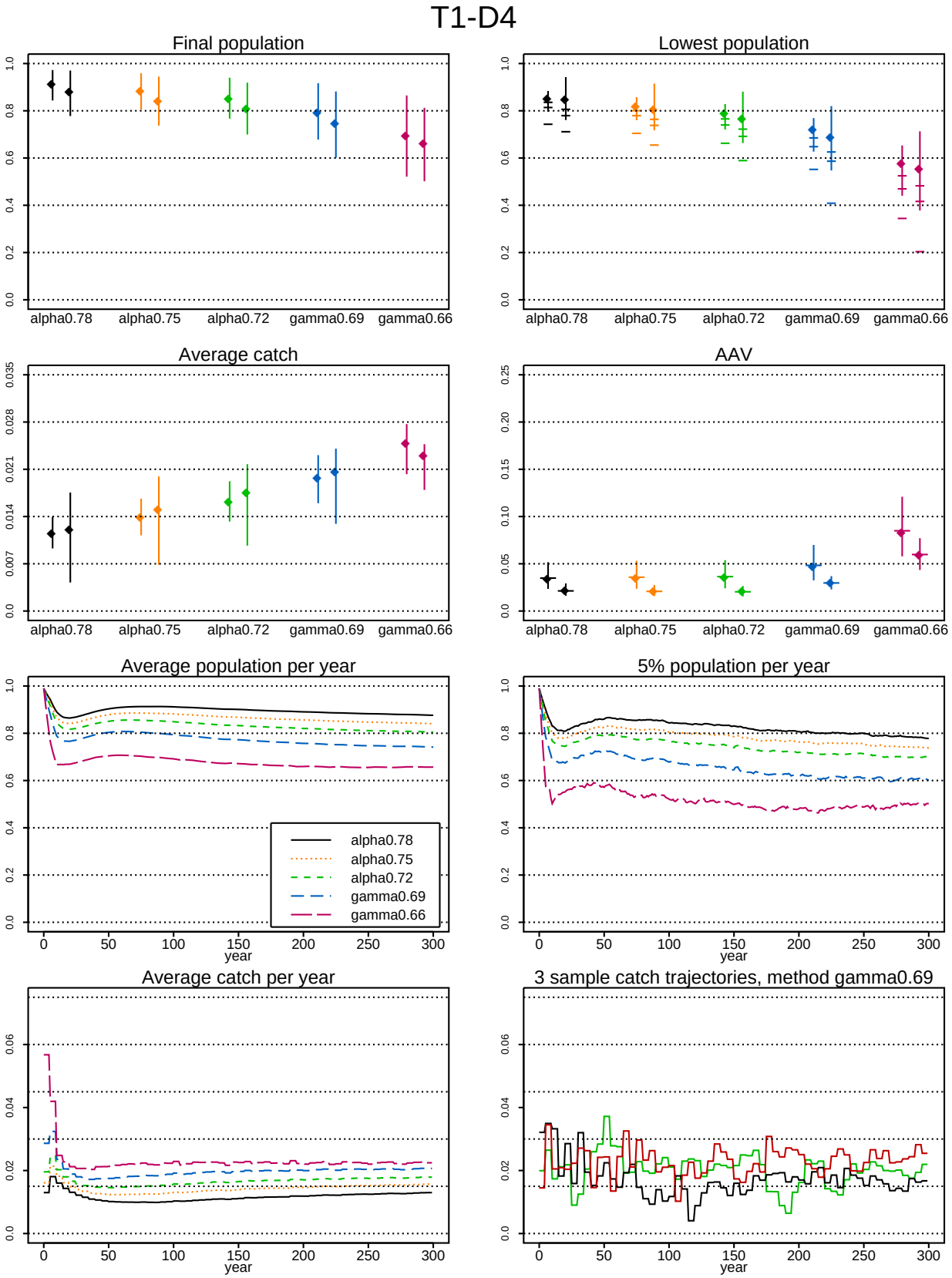


Figure 70. Trial T1-D4. Base case.

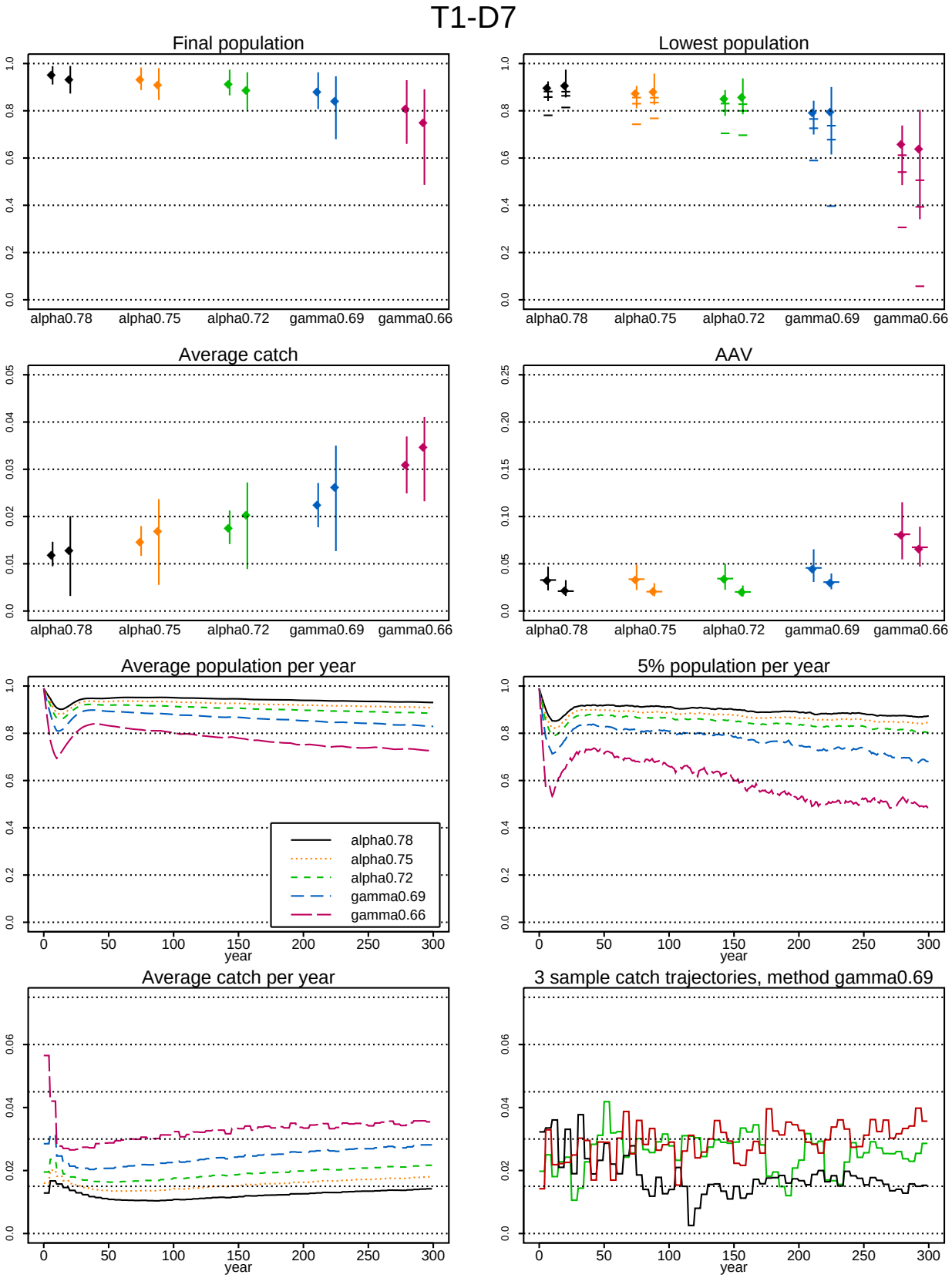


Figure 71. Trial T1-D7. Base case.

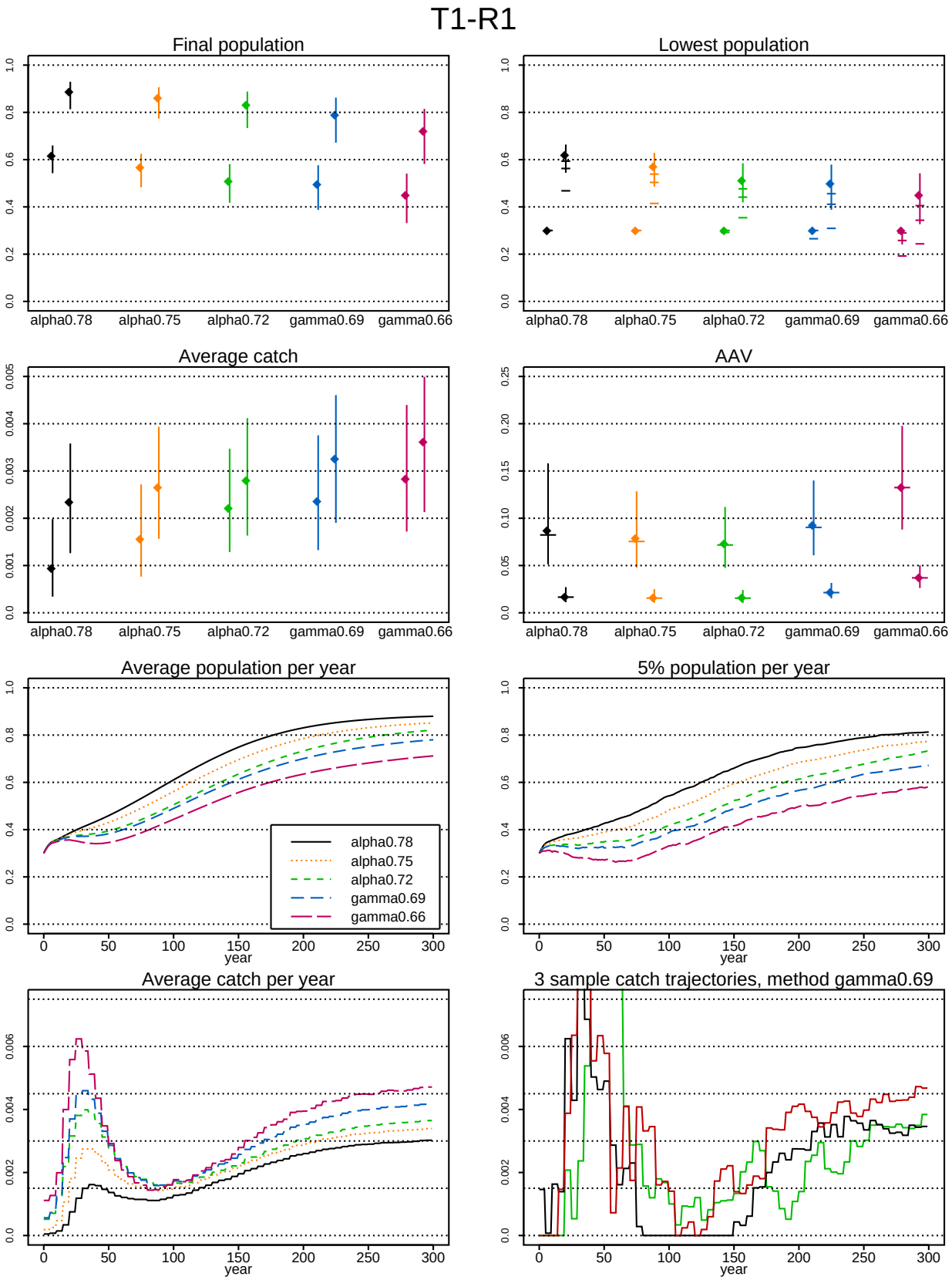


Figure 72. Trial T1-R1. Base case.

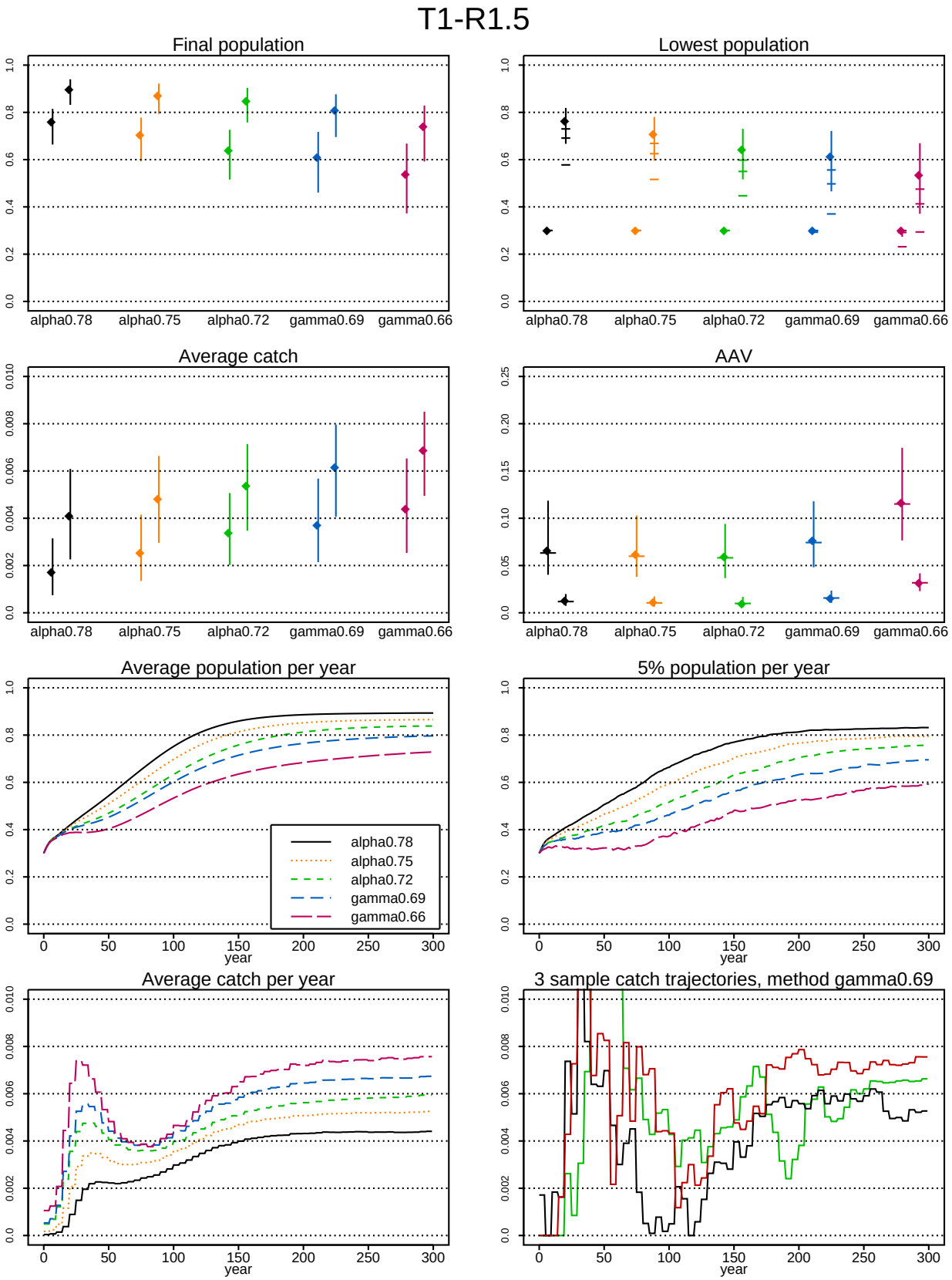


Figure 73. Trial T1-R1.5. Base case.

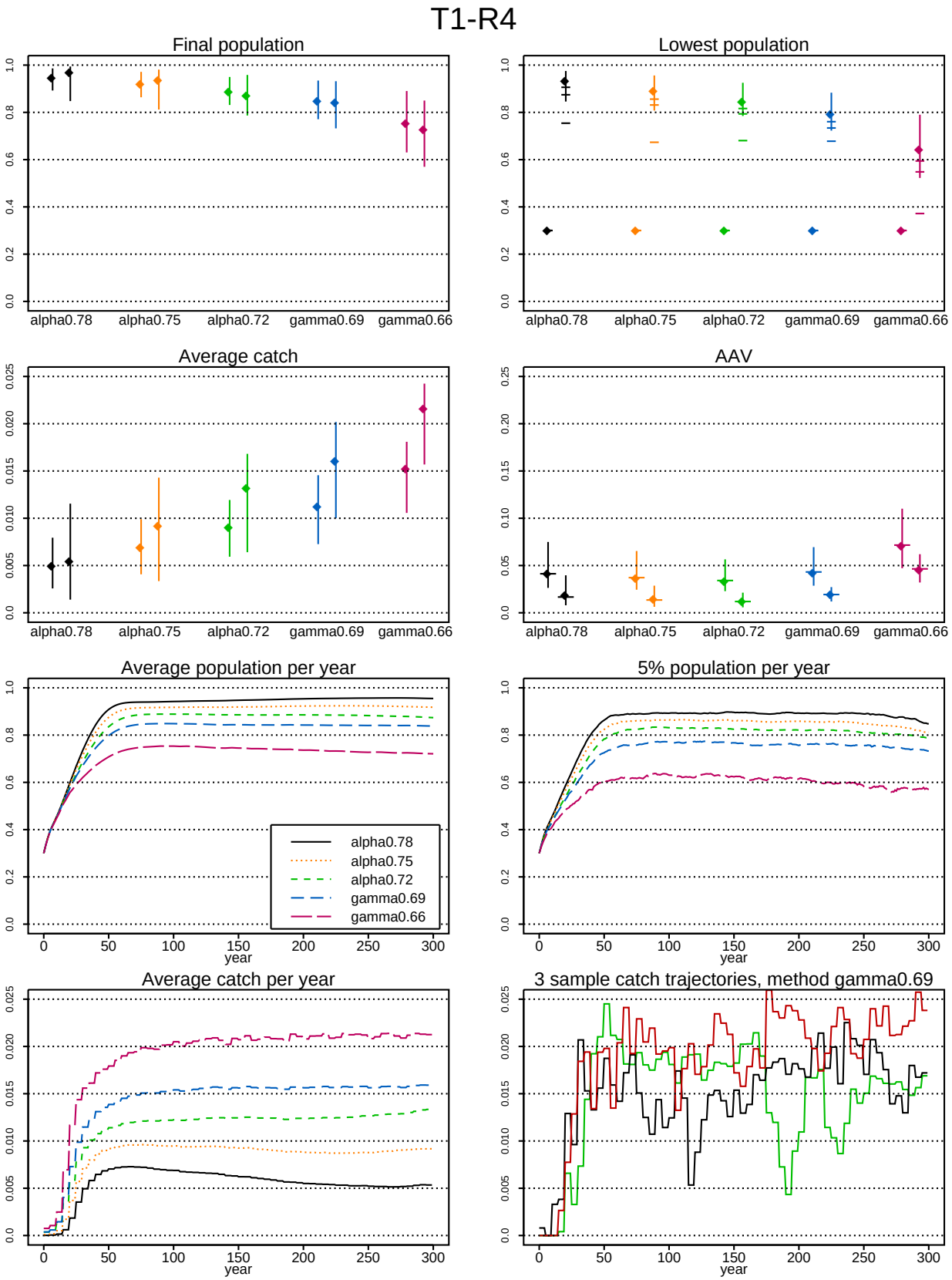


Figure 74. Trial T1-R4. Base case.

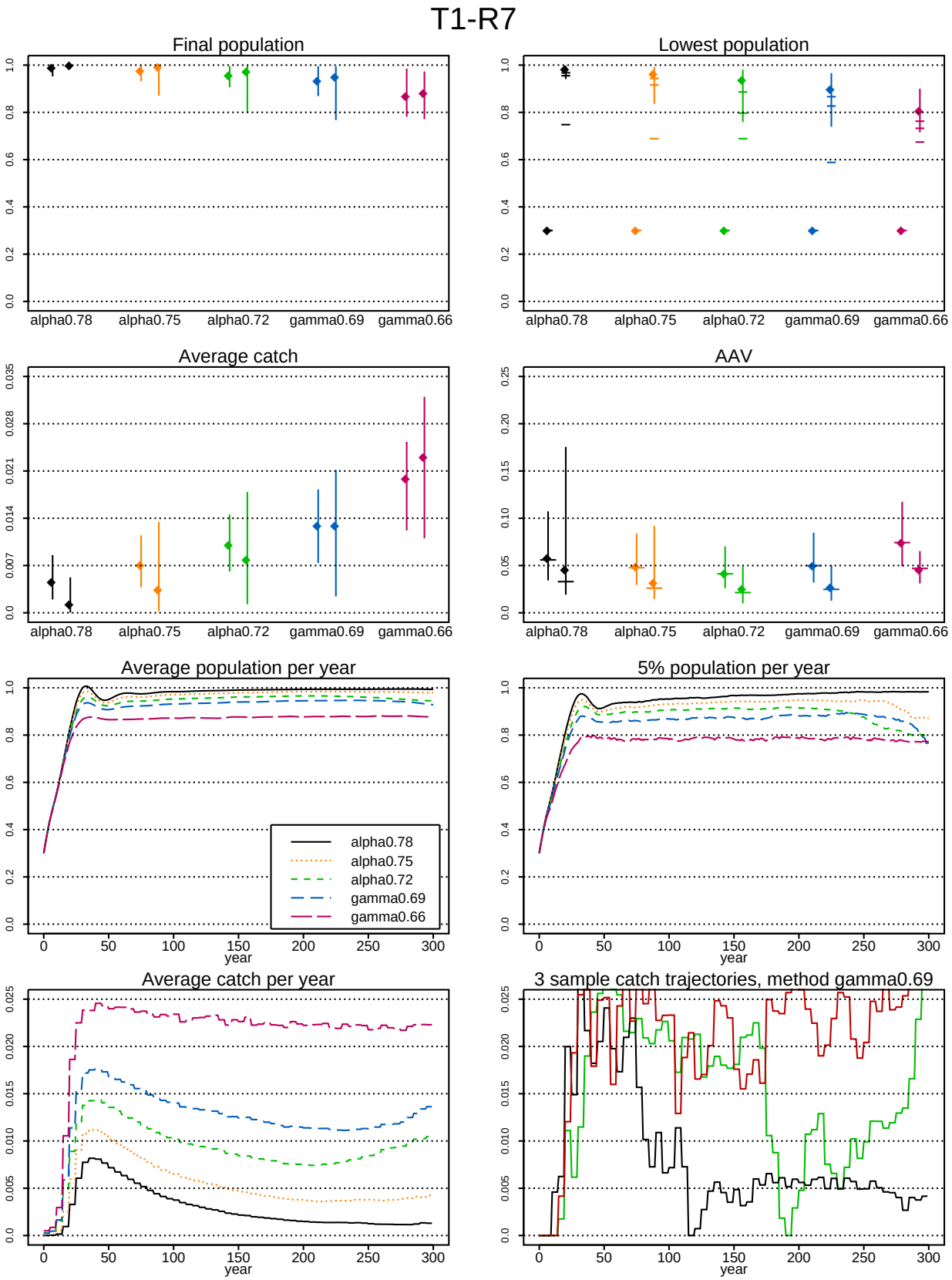


Figure 75. Trial T1-R7. Base case.

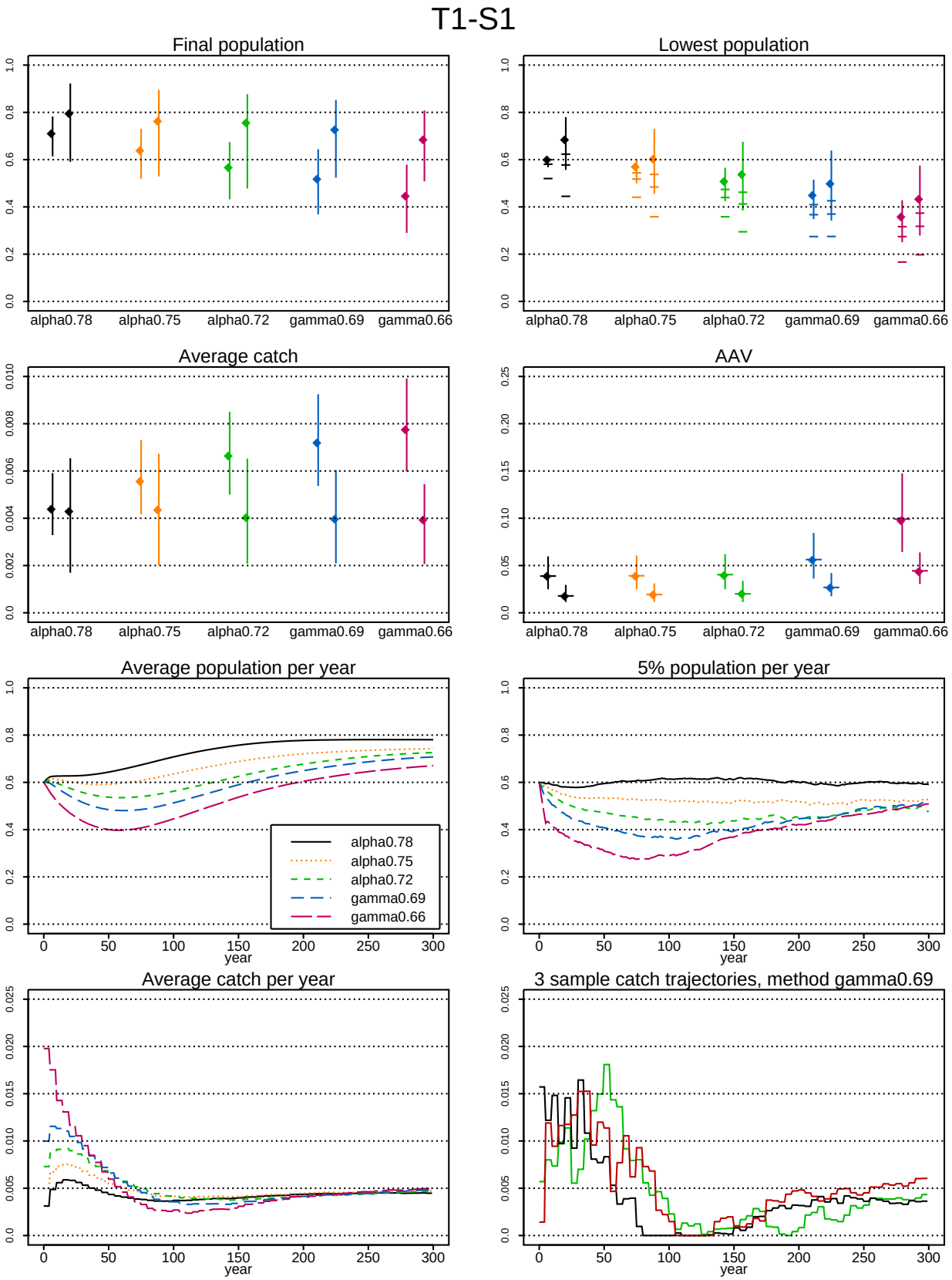


Figure 76. Trial T1-S1. Base case.

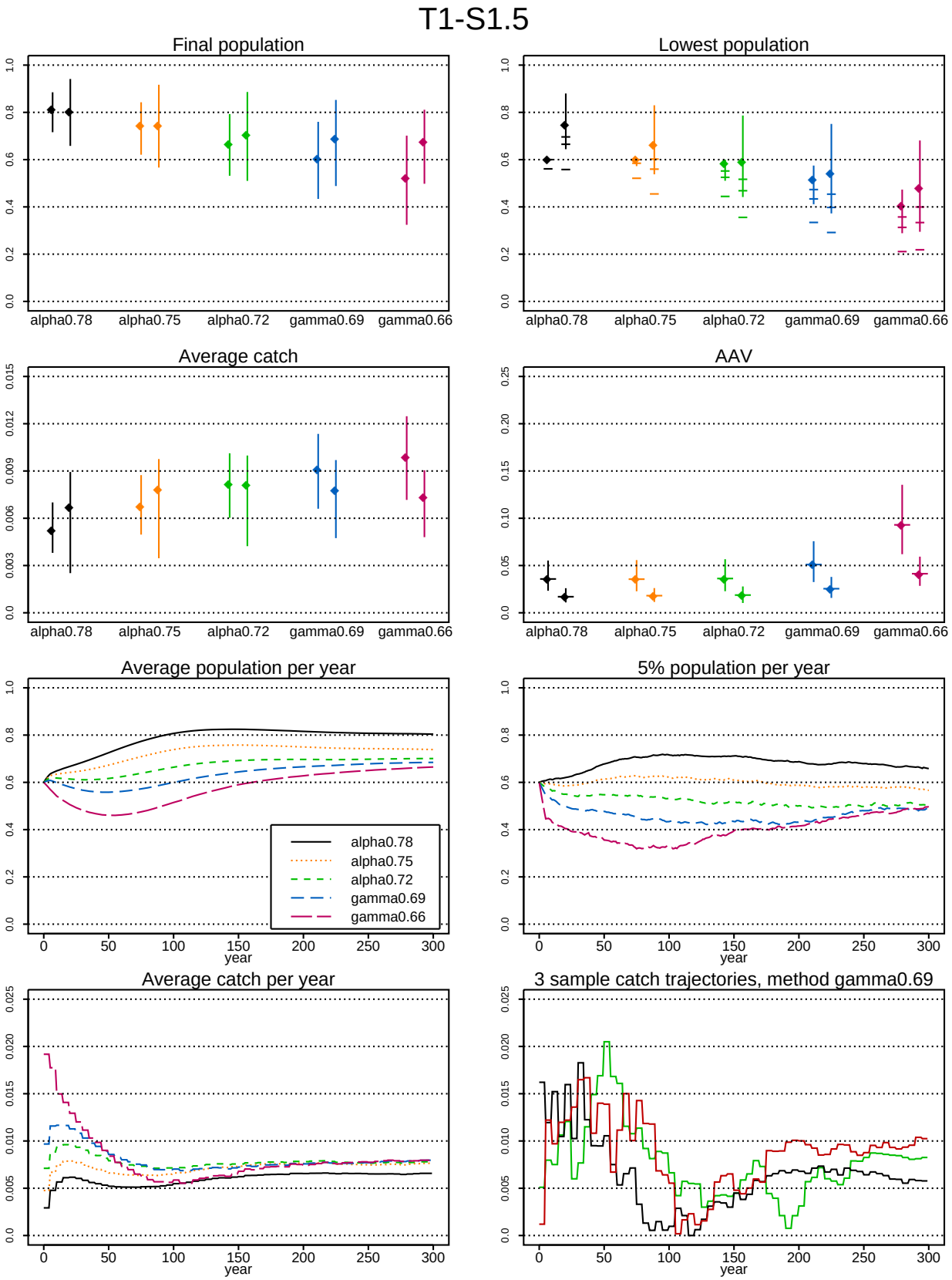


Figure 77. Trial T1-S1.5. Base case.

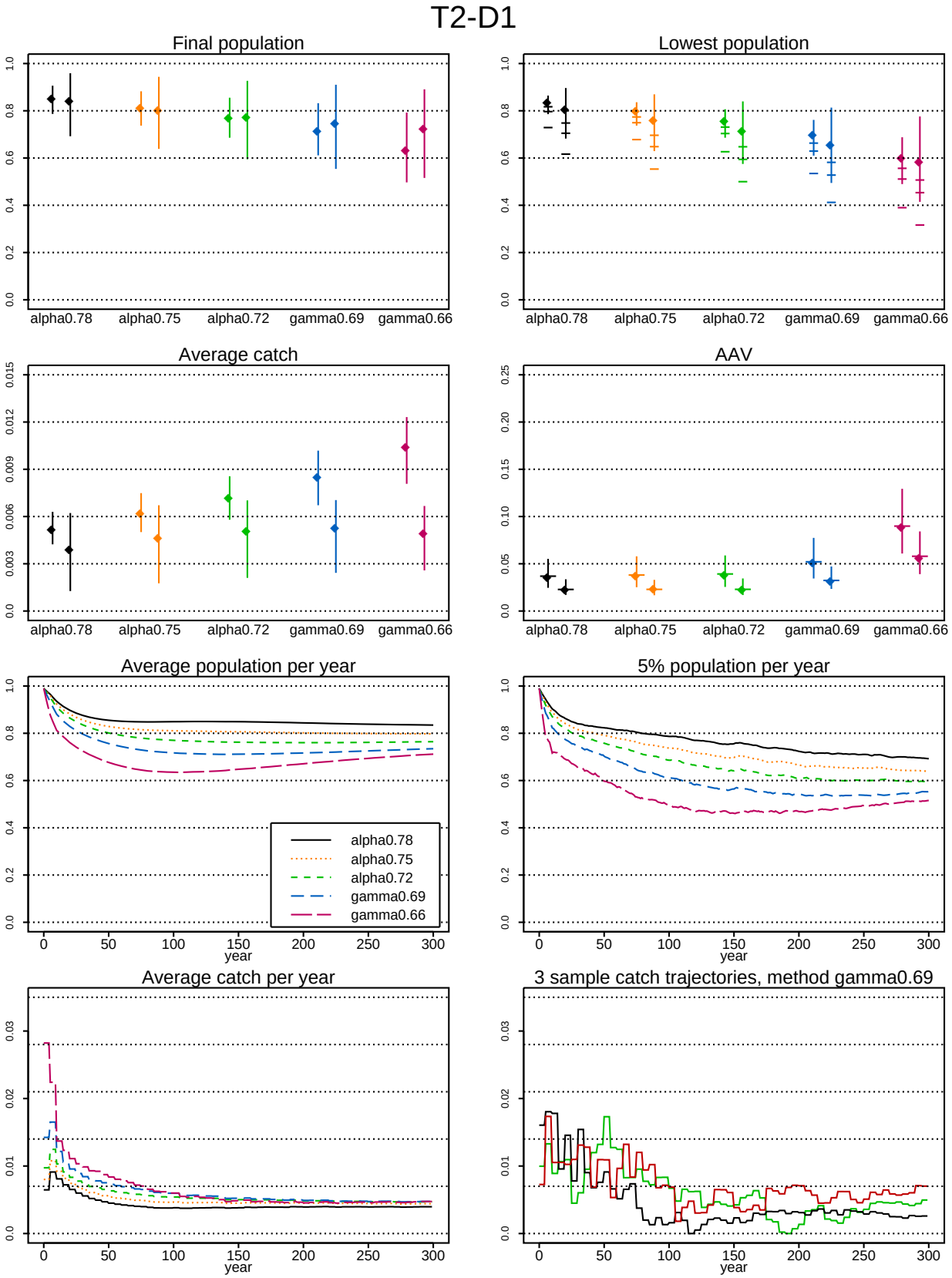


Figure 78. Trial T2-D1. 50% negative bias in abundance estimates.

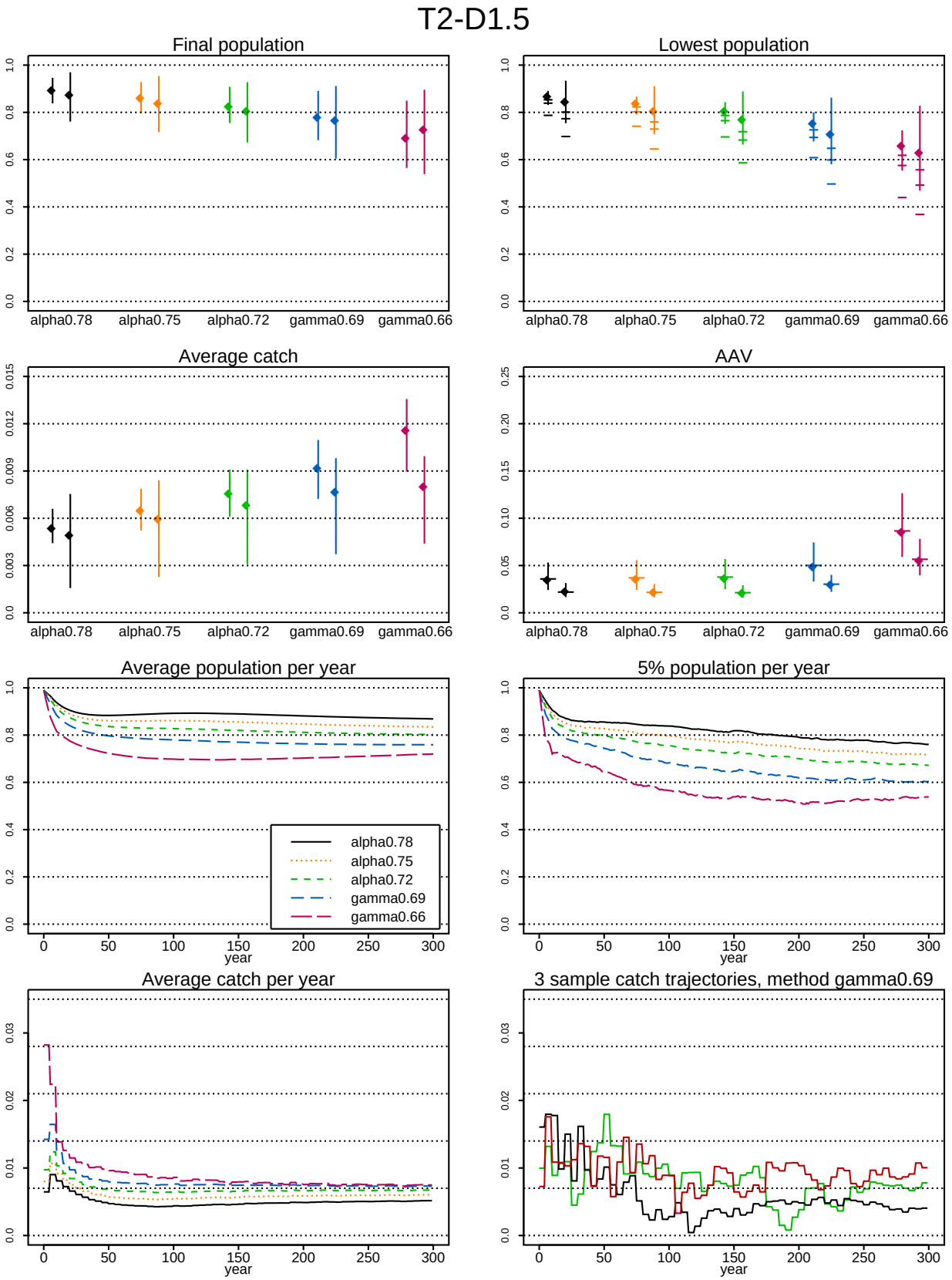


Figure 79. Trial T2-D1.5. 50% negative bias in abundance estimates.

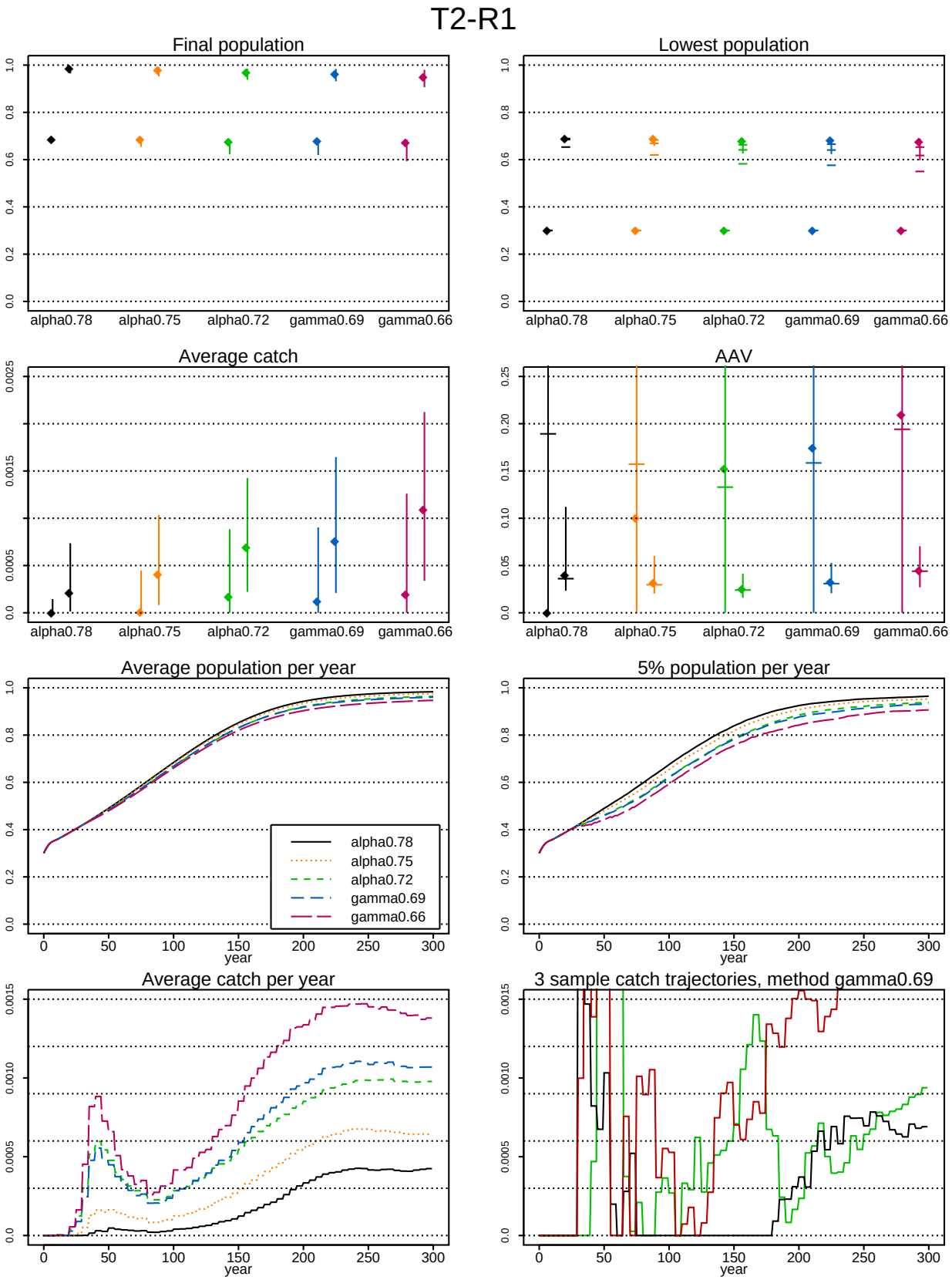


Figure 80. Trial T2-R1. 50% negative bias in abundance estimates.

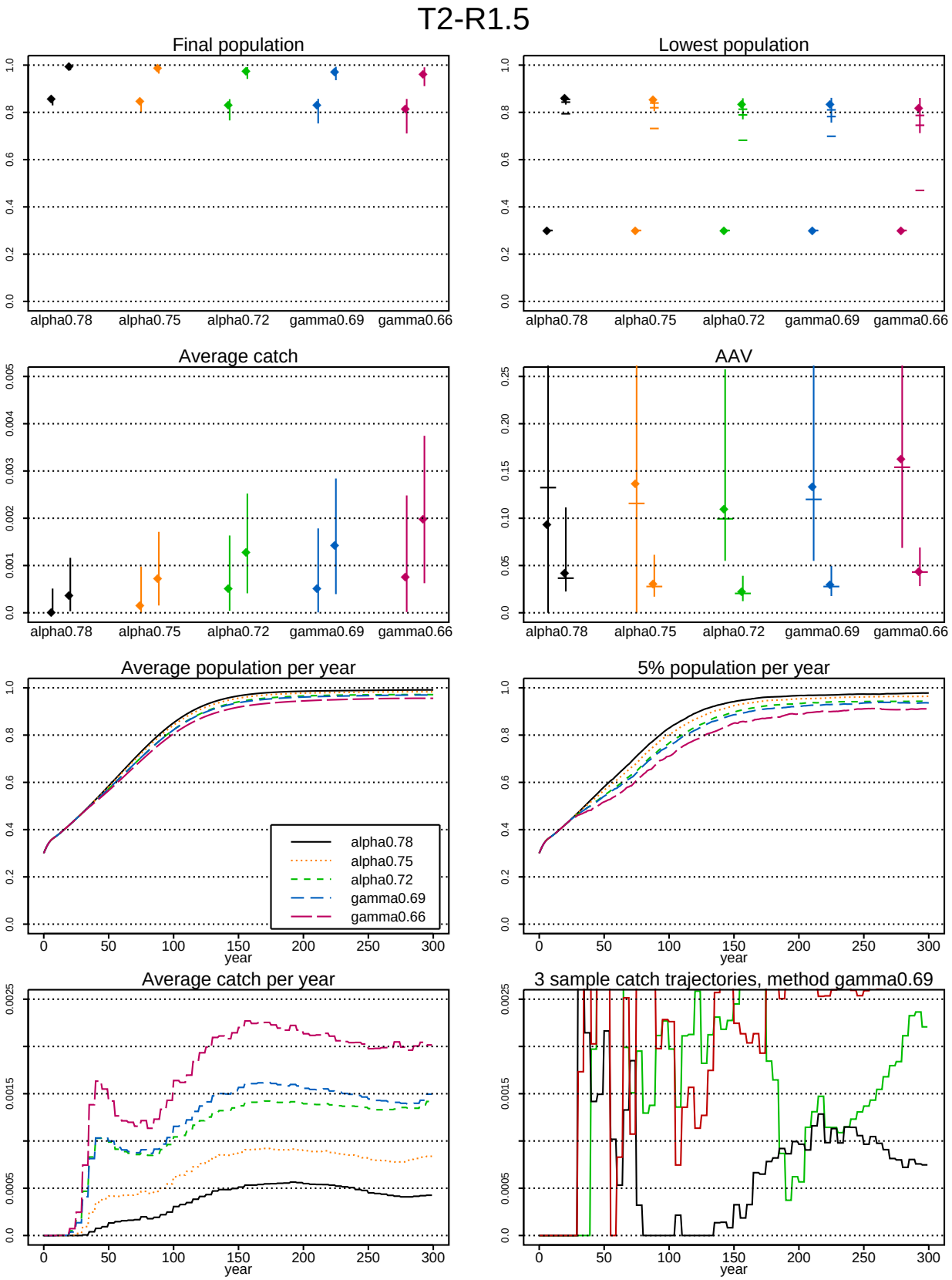


Figure 81. Trial T2-R1.5. 50% negative bias in abundance estimates.

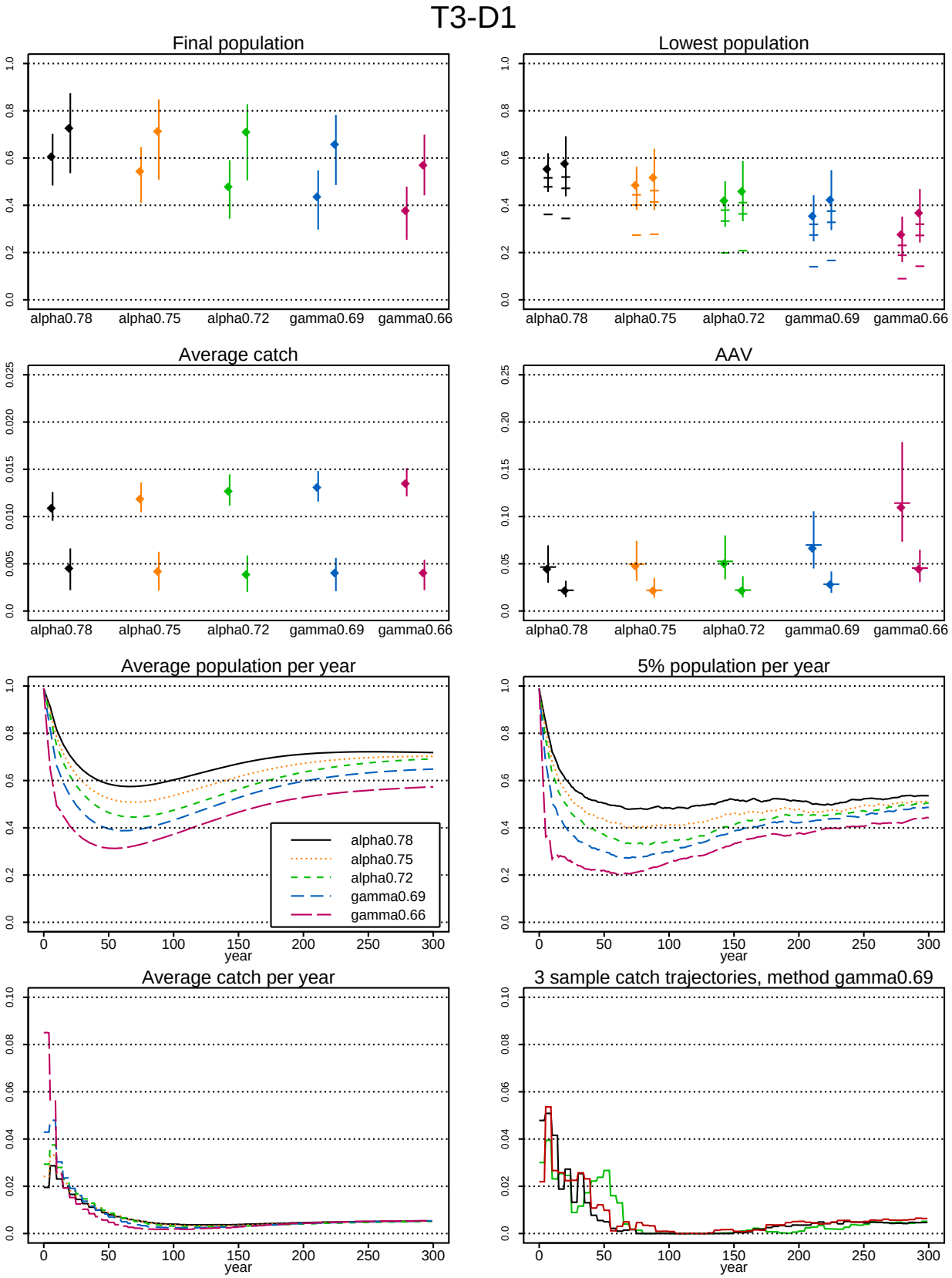


Figure 82. Trial T3-D1. 50% positive bias in abundance estimates.

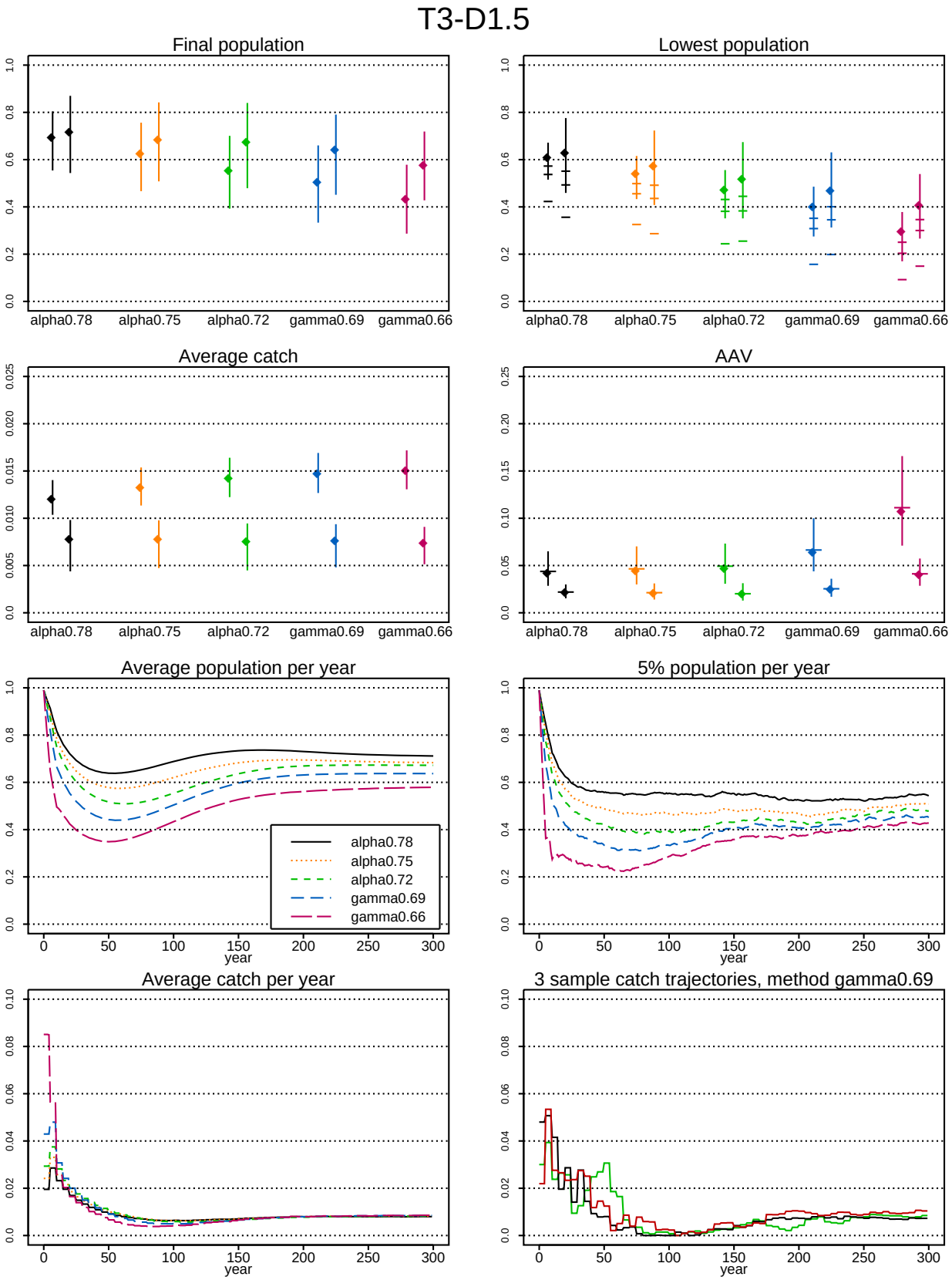


Figure 83. Trial T3-D1.5. 50% positive bias in abundance estimates.

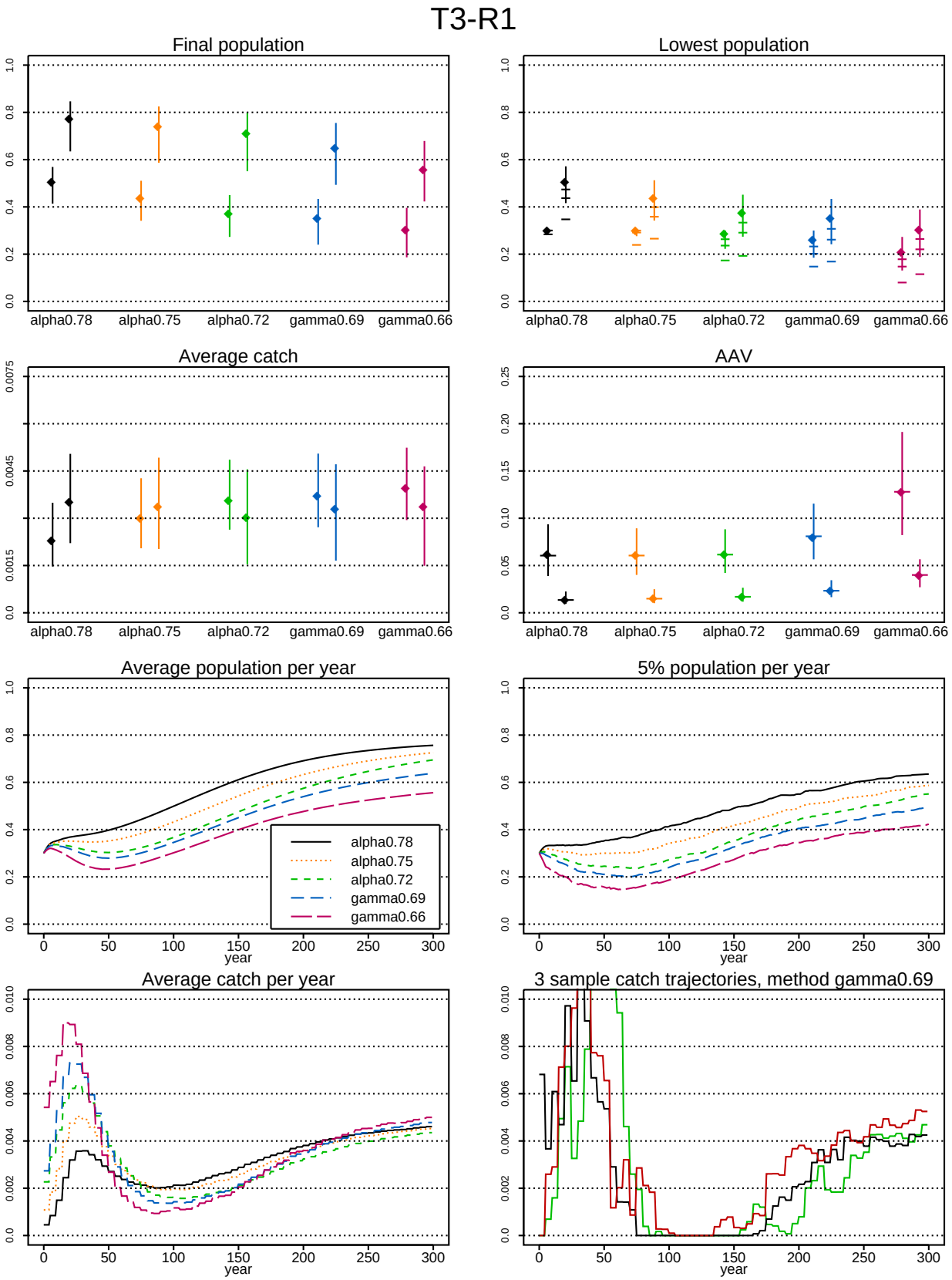


Figure 84. Trial T3-R1. 50% positive bias in abundance estimates.

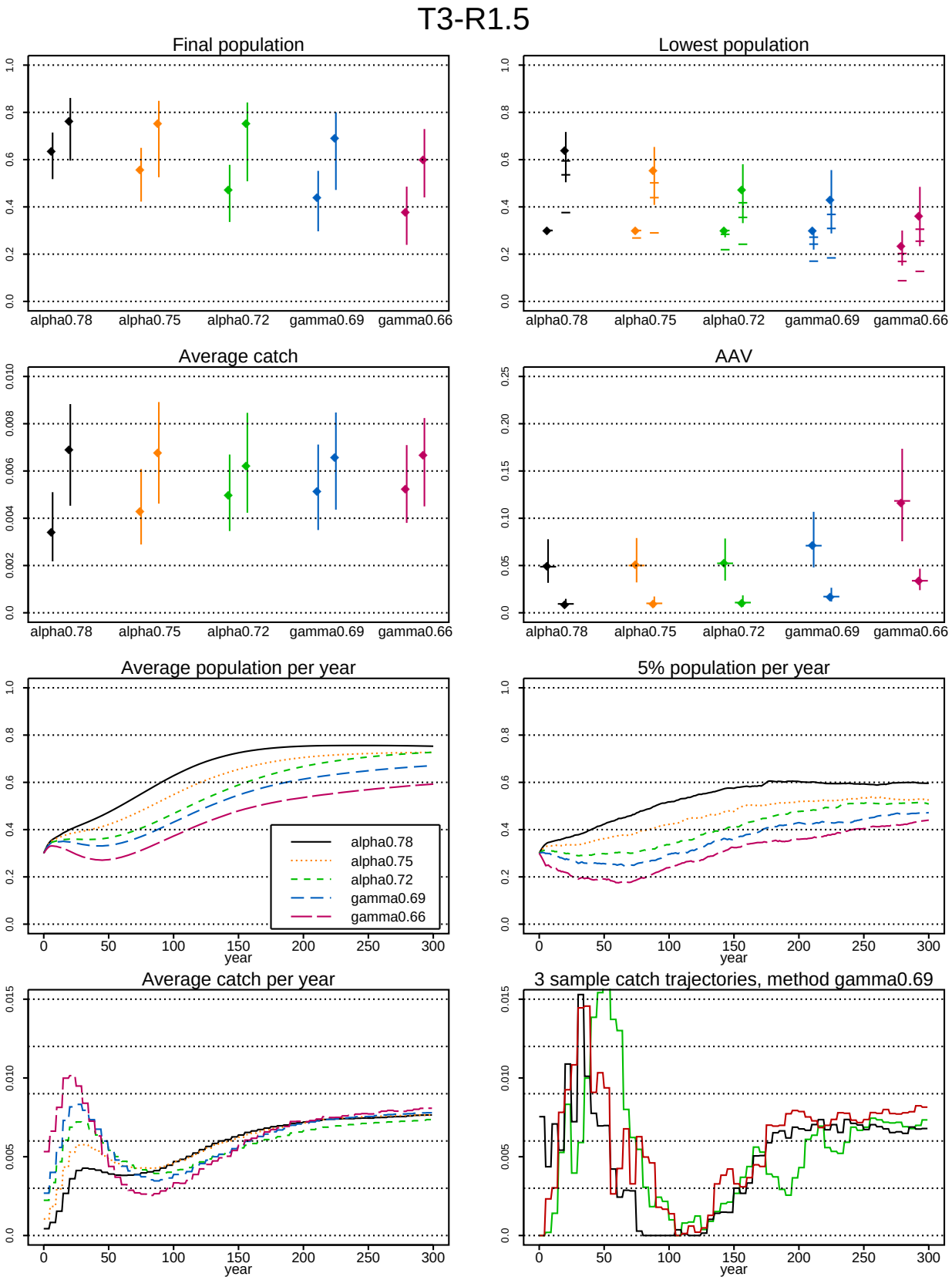


Figure 85. Trial T3-R1.5. 50% positive bias in abundance estimates.

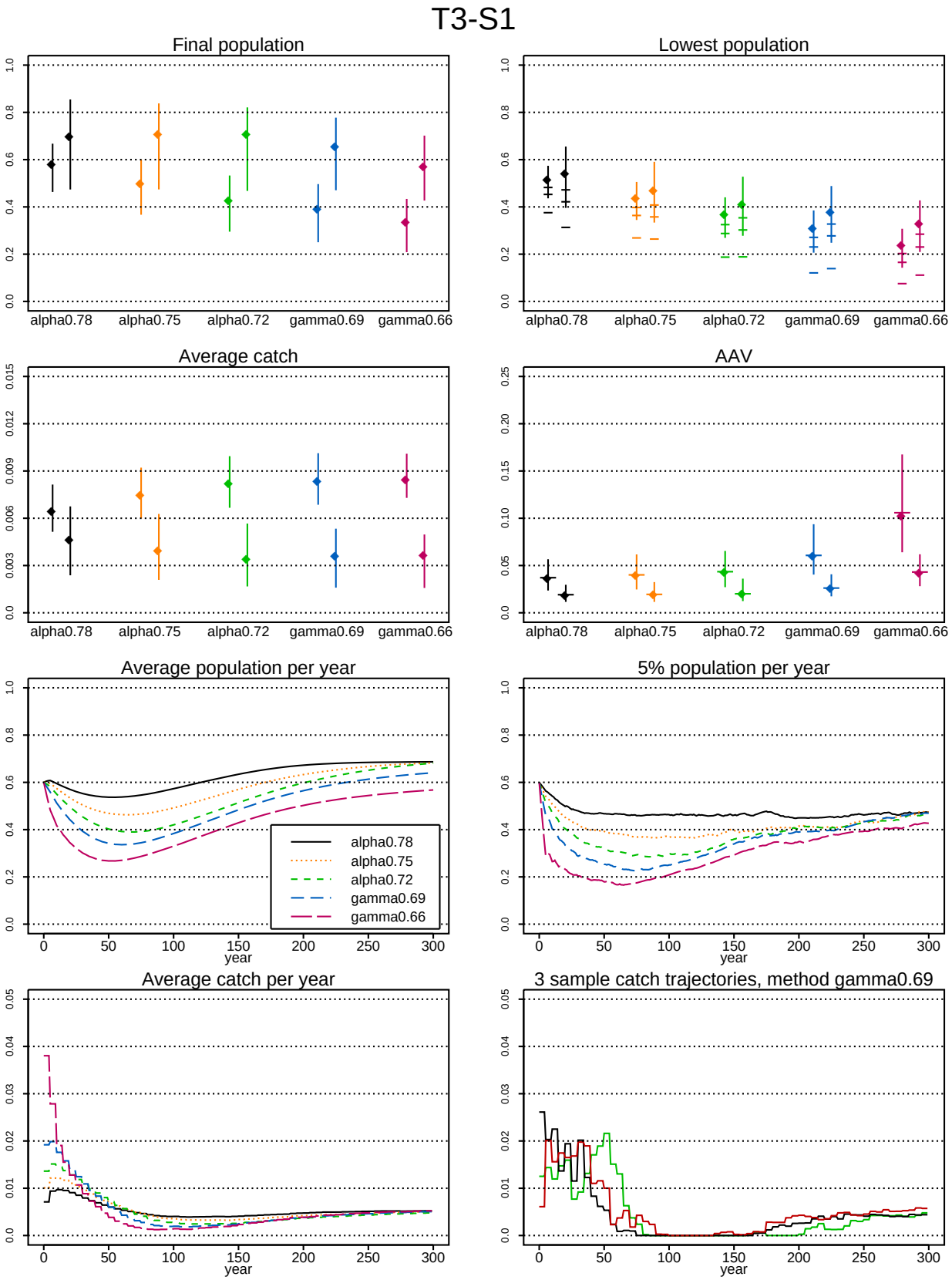


Figure 86. Trial T3-S1. 50% positive bias in abundance estimates.

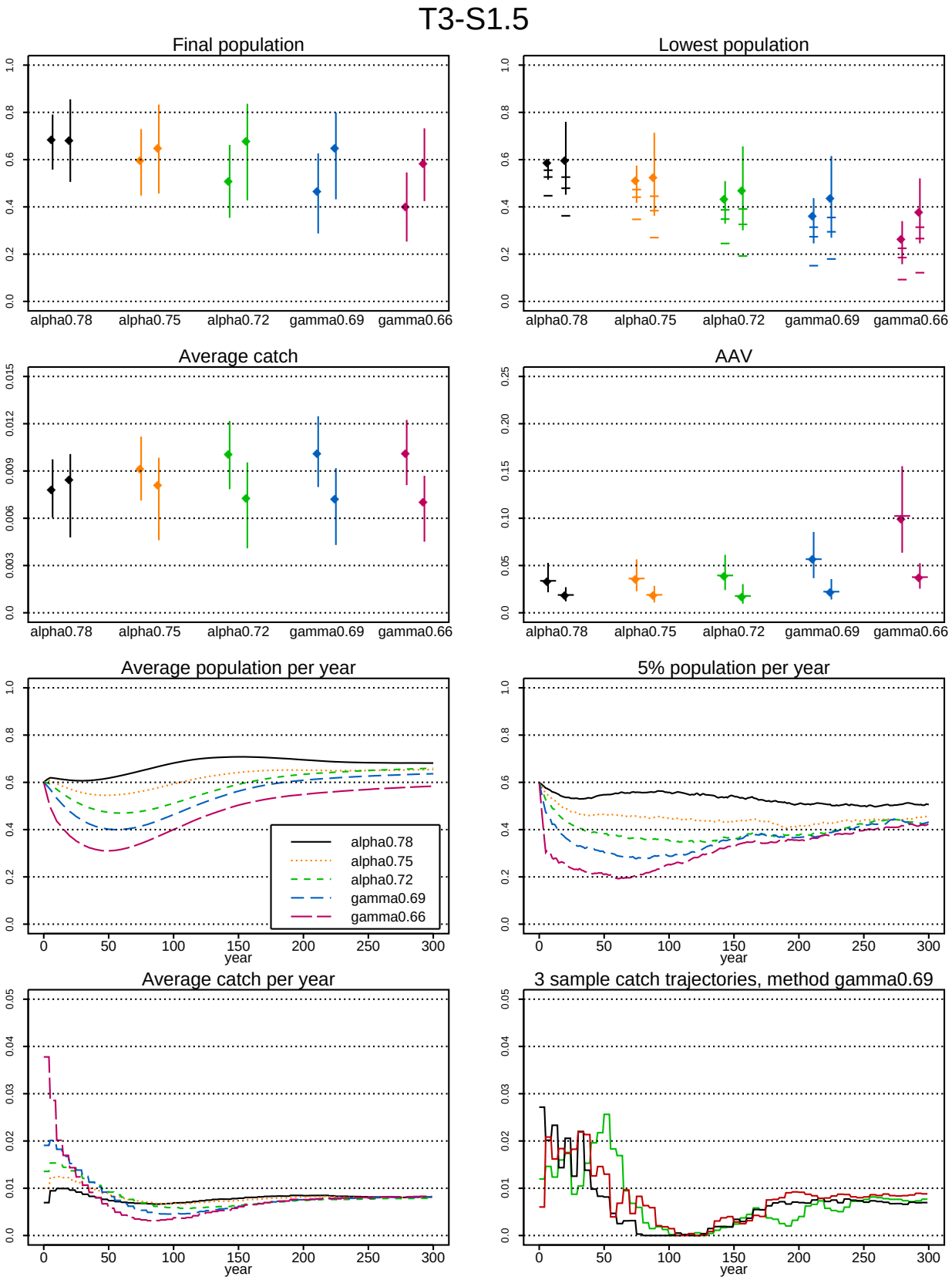


Figure 87. Trial T3-S1.5. 50% positive bias in abundance estimates.

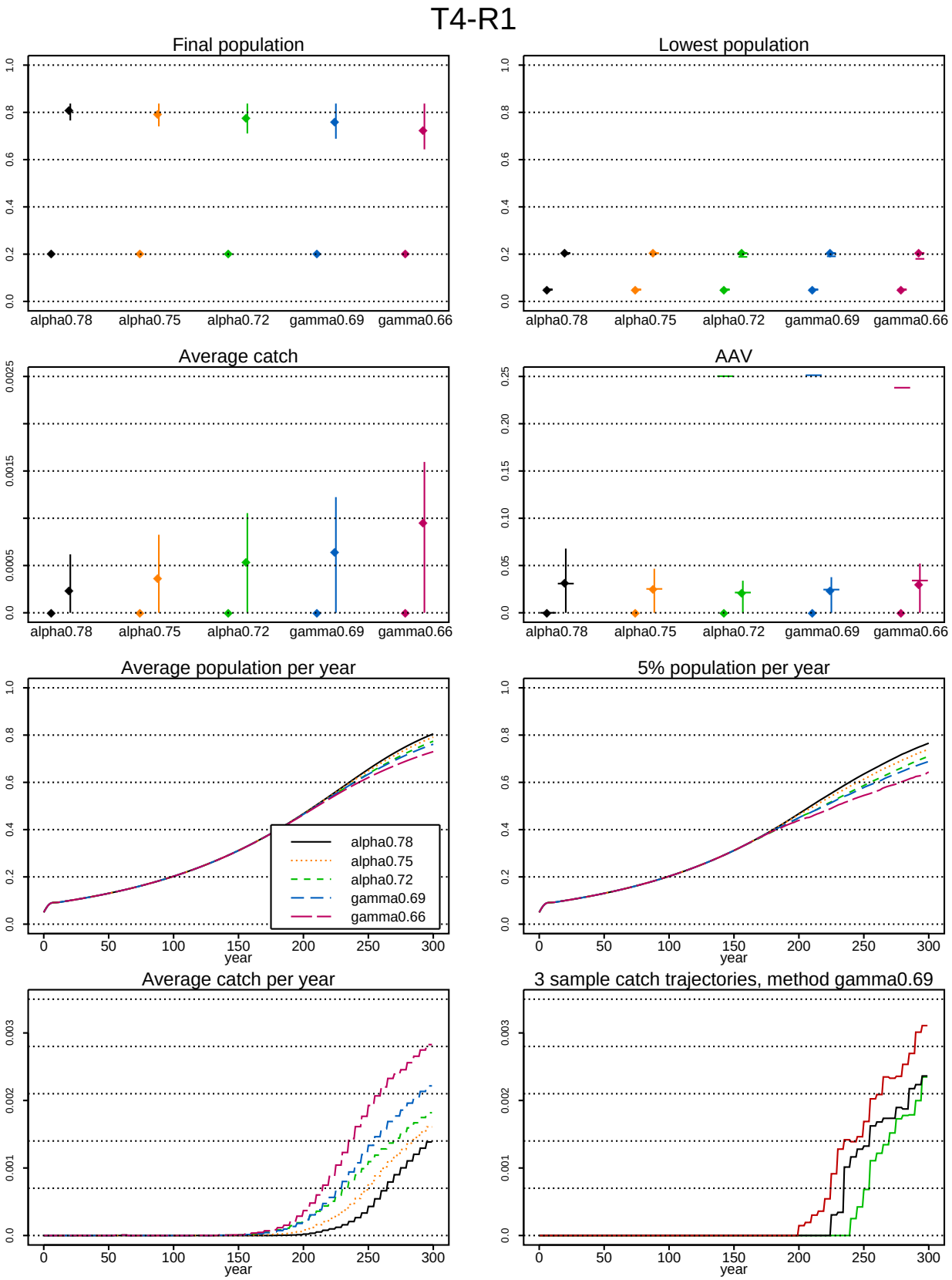


Figure 88. Trial T4-R1. Initial depletion 0.05K.

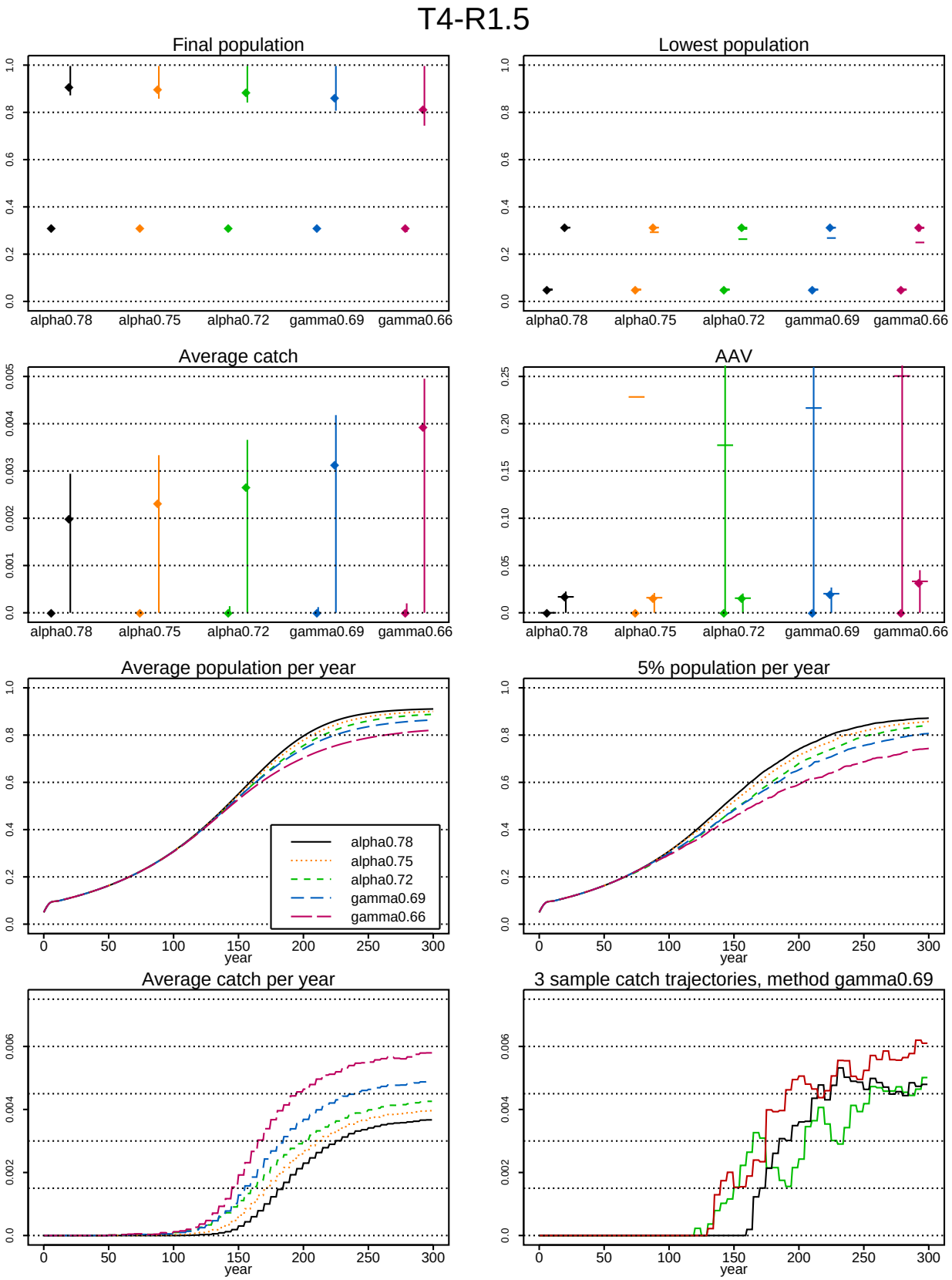


Figure 89. Trial T4-R1.5. Initial depletion 0.05K.

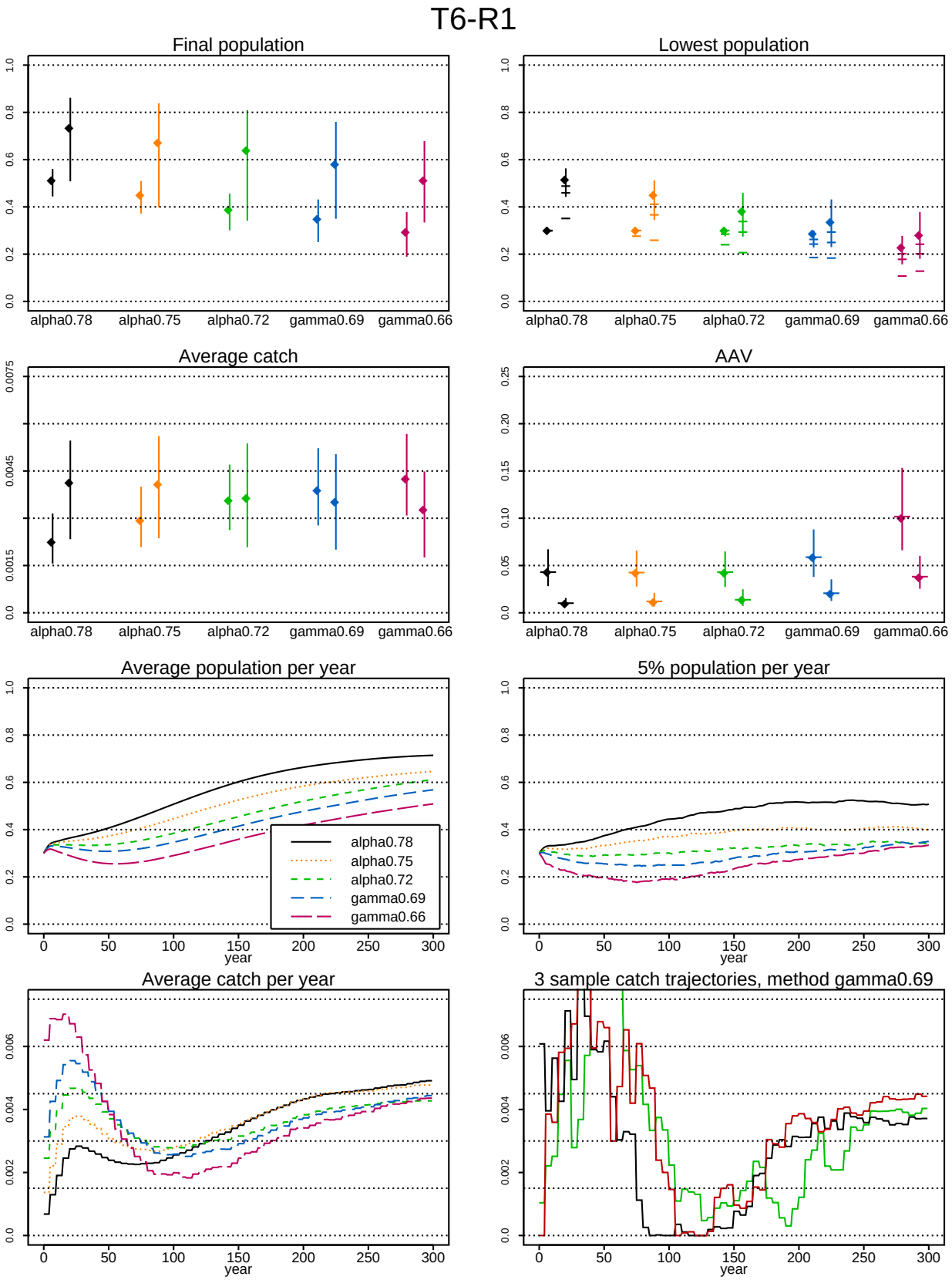


Figure 90. Trial T6-R1. Reported historic catch = 50% of the true catch.

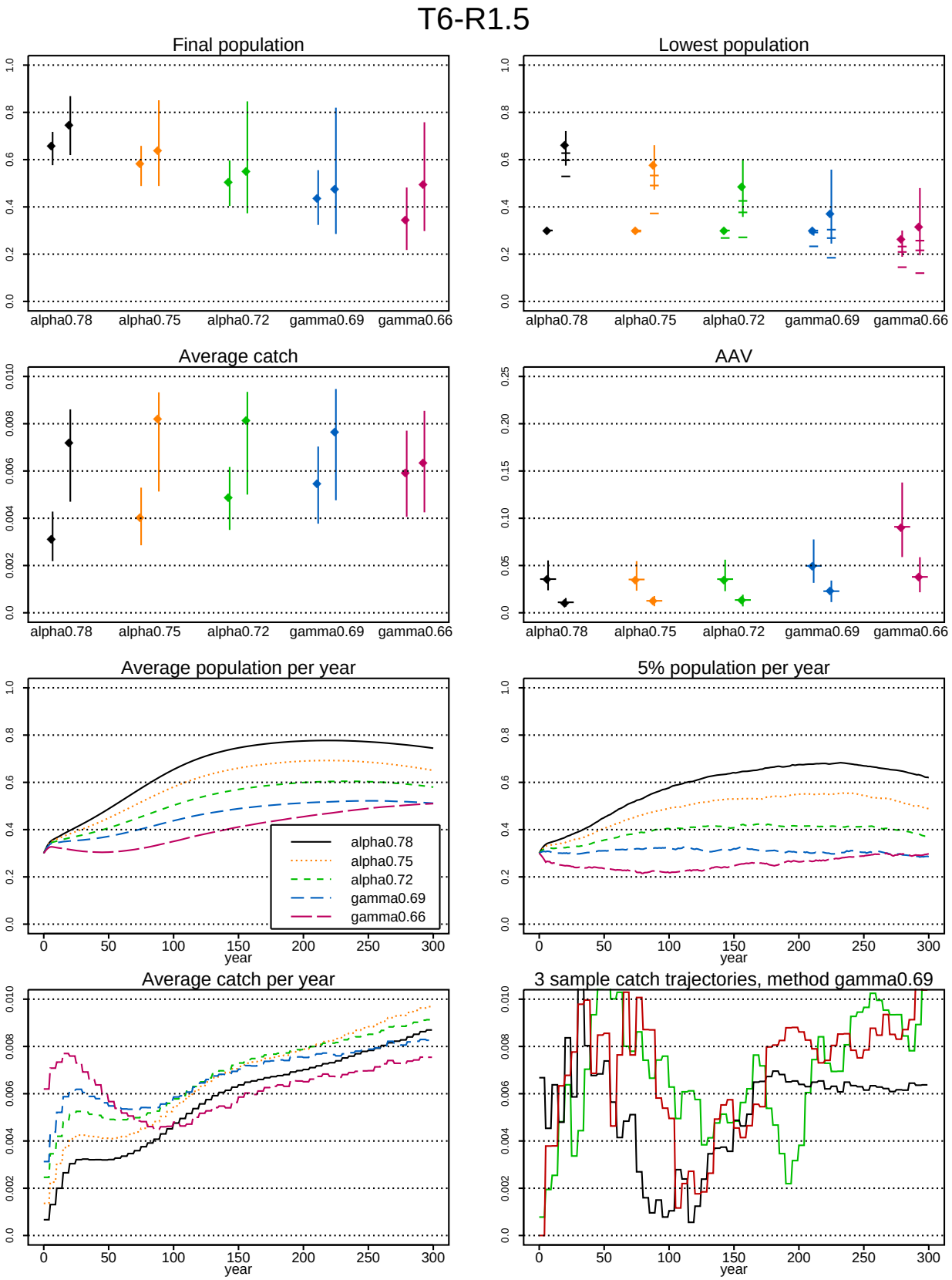


Figure 91. Trial T6-R1.5. Reported historic catch = 50% of the true catch.

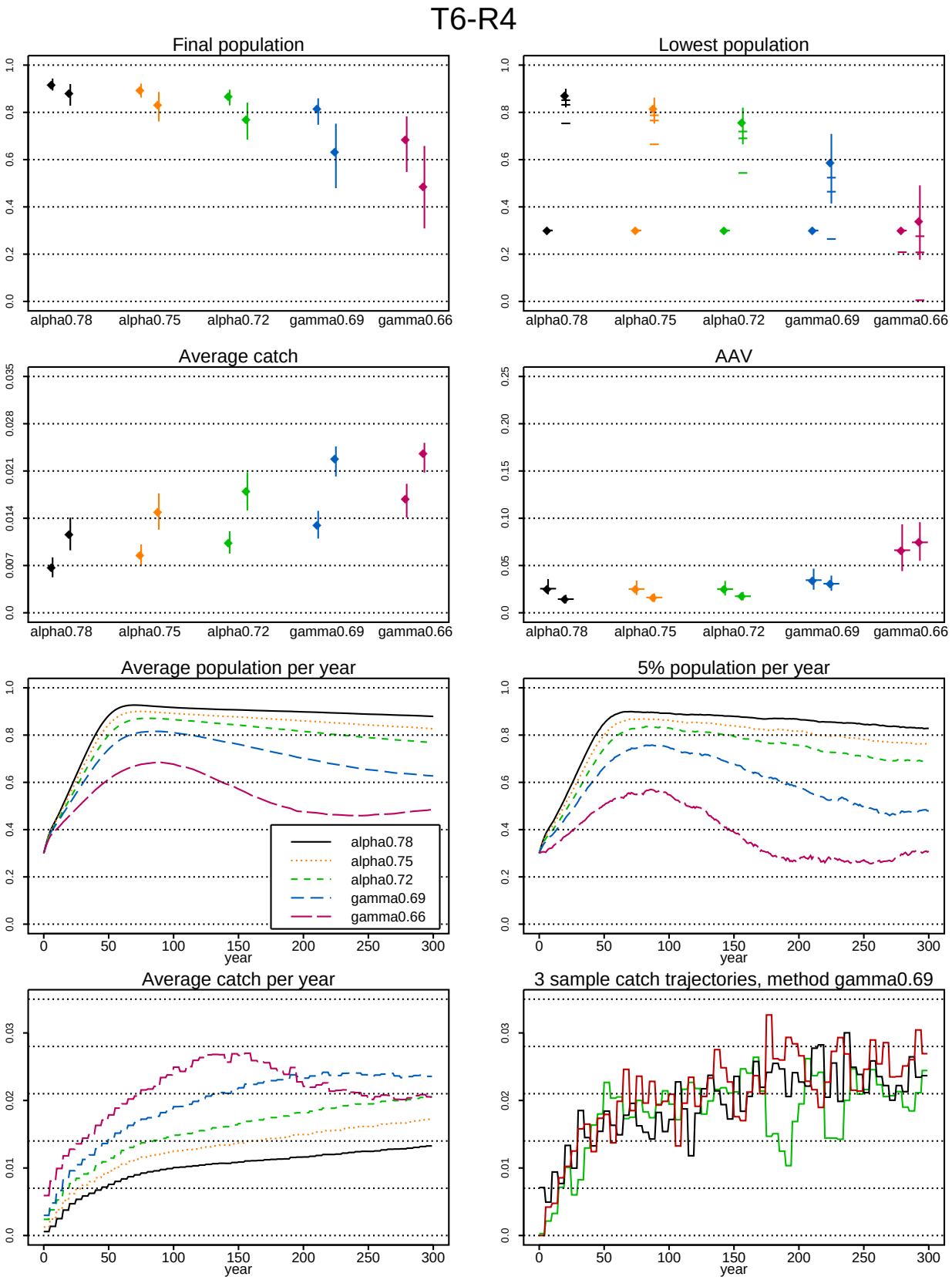


Figure 92. Trial T6-R4. Reported historic catch = 50% of the true catch.

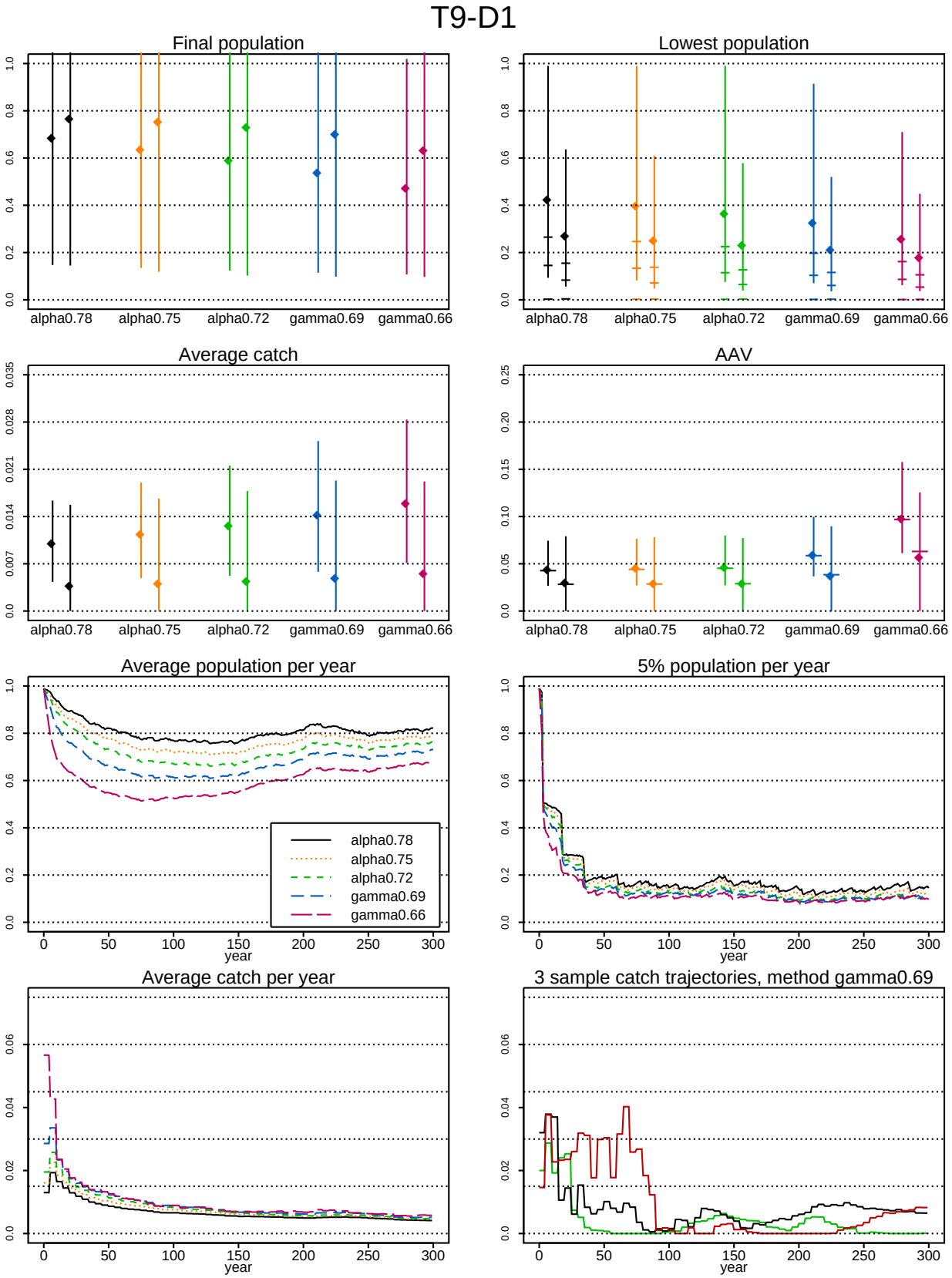


Figure 93. Trial T9-D1. Episodic events; (Rate = 0.02).

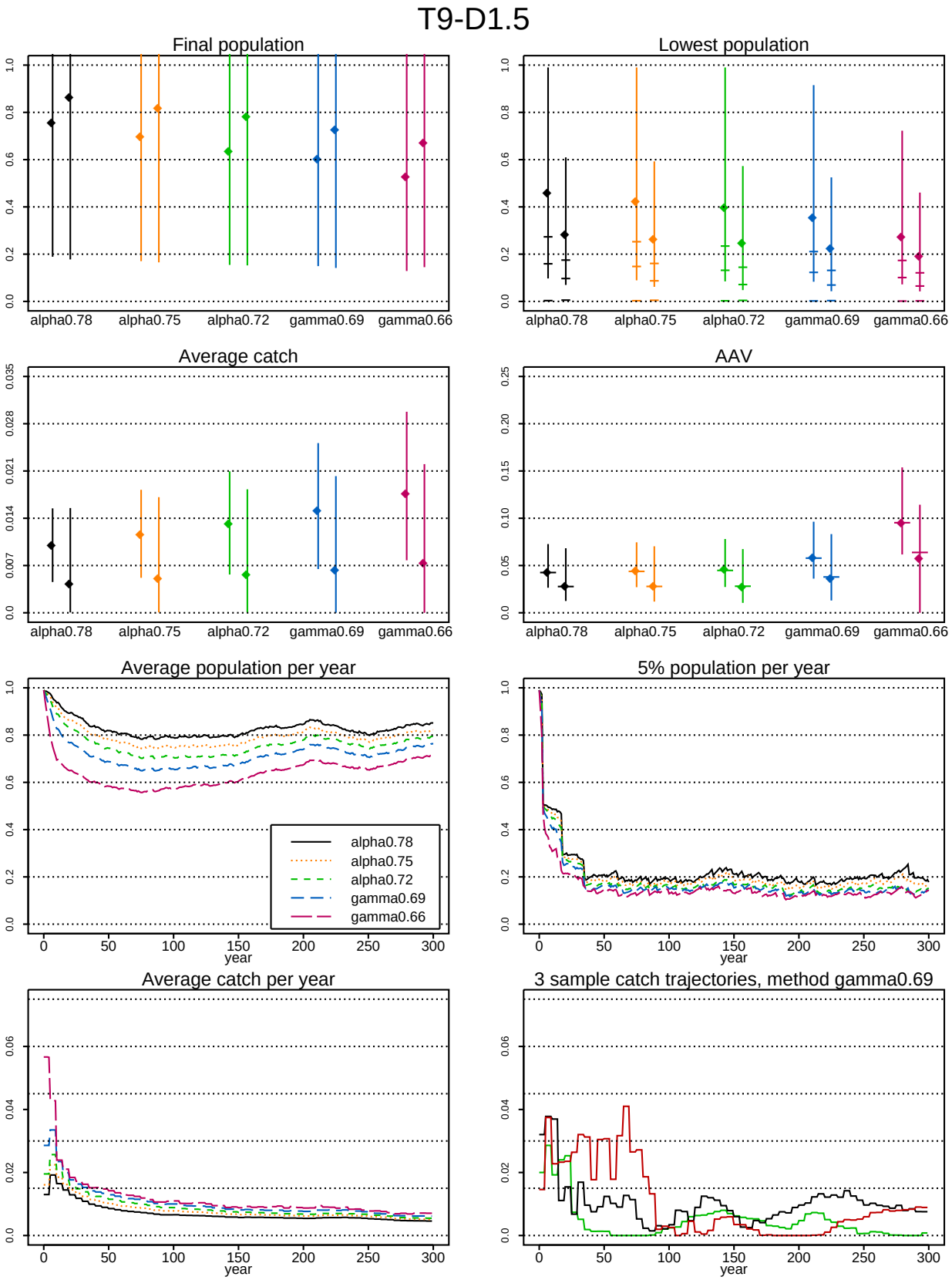


Figure 94. Trial T9-D1.5. Episodic events; (Rate = 0.02).

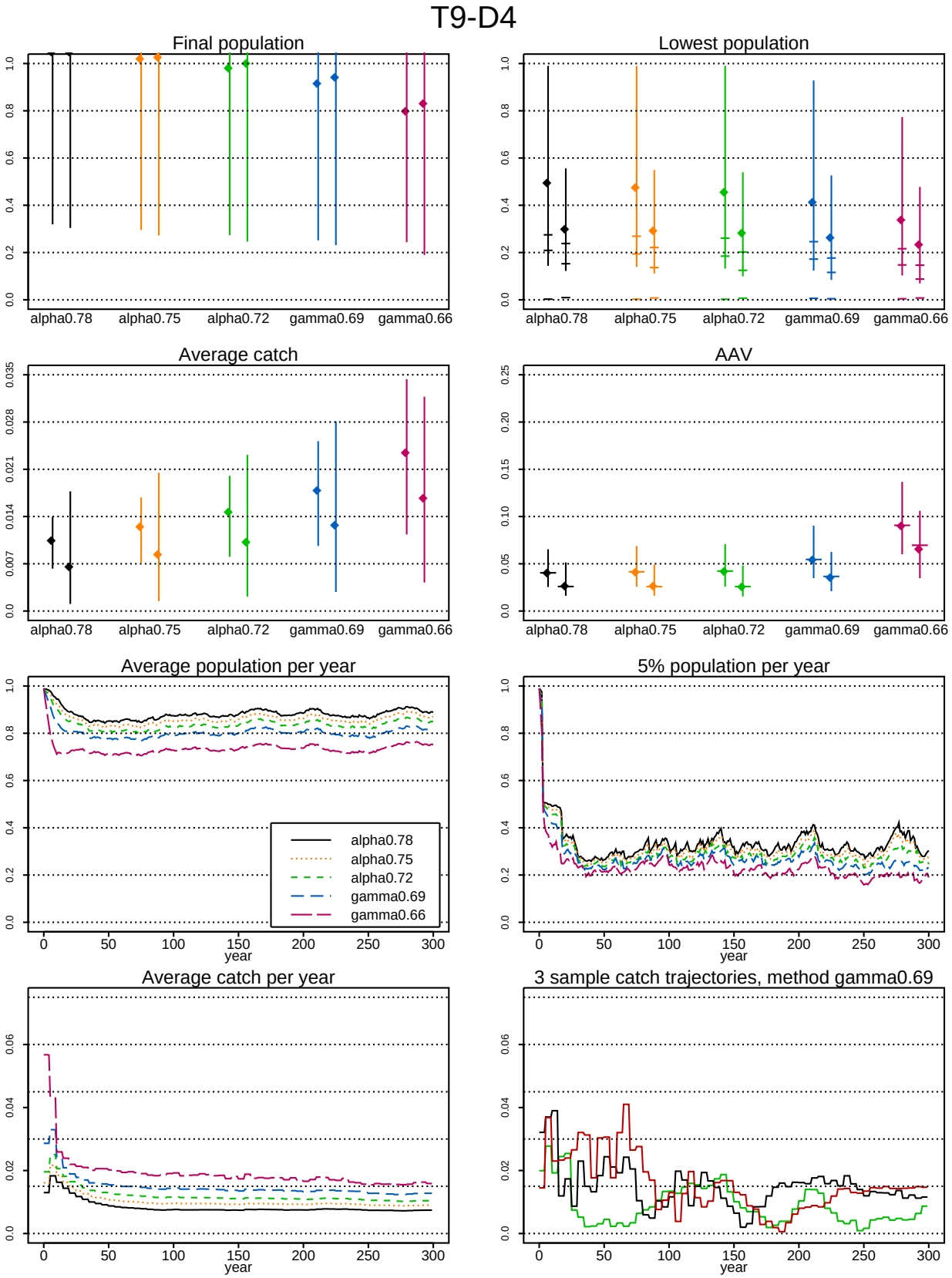


Figure 95. Trial T9-D4. Episodic events; (Rate = 0.02).

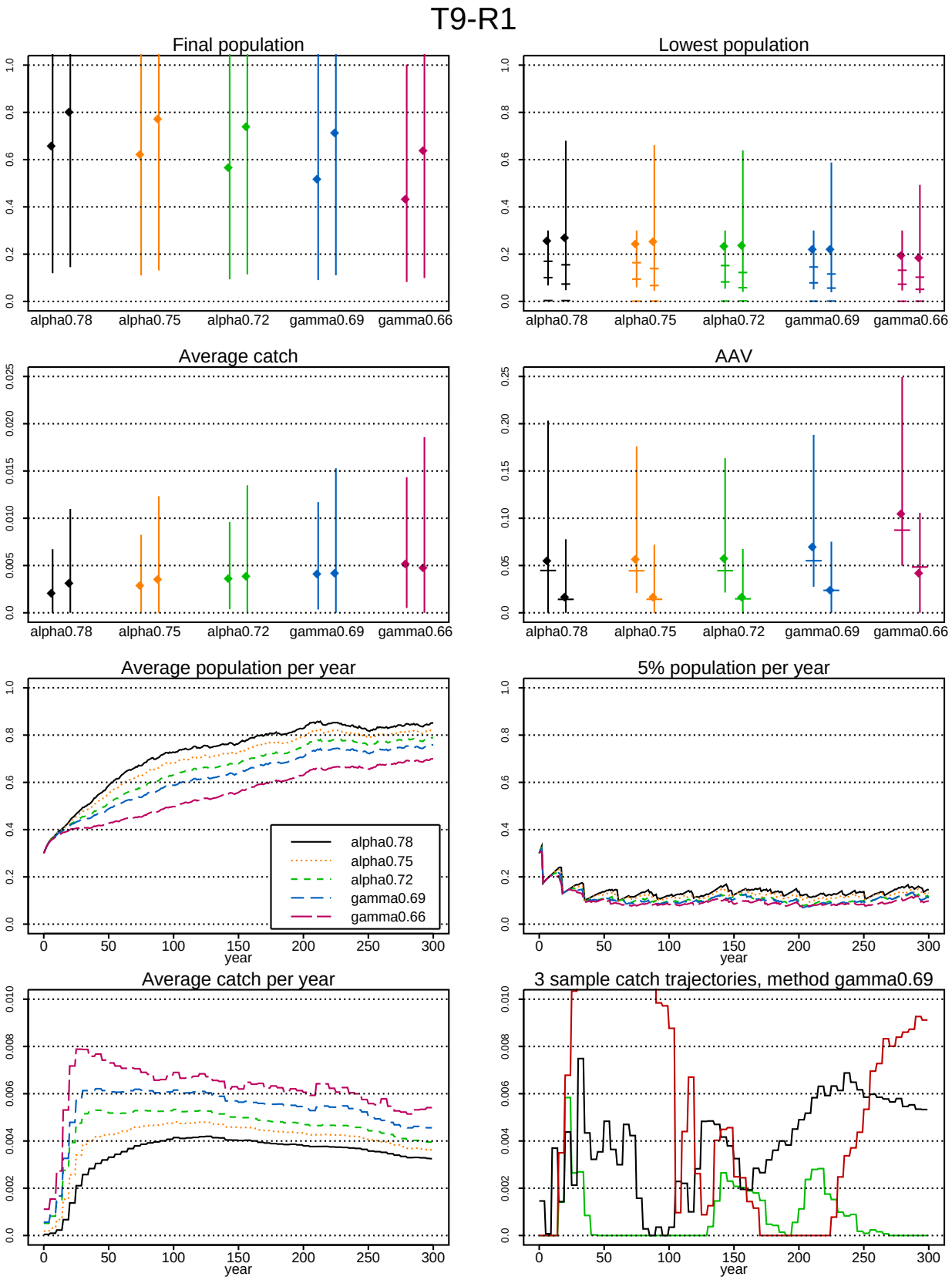


Figure 96. Trial T9-R1. Episodic events; (Rate = 0.02).

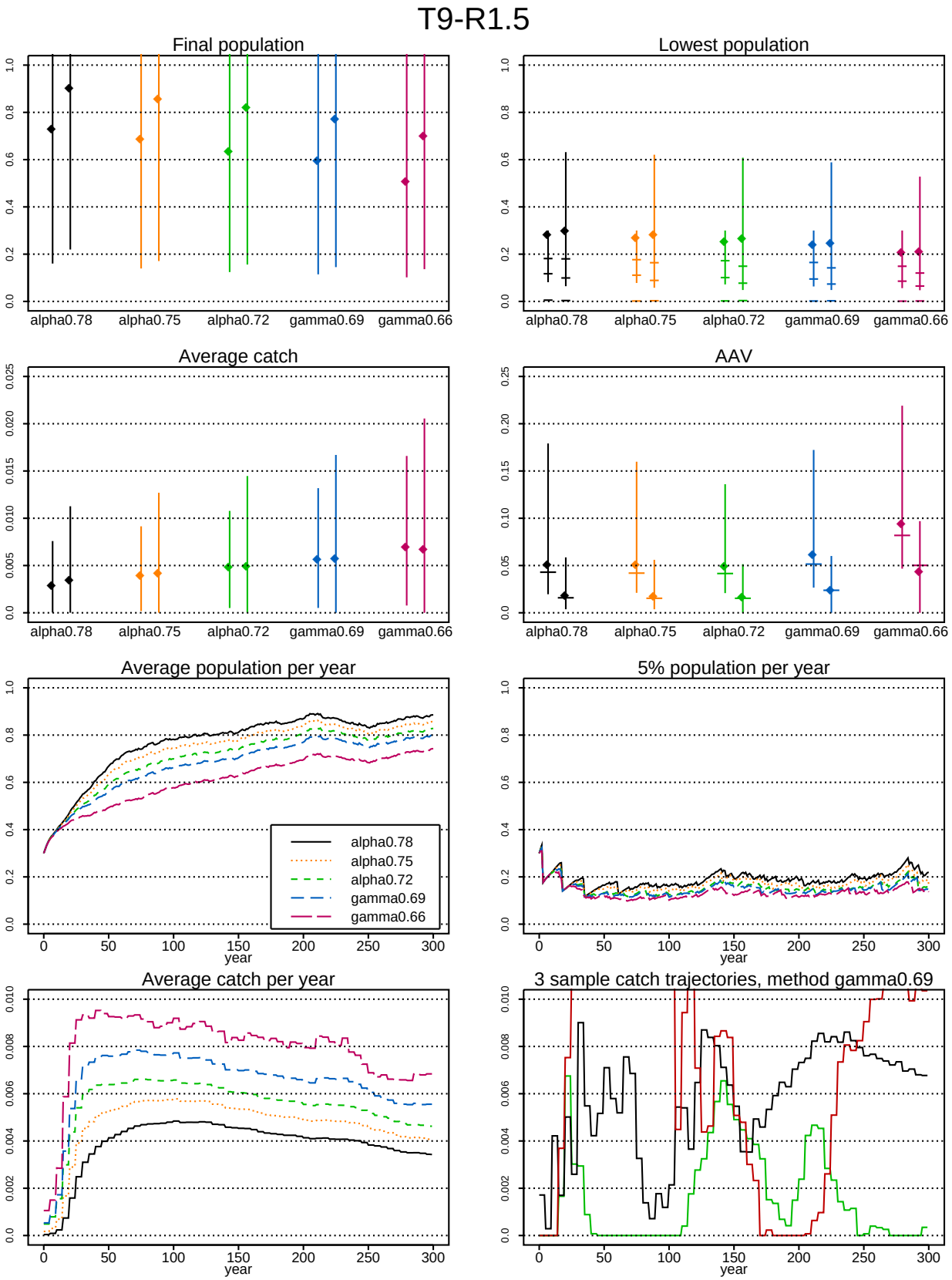


Figure 97. Trial T9-R1.5. Episodic events; (Rate = 0.02).

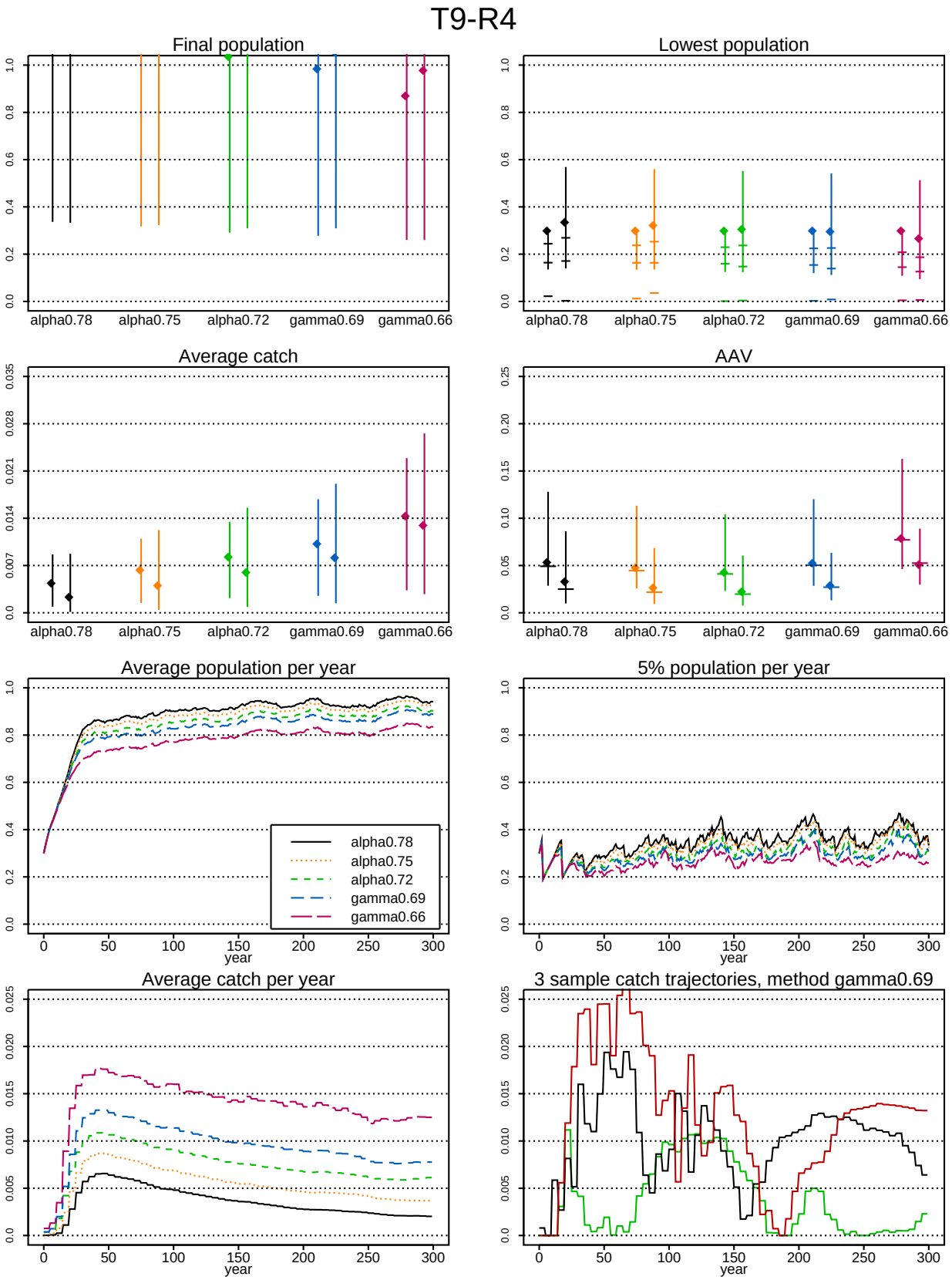


Figure 98. Trial T9-R4. Episodic events; (Rate = 0.02).

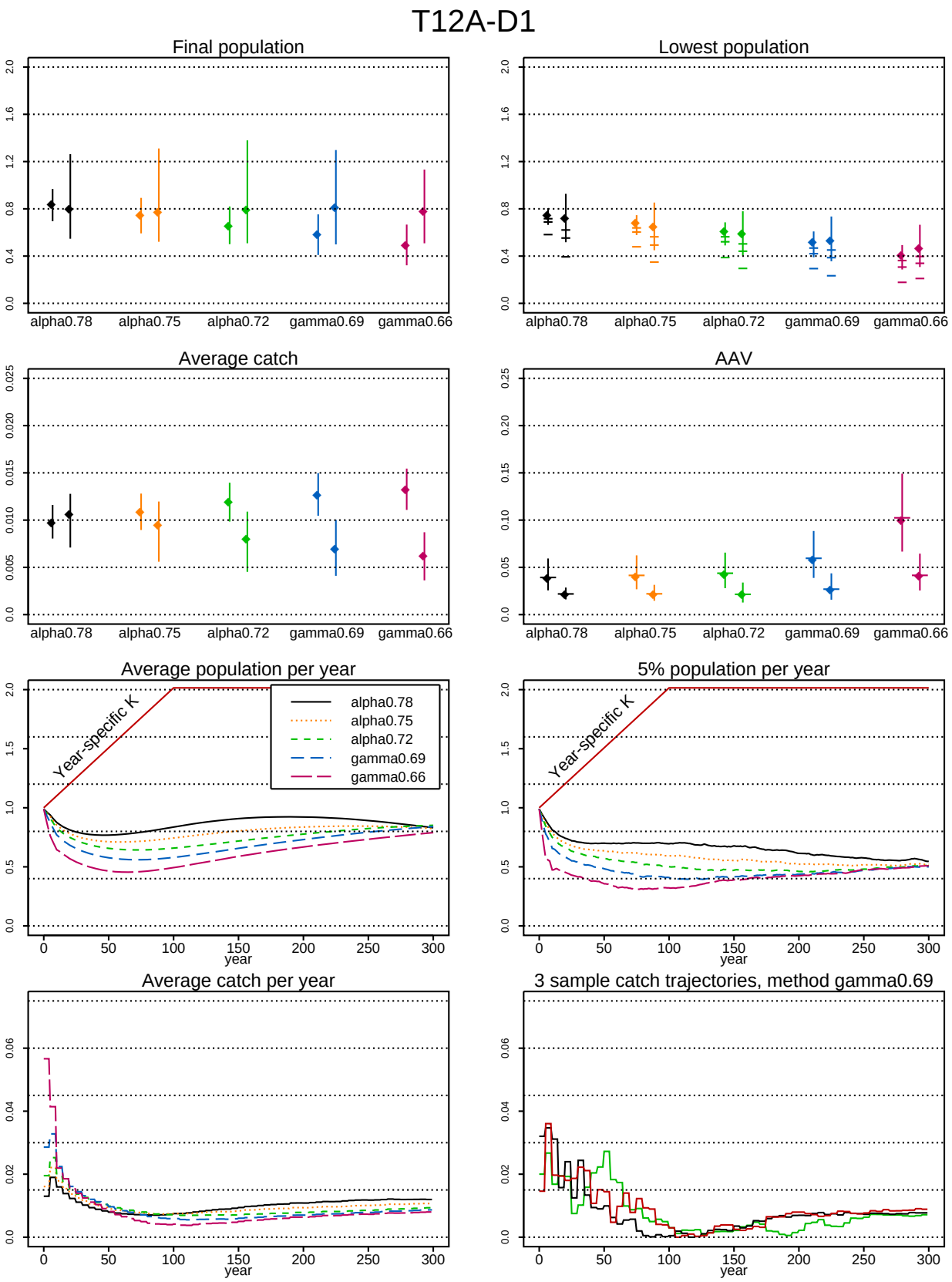


Figure 99. Trial T12A-D1. Linear increase in K from K_0 to a constant level of $2 \cdot K_0$ after 100 years.

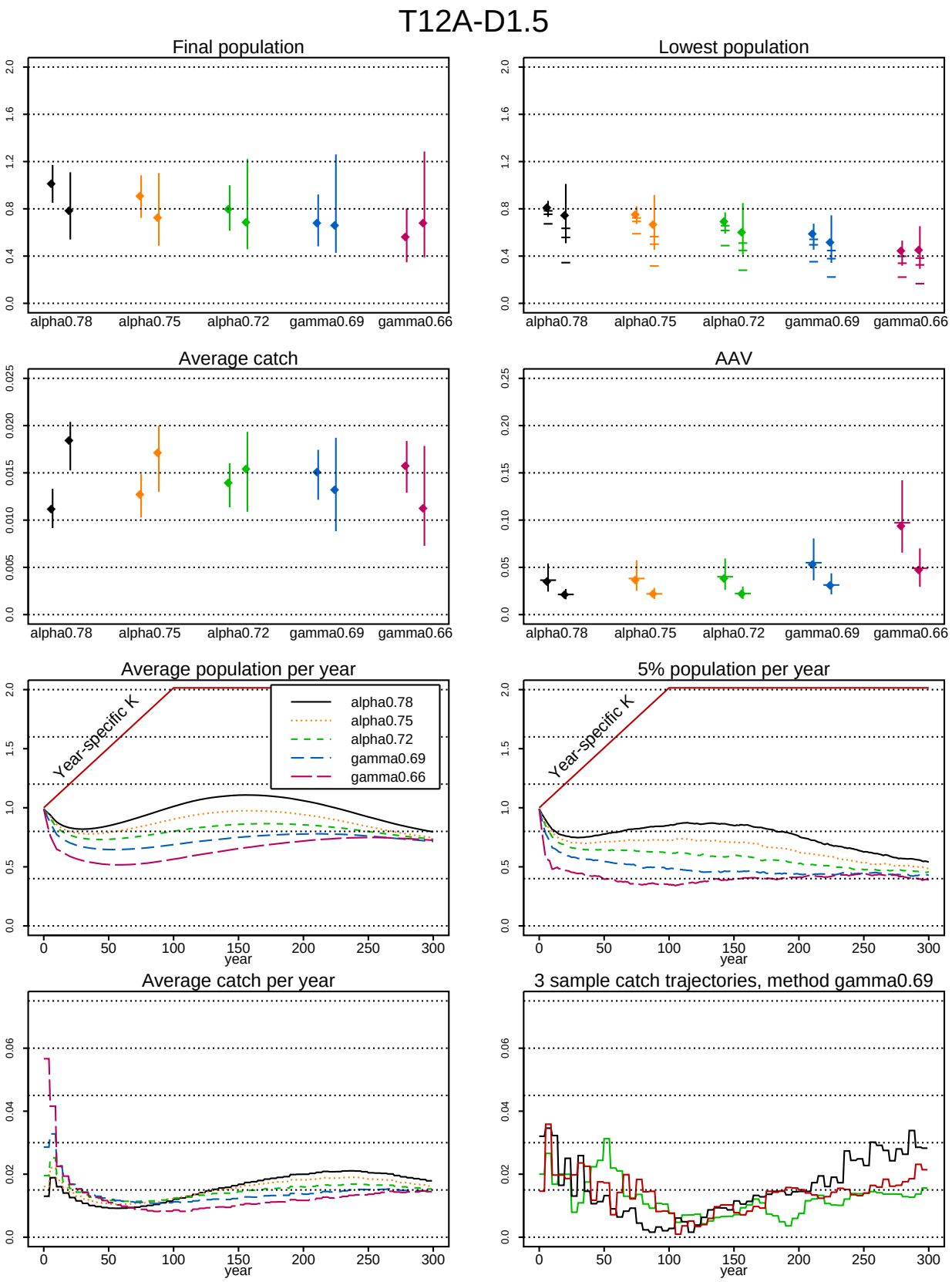


Figure 100. Trial T12A-D1.5. Linear increase in K from K_0 to a constant level of $2 \cdot K_0$ after 100 years.

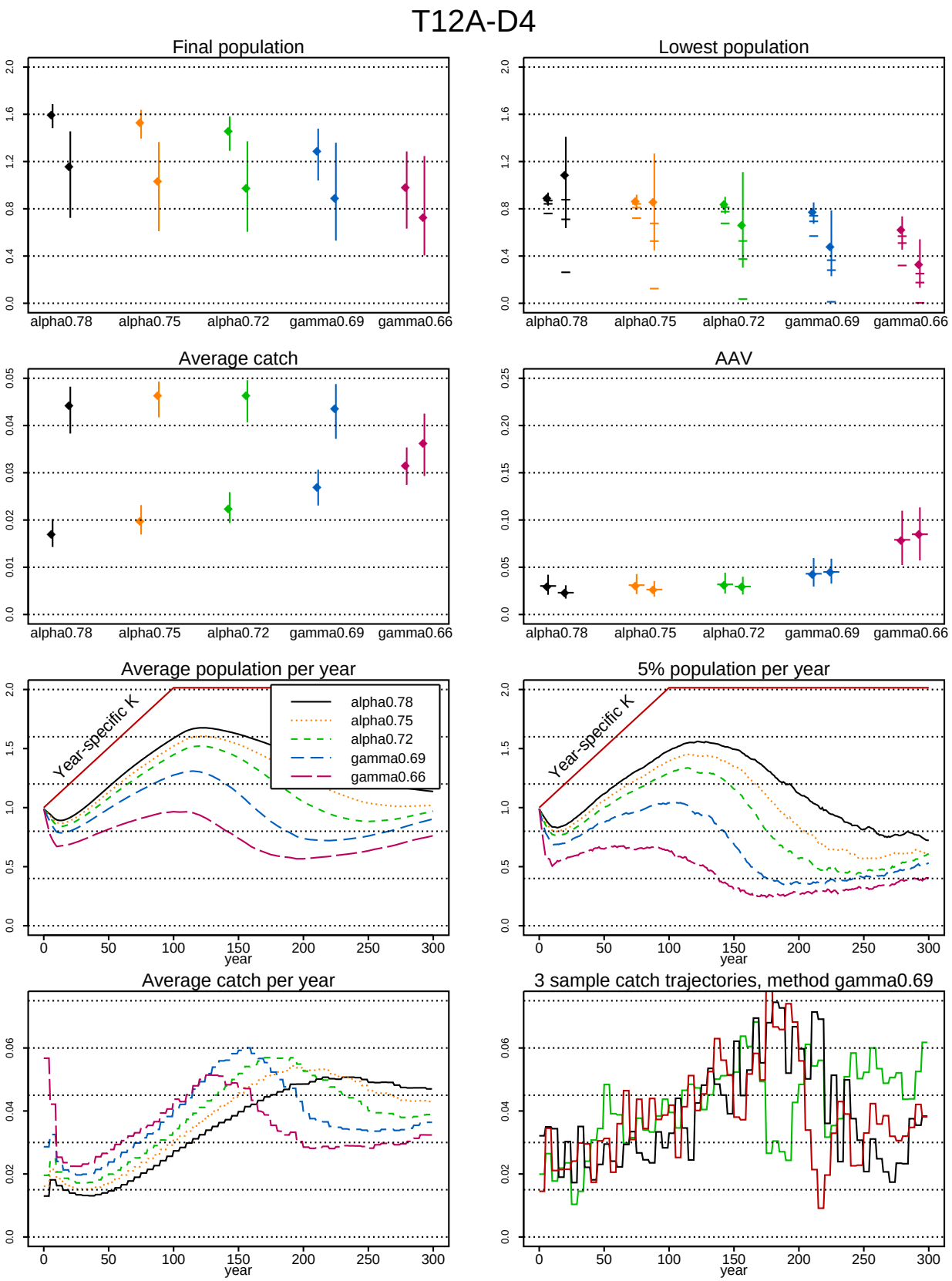


Figure 101. Trial T12A-D4. Linear increase in K from K_0 to a constant level of $2 \cdot K_0$ after 100 years.

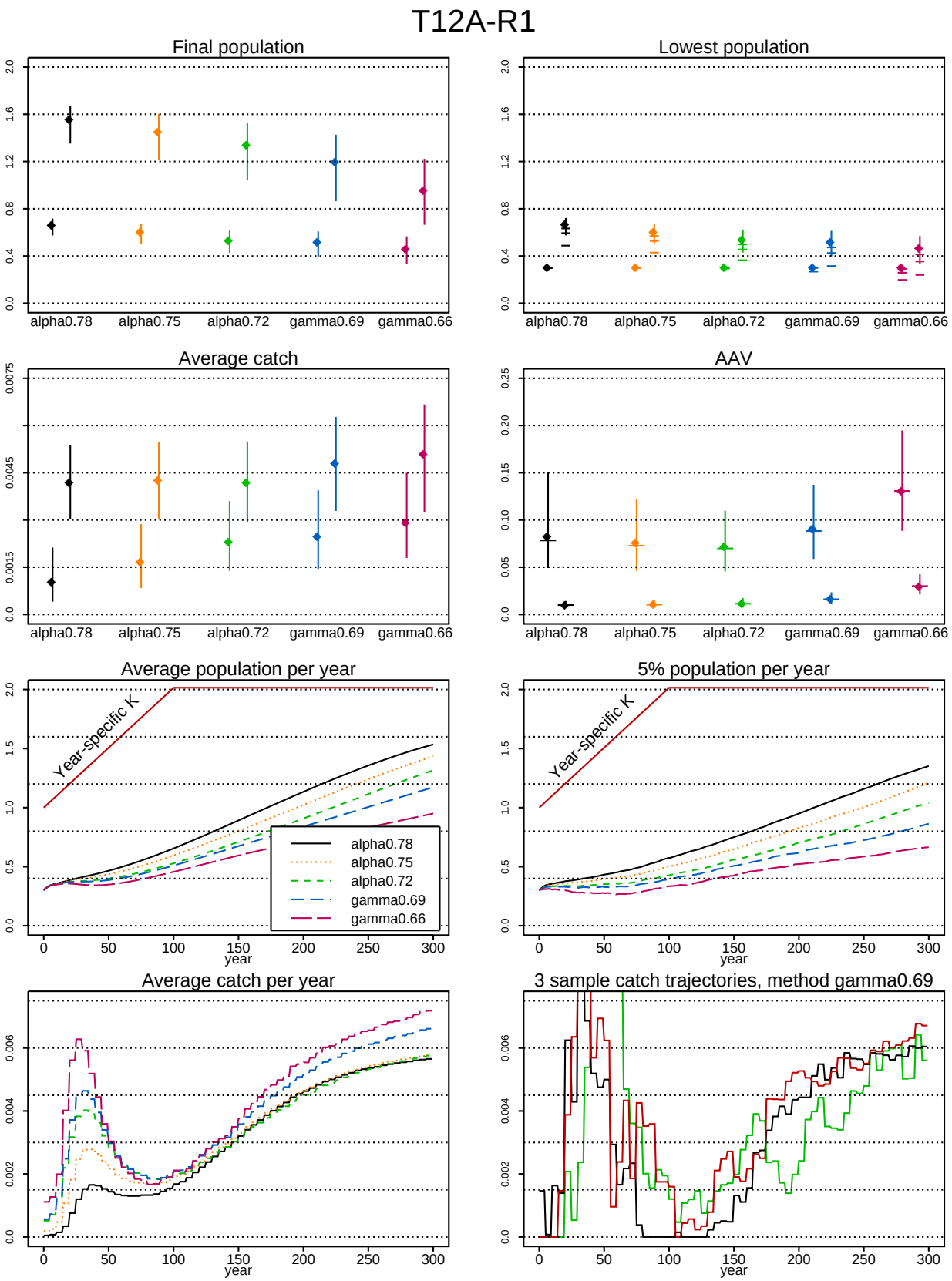


Figure 102. Trial T12A-R1. Linear increase in K from K_0 to a constant level of $2 \cdot K_0$ after 100 years.

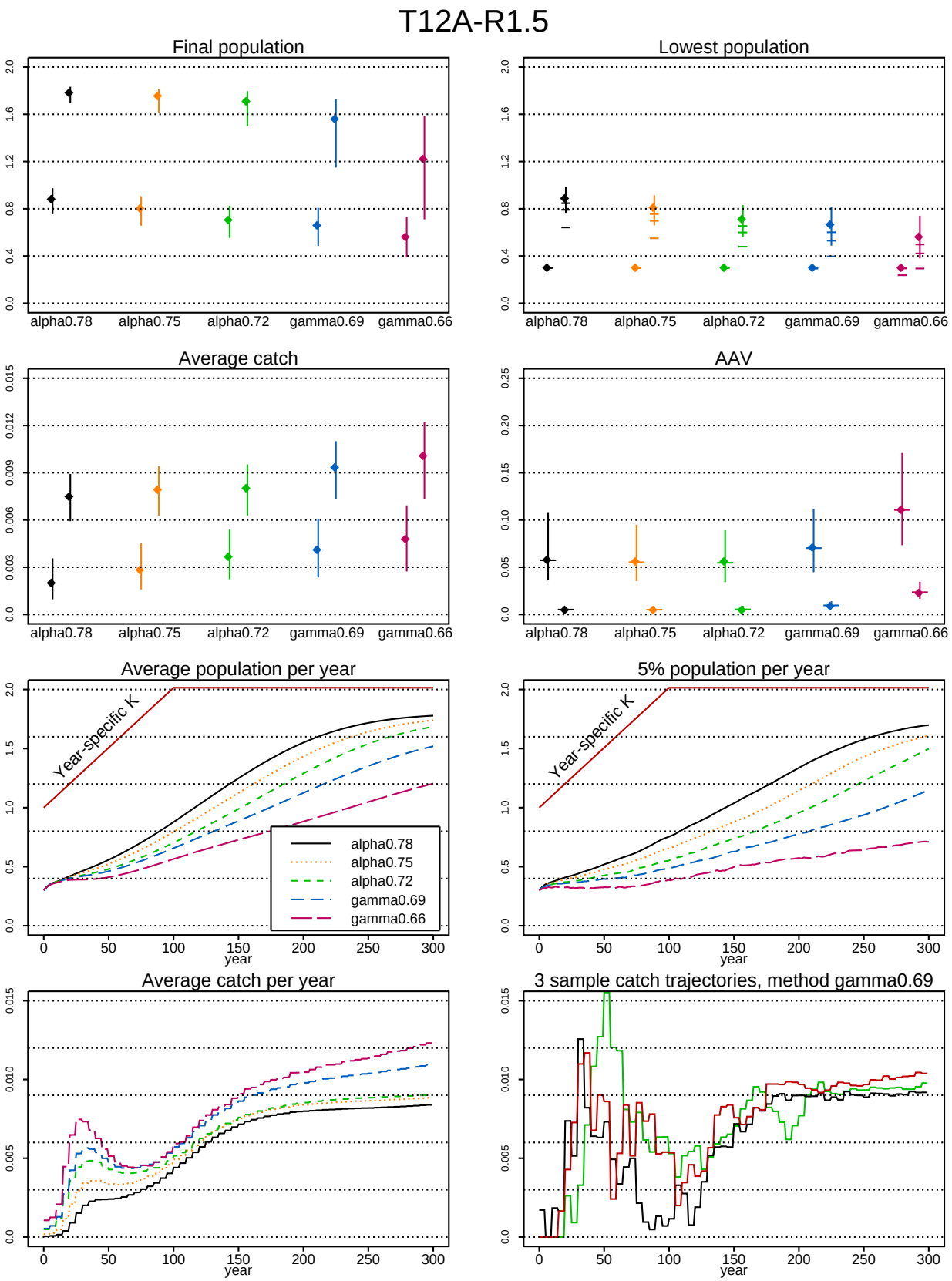


Figure 103. Trial T12A-R1.5. Linear increase in K from K_0 to a constant level of $2 \cdot K_0$ after 100 years.

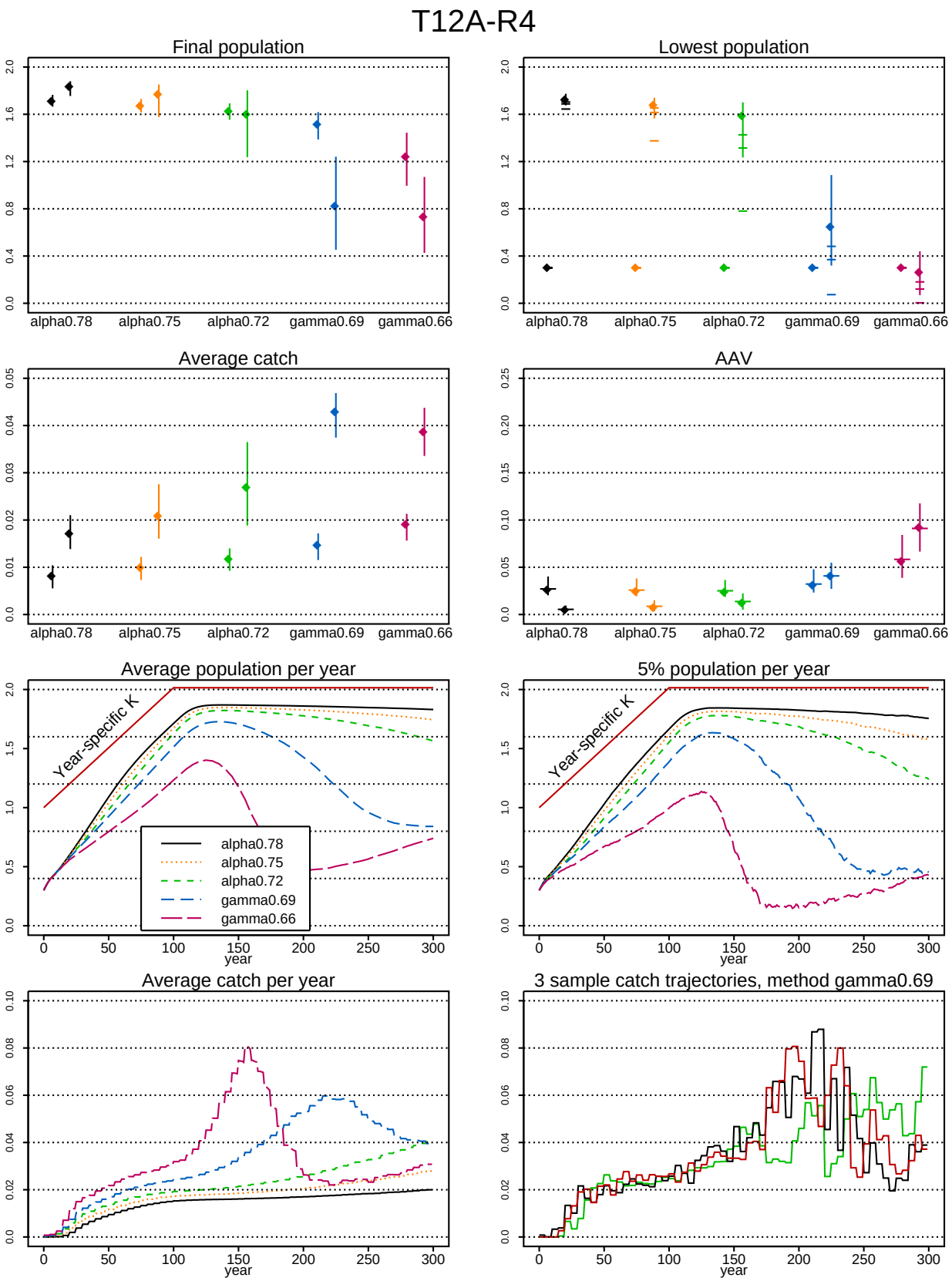


Figure 104. Trial T12A-R4. Linear increase in K from K_0 to a constant level of $2 \cdot K_0$ after 100 years.

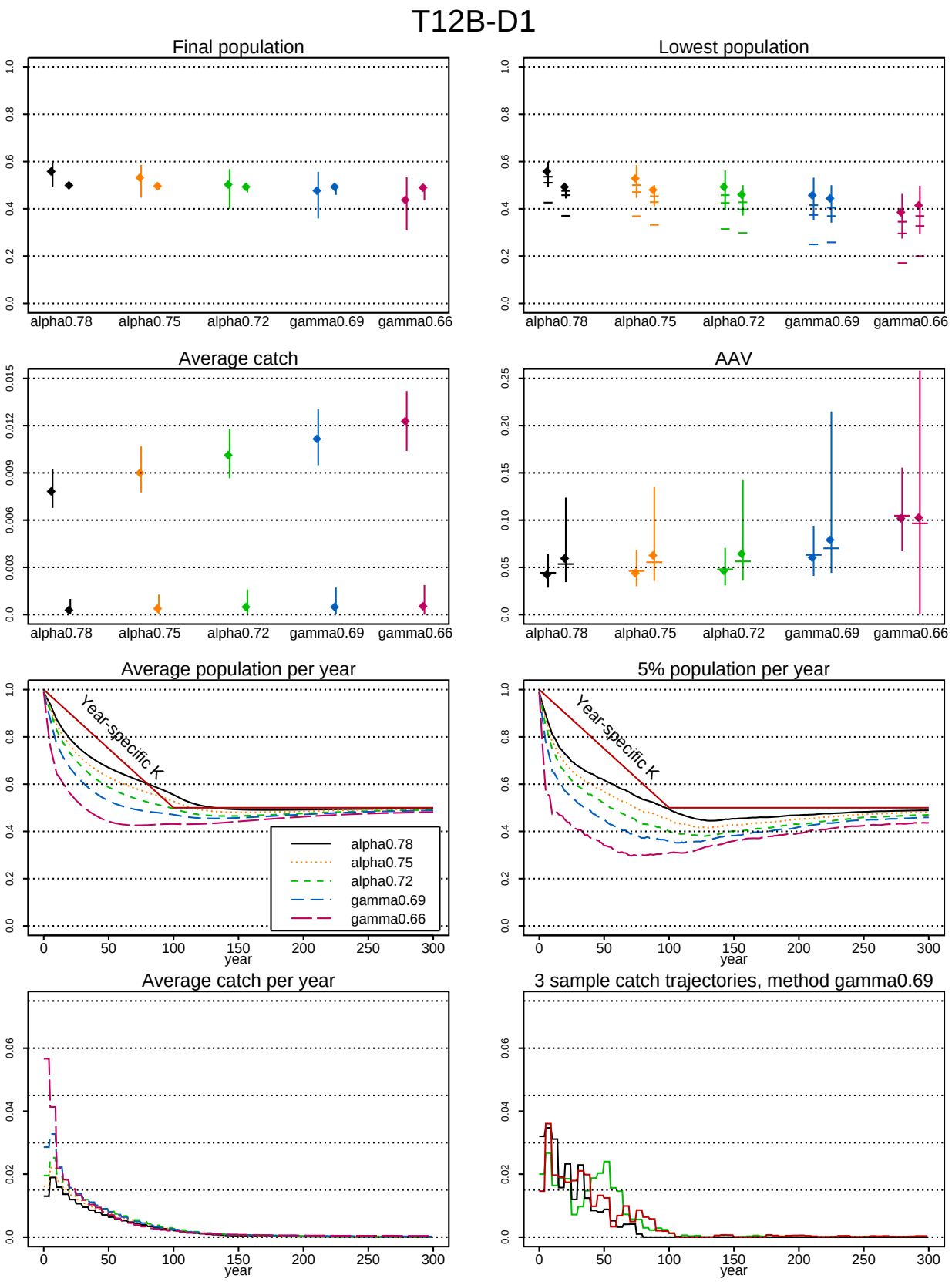


Figure 105. Trial T12B-D1. Linear decrease in K from K_0 to a constant level of $0.5 \cdot K_0$ after 100 years.

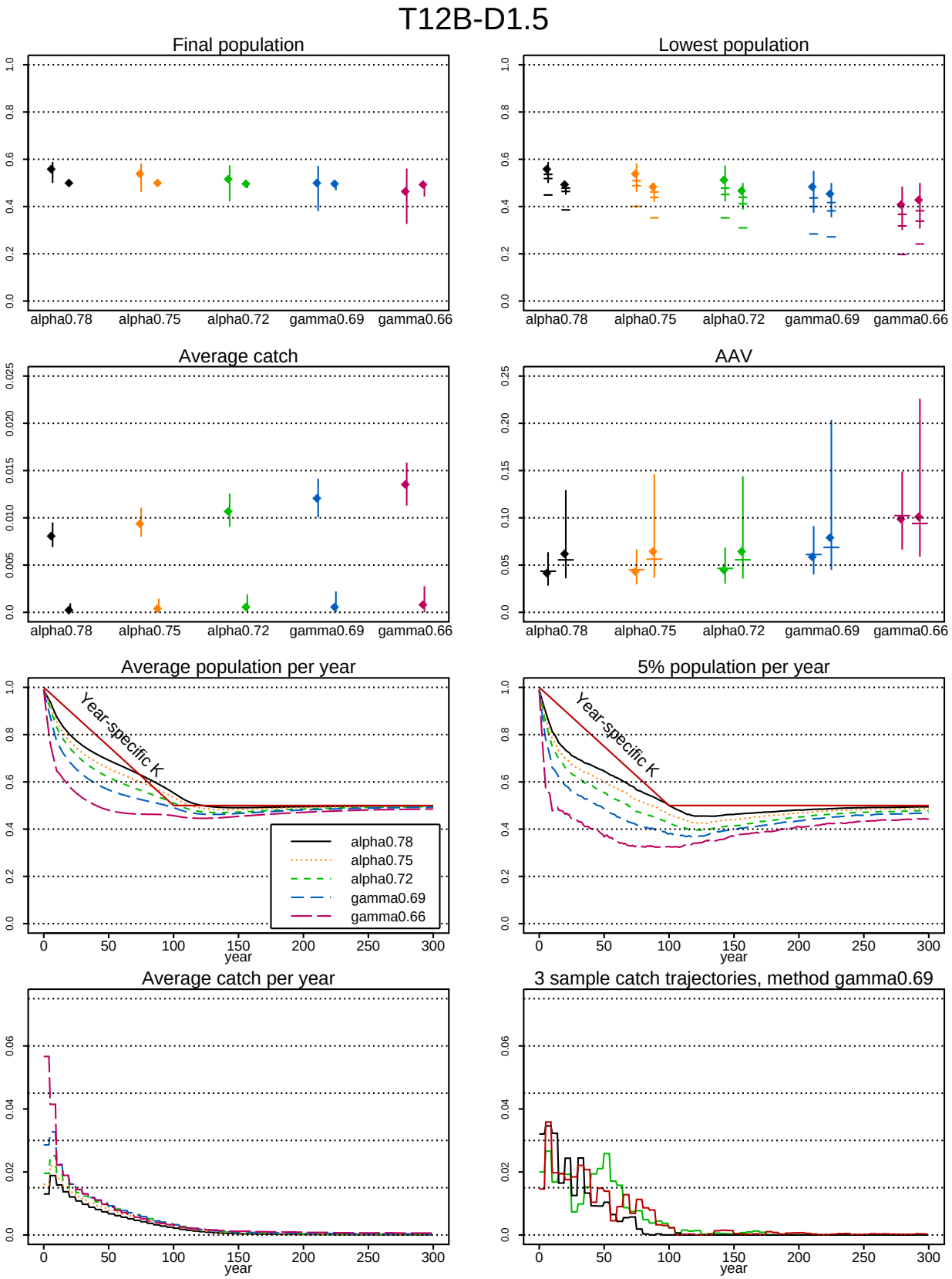


Figure 106. Trial T12B-D1.5. Linear decrease in K from K_0 to a constant level of $0.5 \cdot K_0$ after 100 years.

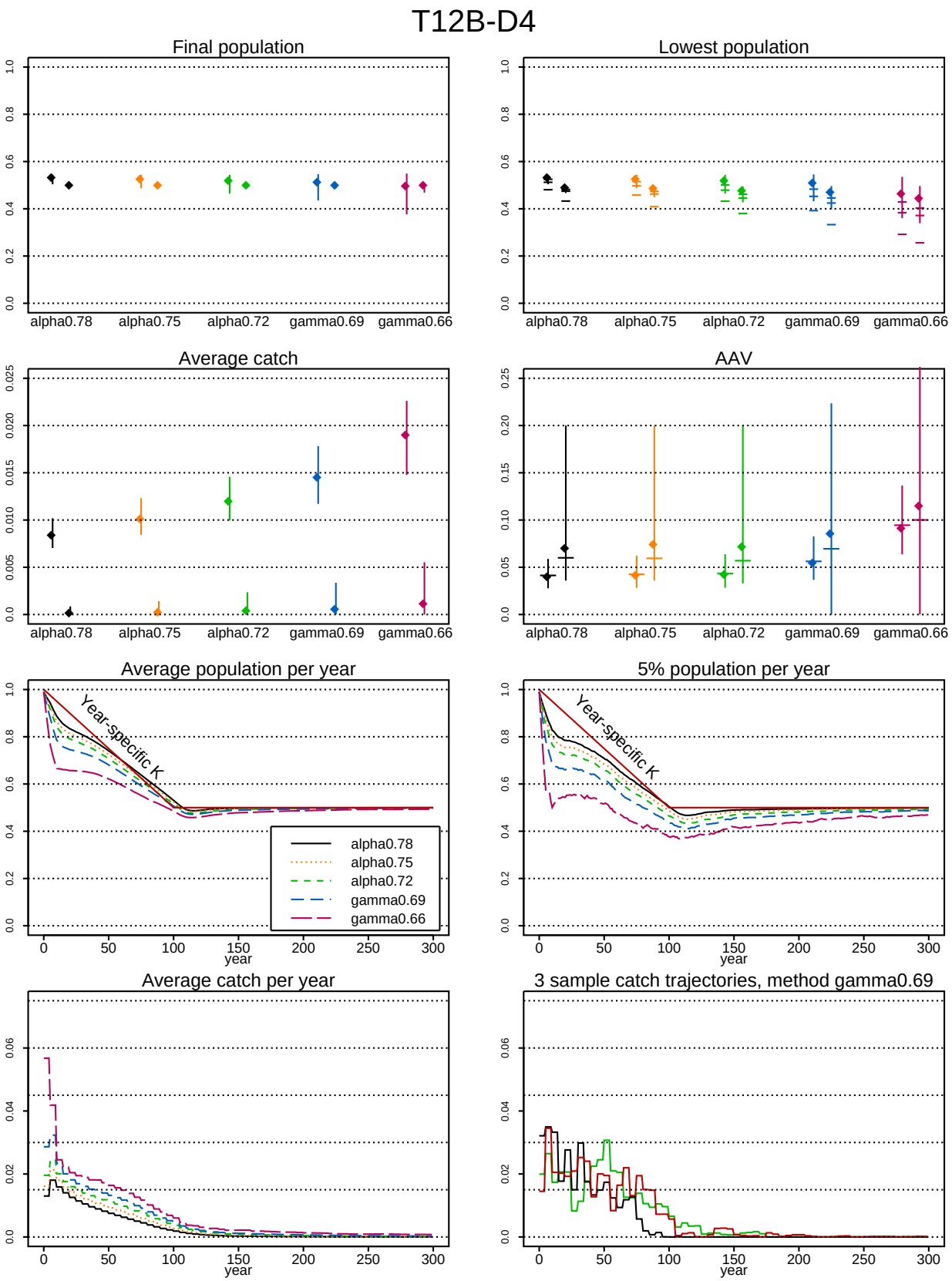


Figure 107. Trial T12B-D4. Linear decrease in K from K_0 to a constant level of $0.5 \cdot K_0$ after 100 years.

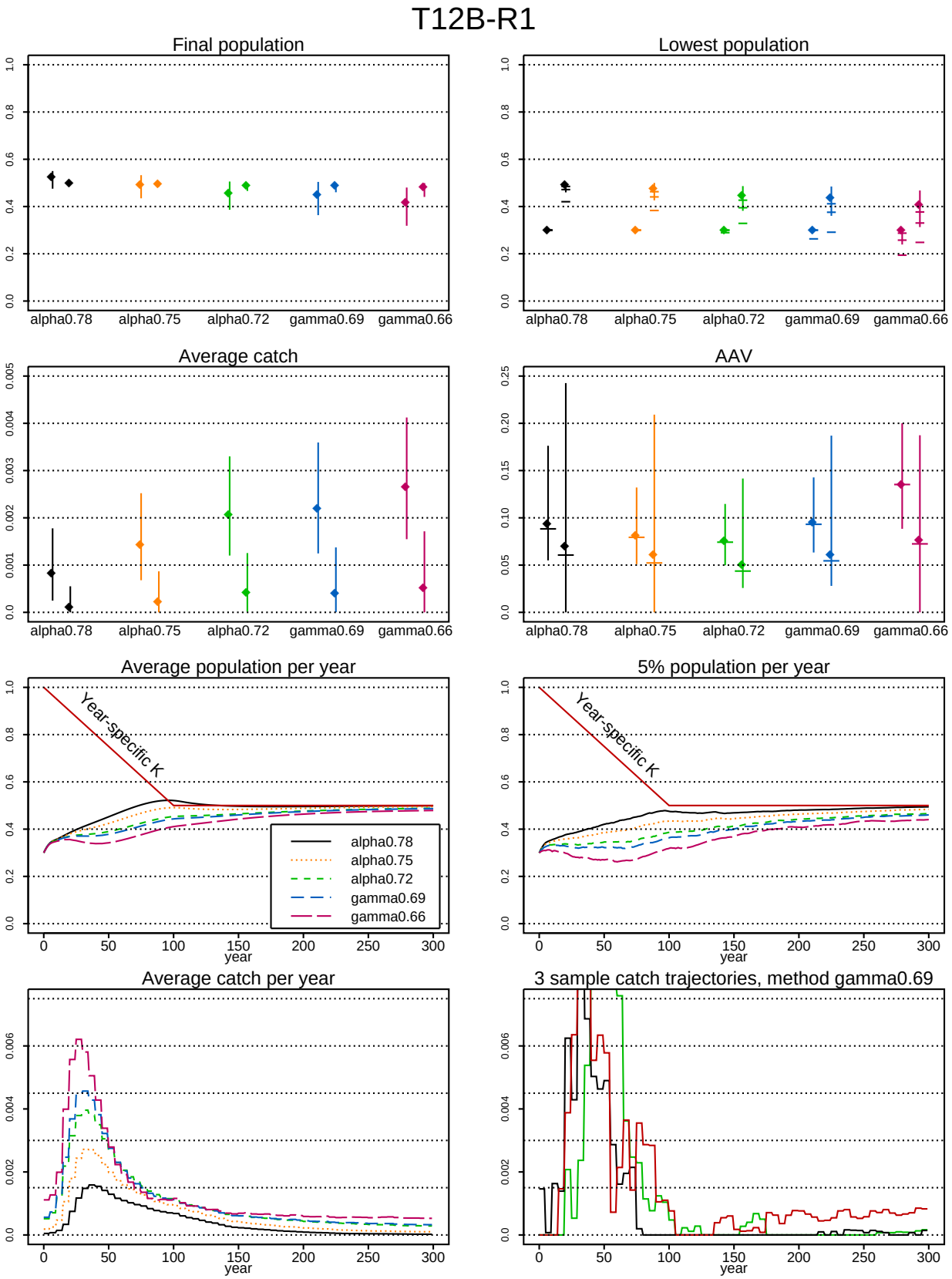


Figure 108. Trial T12B-R1. Linear decrease in K from K_0 to a constant level of $0.5 \cdot K_0$ after 100 years.

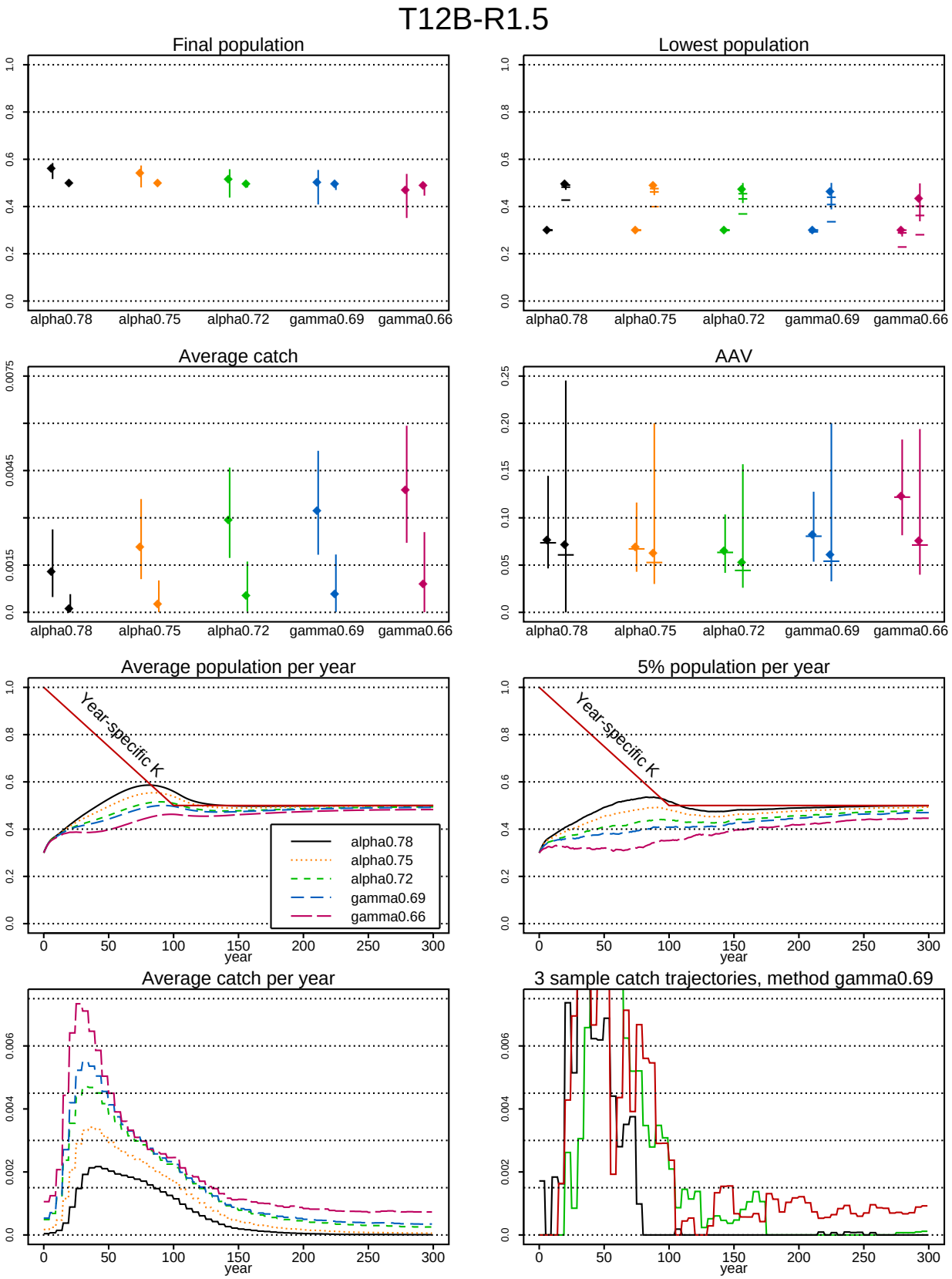


Figure 109. Trial T12B-R1.5. Linear decrease in K from K_0 to a constant level of $0.5 \cdot K_0$ after 100 years.

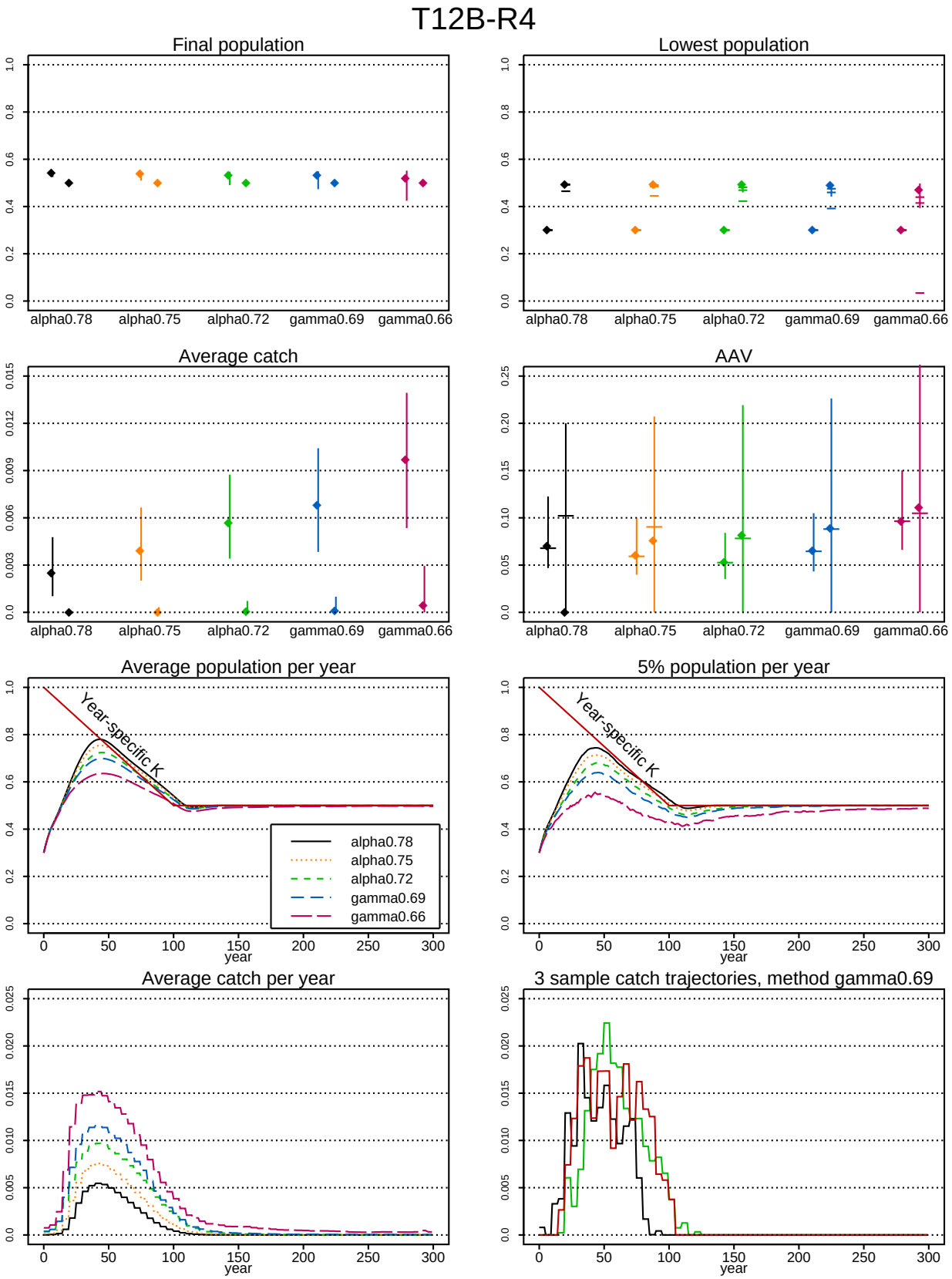


Figure 110. Trial T12B-R4. Linear decrease in K from K_0 to a constant level of $0.5 \cdot K_0$ after 100 years.

Acknowledgements

The authors are grateful to Andre Punt, Tore Schweder, Lars Walløe and Ingrid Hobæk Haff for helpful comments and suggestions during the work with this paper. We also thank Andre Punt for updating the MANRES program to version 9.

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A Appendix Options to the MANTST program

Several options to the MANTST program are specified in an input file called COPY.DAT. The content of this file T1-D1 trial (base case) is shown below, folloved by an explanation of most of the paramaters, extracted from the computer code.

Content of COPY.dat:

```
MANAGEMENT PARAMETERS         CASE: T1-D1

RANDOM PARAMETERS OPTION              OPTRAN    0
VARIABLE BIAS OPTION                  OPTB      0
REPORTED CATCH OPTION                 OPTC      0
PRODUCTION MODEL OPTION               OPTMOD    5
STOCHASTICITY OPTION                  OPTDET    0
SURVEY COSTS OPTION                   OPTSUR    0
No. OF TRIALS                         NTRIAL  400
No. OF YEARS IN SIMULATION            NYEAR   300
No. OF YEARS OF PREMANAGEMENT CATCH   NPCAT    30
YEARS OF PREMANAGEMENT PROTECTION     NPPROT    0
TRUE MSYL(1)                          MSYL     0.60
TRUE MSY RATE(1)                      MSYR1    0.010000
PREMANAGEMENT DEPLETION (1)           DEPL     0.9900
CHANGING K OPTION                     K99      0.000
CHANGING MSYR OPTION                  MSYR99   0.000
CHANGING MSYR STEP                    ISTEP    0
MATURITY PARAMETER                    MAT1     7.00
MATURITY SIGMA                        MSIG     1.20
RECRUITMENT PARAMETER                 REC1     7.00
RECRUITMENT SIGMA                     RSIG     1.20
MORTALITY PARAMETER 1                 MORT1    0.04
MORTALITY PARAMETER 2                 MORT2    0.07

MORTALITY FUNCTION                    MORTIP   -1
MAXIMUM AGE                           MAXAGE   20
EPIDEMIC RATE                         ERATE    0.00
COMPONENTS (0=EXPLOITABLE; 1=TOTAL1+; 2=MATURE)
MSYR COMPONENT                        OPTF      2
```

```
MSYL COMPONENT                          OPTMSYL   2
DENSITY-DEPENDENT COMPONENT             OPTDD     2
FREQUENCY OF ABUNDANCE ESTIMATES        IFREQ     5
YEAR OF LAST SURVEY                     ENDSUR  300
YEAR CV CHANGES                         IYRCV   300
BIAS IN ABUNDANCE ESTIMATES             BIAS0    1.0
CV OF CV ESTIMATES (1st)                CV1EST   0.20
PROCESS ERROR PARAMETER                 ETA      1.00
MINIMUM No. OF DEGREES OF FREEDOM       DOFMIN   5.00
DEPLETION (0:SINGLE VALUE;1:READ IN) OPTDPL   0
DEPLETION FILE                                DEPL99.CSV
```

Explanation of parameters:

```
Population parameters, common to all population models:
NTRIAL Number of trials.
NYEAR  Number of years of management.
NPCAT  Number of years of the (constant) premanagement catch.
       Read in or if OPTRAN=1 a random value from U[15,45] used.
NPPROT Number of years of premanagement protection. Read in.
MSYL   MSY Level.  Read in.
MSYR1  Initial MSY rate used to set A. Read in  or  if OPTRAN=1 a
       random value from U[.001,.05] is generated for each trial.
       If OPTMOD=4 then the value read in = MSY/1+ population at
       MSYL, and the true MSYR is calculated in SMSYR.
DEPL   Depletion level in year 0, =PTRUE(0)/K. Used to set K.
       Read in or if OPTRAN=1 a random value from U[.01,.99] used.
ERATE  Rate at which epidemics occur.   AGE STRUCTURED MODEL ONLY
       If epidemics occur, SUR is reduced after year 0

P-T model parameters: (OPTMOD<2)
M      Mortality rate.  Read in.
TM     Age of maturity.  Read in
K99    If K99>0 then there is a linear change in K
                from  K1 in year KYEAR  to  K1*K99 in year NYEAR-1
       If K99=-1: K cyclic, starting min;  K99=-2: K cyclic, starting max
KYEAR  If K99>0 then K varies linearly from years KYEAR to NYEAR-1
ISTEP  MSYR changes every ISTEP years, P-T model only. Usually=0.
```

```
MSYR99 If MSYR99 > 0 then there is a linear change in MSYR
                from  MSYR1 in year MSYRYR  to   MSYR1*MSYR99 in NYEAR-1
MSYRYR If MSYR99>0 then MSYR varies linearly from year MSYRYR to NYEAR-1

Survey estimate parameters:
BIAS0  Initial bias in absolute abundance estimates
IFREQ  Frequency with which absolute abundance estimates made.
       1st survey made in year -1. If IFREQ=5 the 2nd is in year 4
       If IFREQ=-1, time to next estimate generated from U[1,9]
       If OPTSUR=1 survey costs taken into account & IFREQ ignored
ENDSUR Year after which no surveys take place.  Read in.
CV1EST value of CV(est) when P=0.6K. CV(est) = CV of CVX.  Read in.
IYRCV  Year (if any) when CV(est) changes from CV1EST to CV2EST. Read in.
DOFMIN Minimum number of degrees of freedom in chi-square distribution
ETA    Process error parameter.  If ETA = 0 there is no process error.


OPTIONS -------------------------------------------------------------
OPTRAN Option determining use of random parameters and seeds:
       0: No random parameters;  Use a new seed for each replicate
       1: MSYR1, NPCAT (& INITYR) & DEPL generated for each trial.
       2: The random number generators are NOT reseeded (factorial expt.)
          IRAN defines the inital seeds.
       3: New seeds are generated (tuning trial)
OPTB   Option controlling bias   0: Constant
       1: Linear, doubles        2: Linear, decreases by 1/3 eg 1.5 -> 1.0
OPTC   Defines reported premanagement catch (i.e. as reported to
       the management procedure).
       0: True catch (CATERR=1)
       1: Catch in error; true catch & depletion = base case values
       2: Catch in error; reported catch & PTRUE(0) = base case values
OPTMOD Sets the population model
       0: Standard Pella Tomlinson
       1: P-T with maximum recruitment limitation
       2: Tent Model  (constant MSYR only)
       3: Age structured, maturity = recruitment [base case]
       4: Age structured, differing ages of maturity & recruitment
          with MSY / 1+ population at MSYL = base case ratio
       5: Age structured with MSYL, MSYR and density-dependent
          components entered
```

```
OPTDPL Specifies whether depletion changes among simulations (not randomly)
       0: Constant depletion
       1: Depletion read-in
OPTDET Set on deterministic run    0: stochastic   1:deterministic
OPTSUR Survey control option       0: none
       1: Survey costs taken into account
```