

Examples of input files used in the paper

Input files for the bottleneck scenario in Figure1A

1PopBot20Mb.tpl file

```
//Number of population samples (demes)
1
//Population effective sizes (number of genes)
NCUR
//Sample sizes
20
//Growth rates : negative growth implies population expansion
0
//Number of migration matrices : 0 implies no migration between demes
0
//historical event: time, source, sink, migrants, new size, new growth rate, migr. matrix
2 historical event
TBOT 0 0 0 RESBOT 0 0
TENDBOT 0 0 0 RESENDBOT 0 0
//Number of independent loci [chromosome]
1 0
//Per chromosome: Number of linkage blocks
1
//per Block: data type, num loci, rec. rate and mut rate + optional parameters
FREQ 1 0 2.5e-8
```

1PopBot20Mb.est file

```
// Priors and rules file
// ****
[PARAMETERS]
//#isInt? #name    #dist.#min  #max
//all Ns are in number of haploid individuals
1  NCUR  unif 10  100000 output
1  NANC  unif 10  100000 output
1  NBOT  unif 10  100000 output
1  TBOT  unif 10  10000 output

[RULES]

[COMPLEX PARAMETERS]
0 RESBOT      = NBOT/NCUR hide
0 RESENDBOT   = NANC/NBOT hide
1 TENDBOT     = TBOT+100  hide
```

Command line for parameter estimation

```
./fastsimcoal2 -t 1PopBot20Mb.tpl -n100000 -N100000 -d -e 1PopBot20Mb.est -M 0.001 -l 10 -L 40
-q
```

Example of an observed SFS file

1PopBot20Mb_DAFpop0.obs

```
1 observations
d0_0      d0_1  d0_2      d0_3  d0_4  d0_5  d0_6  d0_7  d0_8  d0_9  d0_10 d0_11 d0_12 d0_13 d0_14 d0_15 d0_16 d0_17 d0_18 d0_19 d0_20
19960052  9331  3572    2530  2221  2059  1963  1952  1730  1682  1572  1520  1426  1453  1335  1179  1195  1069  1129  1030   0
```

Input files for the IM scenario in Figure 1B

IM20Mb.tpl file

```
//Parameters for the coalescence simulation program : simcoal.exe
2 samples to simulate :
//Population effective sizes (number of genes)
NPOP1
NPOP2
//Samples sizes and samples age
20
30
//Growth rates: negative growth implies population expansion
0
0
//Number of migration matrices : 0 implies no migration between demes
2
//Migration matrix 0
0 MIG2
MIG1 0
//Migration matrix 1
0 0
0 0
//historical event: time, source, sink, migrants, new deme size, growth rate, migr mat index
1 historical event
TDIV 0 1 1 RESIZE 0 1
//Number of independent loci [chromosome]
1 0
//Per chromosome: Number of contiguous linkage Block: a block is a set of contiguous loci
1
//per Block::data type, number of loci, per gen recomb and mut rates
FREQ 1 0 2.5e-8
```

IM20Mb.est file

```
// Priors and rules file
// ****
[PARAMETERS]
//#isInt? #name    #dist.#min  #max
//all N are in number of haploid individuals
1 ANCSIZE      unif      100  100000  output
1 NPOP1        unif      100  100000  output
1 NPOP2        unif      100  100000  output
0 N1M1         logunif   1e-2  20      output
0 N2M2         logunif   1e-2  20      output
1 TDIV         unif      100   20000  output

[RULES]

[COMPLEX PARAMETERS]

0 2NM1 = 2*N1M1          hide
0 2NM2 = 2*N2M2          hide
0 RESIZE = ANCSIZE/NPOP2 hide
0 MIG1   = 2NM1/NPOP1    hide
0 MIG2   = 2NM2/NPOP2    hide
```

Command line for parameter estimation

```
./fastsimcoal2 -t IM20Mb.tpl -n100000 -N100000 -d -e IM20Mb.est -M 0.001 -l 10 -L 40 -q
```

Example of a joint observed SFS file

IM20Mb_jointDAFpop1_0.obs

1 observations		d0_0	d0_1	d0_2	d0_3	d0_4	d0_5	d0_6	d0_7	d0_8	d0_9	d0_10	d0_11	d0_12	d0_13	d0_14	d0_15	d0_16	d0_17	d0_18	d0_19	d0_20
1	observation	d1_0	19928211	15071	5514	2678	1397	799	498	259	173	83	54	27	16	2	3	1	1	0	0	0
		d1_1	2103	646	481	385	282	211	183	116	70	47	42	16	12	11	3	0	1	0	0	0
		d1_2	900	515	386	313	240	171	145	123	81	38	38	25	14	11	5	2	3	1	0	0
		d1_3	537	397	345	291	229	192	151	115	89	59	41	26	21	12	8	3	2	0	0	0
		d1_4	349	317	318	284	229	199	147	119	95	62	30	29	22	15	10	7	1	2	0	0
		d1_5	284	237	256	252	230	202	166	103	95	63	63	36	30	13	11	4	2	3	1	0
		d1_6	205	223	246	230	203	187	150	121	102	77	55	42	34	23	12	8	3	0	0	0
		d1_7	130	196	213	201	202	184	155	138	117	94	56	41	32	21	11	9	4	1	1	0
		d1_8	109	160	188	194	169	184	139	128	106	82	55	52	40	22	14	16	5	1	1	0
		d1_9	68	118	123	189	158	167	148	128	101	103	74	55	39	36	19	13	13	5	0	1
		d1_10	46	86	150	167	168	149	138	118	102	68	67	48	59	23	28	13	9	6	2	1
		d1_11	39	79	108	129	155	151	162	115	122	78	83	72	60	32	39	21	13	10	1	1
		d1_12	26	68	91	135	141	131	118	119	106	106	92	51	38	39	29	28	11	7	4	1
		d1_13	25	39	67	95	111	113	141	112	94	120	101	85	73	55	39	15	23	16	4	0
		d1_14	16	34	73	89	100	110	105	112	95	94	74	57	62	49	54	33	23	9	7	4
		d1_15	5	30	43	62	96	93	102	118	100	108	89	68	55	44	40	32	25	12	8	7
		d1_16	8	19	46	60	81	95	89	108	99	90	79	71	68	71	49	41	20	16	17	9
		d1_17	3	14	34	42	63	77	84	102	86	99	101	85	65	55	52	29	23	20	14	6
		d1_18	3	13	35	50	49	79	87	83	104	90	93	72	73	69	55	30	29	24	15	10
		d1_19	2	8	19	44	47	71	63	80	84	91	78	68	78	60	60	51	30	35	14	12
		d1_20	2	9	15	33	42	57	64	62	82	77	66	77	92	63	40	45	41	25	22	9
		d1_21	3	8	15	25	33	41	59	63	79	75	72	82	80	76	60	51	50	20	25	10
		d1_22	1	5	12	15	29	27	41	44	64	71	89	71	73	66	70	61	40	34	29	15
		d1_23	0	5	3	13	27	21	43	55	71	54	63	82	75	88	70	70	53	36	35	19
		d1_24	0	0	6	13	19	25	33	45	52	52	48	50	64	73	86	58	55	47	38	23
		d1_25	1	1	2	9	11	29	18	33	40	59	65	65	81	72	56	54	63	59	35	19
		d1_26	0	2	0	8	8	16	15	32	41	48	60	59	59	73	68	59	69	57	38	21
		d1_27	0	0	2	3	8	10	13	20	30	42	63	63	61	65	68	68	72	71	47	44
		d1_28	0	0	0	2	5	3	11	19	25	28	38	41	69	64	64	71	90	82	67	57
		d1_29	0	0	3	2	3	3	7	10	23	40	45	55	53	70	75	75	70	91	80	49
		d1_30	0	0	0	2	4	4	7	14	29	37	60	85	105	183	201	312	371	490	638	830

Input files for the 3-population scenario in Figure 1C

3PopExpBot20Mb.tpl

```
//Parameters for the coalescence simulation program : fastsimcoal.exe
3 samples to simulate :
//Population effective sizes (number of genes)
NPOPAF
2000000
2000000
//Samples sizes and samples age
20
20
20
//Growth rates : negative growth implies population expansion
0
R1
R1
//Number of migration matrices : 0 implies no migration between demes
2
//Migration matrix 0
0.0000 0.0000 0.0000
0.0000 0.0000 MIG
0.0000 MIG 0.0000
//Migration matrix 1
0 0 0
0 0 0
0 0 0
//historical event: time, source, sink, migrants, new deme size, growth rate, migr mat index
4 historical event
TDIV 2 0 1 1 0 1
TDIV 1 0 1 1 0 1
TBOT 0 0 0 RES1 0 1
TENDBOT 0 0 0 RES2 0 1
//Number of independent loci [chromosome]
1 0
//Per chromosome: Number of contiguous linkage Block: a block is a set of contiguous loci
1
//per Block:data type, number of loci, per gen recomb and mut rates
FREQ 1 0 2.5e-8
```

3PopExpBot20Mb.est

```
// Priors and rules file
// ****
[PARAMETERS]
//#isInt? #name    #dist.#min  #max
//all Ns are in number of haploid individuals
1  ANCSIZE      unif     1000   100000  output
1  NBOT         unif     10     2000   output
1  NPOPAF       unif     1000   100000  output
1  NPOPOOA      unif     10     10000  output
1  TDIV          unif     10     10000  output
1  TPLUSDIV     unif     10     10000  hide
0  MIG           logunif  1e-5   1e-2   output

[RULES]

[COMPLEX PARAMETERS]
1  TBOT = TDIV+TPLUSDIV          output
0  RATIO_OOA_EA = NPOPOOA/2000000 hide
0  RTEA = log(RATIO_OOA_EA)      hide
0  R1 = RTEA/TDIV                hide
1  TENDBOT = TBOT+500            hide
0  RES1 = NBOT/NPOPAF           hide
0  RES2 = ANCSIZE/NBOT          hide
```

Command line for parameter estimation

```
./fastsimcoal2 -t 3PopExpBot20Mb.tpl -n100000 -N100000 -d -e 3PopExpBot20Mb.est -M 0.001 -l 10
-L 40 -q --multiSFS -C10
```

Input files for the 10-population scenario in Figure 1D

10Pop2ContilsI.tpl

```

13 historical event
TISLAND1 0 10 1 1 0 1
TISLAND1 1 10 1 1 0 1
TISLAND1 2 10 1 1 0 1
TISLAND1 3 10 1 1 0 1
TISLAND1 4 10 1 1 0 1
TISLAND1 10 10 0 0.0001 0 1
TISLAND2 5 11 1 1 0 2
TISLAND2 6 11 1 1 0 2
TISLAND2 7 11 1 1 0 2
TISLAND2 8 11 1 1 0 2
TISLAND2 9 11 1 1 0 2
TISLAND2 10 11 1 1 0 2
TISLAND2 11 11 0 RESIZE 0 2//Number of independent loci [chromosome]
1 0
//Per chromosome: Number of contiguous linkage Block: a block is a set of contiguous loci
1
//per Block:data type, number of loci, per gen recomb and mut rates
FREQ 1 0 2.5e-8

```

10Pop2ContiIsl.est

```

// Priors and rules file
// ****

[PARAMETERS]
//#isInt? #name    #dist.#min  #max
//all Ns are in number of haploid individuals
1  ANCSIZE      unif      10   100000  output
0  NM0          logunif   0.01  100   output
0  NM1          logunif   0.01  100   output
0  NM2          logunif   0.01  100   output
0  NM3          logunif   0.01  100   output
0  NM4          logunif   0.01  100   output
0  NM5          logunif   0.01  100   output
0  NM6          logunif   0.01  100   output
0  NM7          logunif   0.01  100   output
0  NM8          logunif   0.01  100   output
0  NM9          logunif   0.01  100   output
0  NM_12         logunif   0.01  100   output
1  TISLAND1     unif      10   20000  output
1  TPLUS         unif      10   20000  hide

[RULES]

[COMPLEX PARAMETERS]

//Assume an island haploid population size of 1000 for all islands
1  TISLAND2 = TISLAND1+TPLUS output
0  M010 =  NM0/1000           hide
0  M110 =  NM1/1000           hide
0  M210 =  NM2/1000           hide
0  M310 =  NM3/1000           hide
0  M410 =  NM4/1000           hide
0  M511 =  NM5/1000           hide
0  M611 =  NM6/1000           hide
0  M711 =  NM7/1000           hide
0  M811 =  NM8/1000           hide
0  M911 =  NM9/1000           hide
0  M1211 = NM_12/2000         hide
0  RESIZE = ANCSIZE/20000000 hide

```

Command line for parameter estimation

```

./fastsimcoal2 -t 10Pop2ContiIsl.tpl -n50000 -N50000 -d -e 10Pop2ContiIsl.est -M 0.001 - 110 -
L 30 -q

```

Input files for the African demography with SNP ascertainment as in Figure 5

Model A

p4NocpgSanYor4.tpl

```
//Parameters for the coalescence simulation program : simcoal.exe
3 samples to simulate : Exponential growth : 1000 to 100,000,000 started 3000 generations ago
//Population effective sizes (number of genes)
NSan
NYor
1000
//Samples sizes
12
44
1 1600
//Growth rates : negative growth implies population expansion
0
0
0
//Number of migration matrices : 0 implies no migration between demes
0
//historical event: time, source, sink, migrants, new deme size, new growth rate, migration matrix index
6 historical event
TGSan 0 0 0 RES_SAN 0 0
TGYor 1 1 0 RES_YOR 0 0
TAdm 0 1 AYS 1 0 0
TAdm 1 0 ASY 1 0 0
TDIVSanYor 1 0 1 RES_AF 0 0
16000 2 0 1 RES_ANC 0 0
//Number of independent loci [chromosome]
1 0
//Per chromosome: Number of contiguous linkage Block: a block is a set of contiguous loci
1
//per Block:data type, number of loci, per gen recomb and mut rates
FREQ 1 0 1e-7
```

p4NocpgSanYor4.est

```
// Priors and rules file
// ****
[PARAMETERS]
//#isInt? #name    #dist.#min  #max
//all Ns are in number of haploid individuals
1  NSan      unif    1000   2e6  output
1  NYor      unif    1000   2e6  output
1  NASan     unif    1000   1e5  output
1  NAYor     unif    1000   1e5  output
1  HSIZE     unif    1000   1e5  output
1  ANCSIZE   unif    1000   1e5  output
1  TGSan     unif     10    500  output
1  TGYor     unif     10    500  output
1  TAdm      unif     10    500  output
1  TPlusAdm  unif      1    5000 hide
0  AYS       unif      0     0.2  output
0  ASY       unif      0     0.2  output

[RULES]

[COMPLEX PARAMETERS]
1  TDIVSanYor = TAdm+TPlusAdm  output
0  RES_SAN   = NASan/NSan    hide
0  RES_YOR   = NAYor/NYor    hide
0  RES_AF    = HSIZE/NASan   hide
0  RES_ANC   = ANCSIZE/HSIZE hide
```

Command line for parameter estimation

```
./fastsimcoal2 -t p4NocpgSanYor4.tpl -n100000 -N100000 -d -e p4NocpgSanYor4.est -M 0.001 -l 10
-L 20 -a0 -A2 -q -0 -C2 -multiSFS
```

Model B

p4NocpgSanYor4.tpl

```

//Parameters for the coalescence simulation program : simcoal.exe
5 samples to simulate : Exponential growth : 1000 to 100,000,000 started 3000 generations ago
//Population effective sizes: San, Yoruba, Cont San, Cont Yor, Denisova
500
500
1000
NCSan
NCYor
//Samples sizes
12
44
1 1600
0
0
//Growth rates : negative growth implies population expansion
0
0
0
RSan
RYor
//Number of migration matrices : 0 implies no migration between demes
3
//Current migration matrix 0
0      0      0      mS      0
0      0      0      0      mY
0      0      0      0      0
0      0      0      0      0
0      0      0      0      0
//Current migration matrix 1
0      0      0      mS      0
0      0      0      0      0
0      0      0      0      0
0      0      0      0      m_YS
0      0      0      m_SY     0
//No migration matrix 2
0      0      0      0      0
0      0      0      0      0
0      0      0      0      0
0      0      0      0      0
0      0      0      0      0
//historical event: time, source, sink, migrants, new deme size, new growth rate, migration matrix index
8 historical event
TAdm 3 4 a_YS 1 RYor 0
TAdm 4 3 a_SY 1 RSan 0
TEY 1 4 1 RESYOR 0 1
TES 3 3 0 1 0 1
TES 0 4 1 RESNH 0 2
TES 1 4 1 1 0 2
TES 3 4 1 1 0 2
16000 2 4 1 RESANC 0 2
//Number of independent loci [chromosome]
1 0
//Per chromosome: Number of contiguous linkage Block: a block is a set of contiguous loci
1
//per Block: data type, number of loci, per generation recombination and mutation rates and optional
parameters
FREQ 1 0 2.5e-8 OUTEXP

```

p4NocpgSanYor4.est

```
// Priors and rules file
// ****

[PARAMETERS]
//#isInt? #name    #dist.#min  #max
//all Ns are in number of haploid individuals
1  ANCSIZE      unif      1000    100000   output
1  HSIZE         unif      1000    100000   output
1  NAYor         unif      1000    100000   output
1  NDivSan       unif      100     10000    output
1  NDivYor       unif      100     10000    output
1  NCYor         unif      1000    1000000  output
1  NCSan         unif      1000    1000000  output
0  Nm_S          unif      0       100      output
0  Nm_Y          unif      0       100      output
1  TAdm          unif      0       100      output
0  a_BS          unif      0       0.2      output
0  a_SY          unif      0       0.2      output
0  m_SY          logunif  1e-8    1e-3     output
0  m_BS          logunif  1e-8    1e-3     output
1  TExtraGrowth unif      1       500      hide
1  TExtraDiv    unif      1       5000     hide

[RULES]

[COMPLEX PARAMETERS]

1  TEY           = TAdm+TExtraGrowth output
1  TES           = TEY+TExtraDiv    output

//Computation of Yoruba growth rate
0  RatioYor     = NDivYor/NCYor   hide
0  logRYor      = log(RatioYor)  hide
0  RYor          = logRYor/TEY   hide

//Computation of San growth rate
0  RatioSan     = NDivSan/NCSan  hide
0  logRSan      = log(RatioSan)  hide
0  RSan          = logRSan/TES   hide

0  mS            = Nm_S/500     hide
0  mY            = Nm_Y/500     hide

0  RESYOR        = NAYor/NDivYor  hide
0  RESNH         = HSIZE/NAYor   hide
0  RESANC        = ANCSIZE/HSIZE hide
```

Observed joint multidimensional SFS in San, Yoruba and Denisova for Affymetrix panel 4

p4NocpgSanYor4_DSFS-asc2.obs (the multidimensional SFS is given on a single line) using the same representation as $\partial a \partial i$.

1 observation. No. of demes and sample sizes are on next line																			
3	12	44	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
11407	127	1701	71	1237	55	1096	60	829	65	662	44	600	26	510	29	442	29		
388	50	325	28	291	34	271	21	192	18	198	21	173	18	114	12	106	13		
95	10	93	14	84	10	88	8	43	4	44	10	34	8	39	6	30	6		
23	3	24	4	18	2	12	1	10	4	8	4	9	1	6	0	5	4		
4	3	5	2	1	0	1	0	0	0	1	0	0	0	0	0	1	0	0	
7796	148	1454	77	1111	85	917	75	819	56	757	67	603	63	584	50	507	68		
509	52	420	46	383	37	337	33	302	46	242	36	239	44	227	45	200	35		
191	29	147	20	140	25	117	24	128	30	107	17	92	18	76	11	68	14		
74	17	36	14	32	10	38	8	37	10	31	9	26	5	21	5	13	6		
7	2	12	11	11	1	3	1	5	3	2	0	1	2	0	2	2	0		
4478	115	993	68	815	64	661	65	663	47	563	68	548	53	449	63	477	59		
377	65	390	53	326	46	296	46	307	54	288	50	279	36	226	45	221	36		
225	38	191	28	188	41	184	41	152	32	145	49	107	24	107	33	98	35		
88	21	75	37	58	20	51	22	55	32	46	15	33	11	36	15	22	10		
24	7	21	14	12	6	8	9	9	4	8	4	1	7	1	1	3	6		
2194	65	699	55	563	50	478	46	459	54	447	54	404	53	380	62	387	64		
321	57	303	67	278	68	334	67	253	51	237	64	256	43	245	39	217	55		
220	66	210	48	179	44	192	46	170	51	144	41	129	31	129	42	94	43		
104	28	98	42	79	31	92	26	58	33	53	25	59	23	50	17	40	18		
34	22	38	15	22	20	19	7	15	12	13	9	16	6	12	5	4	8		
1117	41	371	36	333	39	307	43	299	41	288	53	255	60	283	60	265	47		
254	57	245	49	248	53	245	64	216	59	207	56	209	70	210	67	220	60		
193	47	227	61	176	58	176	50	184	58	140	45	142	66	149	50	124	55		
118	37	107	55	95	43	106	38	87	40	68	50	64	38	59	33	59	38		
40	29	57	31	35	30	30	26	33	12	13	12	14	20	15	6	15	14		
495	17	198	15	206	27	195	26	207	26	165	29	167	27	159	42	179	52		
210	58	158	36	170	36	171	66	174	55	185	43	183	39	173	53	175	47		
171	57	162	65	138	70	148	54	142	43	123	63	142	59	126	51	108	74		
112	60	117	61	70	61	78	44	92	51	100	52	77	51	83	36	62	46		
75	44	40	44	32	38	52	28	33	34	29	23	18	20	14	20	15	19		
204	10	100	20	123	16	95	16	107	18	101	22	113	23	103	27	117	26		
107	18	115	46	128	43	120	35	123	45	138	45	124	46	120	47	143	33		
109	38	134	49	107	52	130	48	120	56	125	66	99	55	103	69	97	61		
100	69	108	58	106	54	91	48	100	60	88	49	96	60	73	71	86	61		
68	56	60	56	73	59	42	53	61	36	41	33	37	38	29	40	28	40		
92	6	60	8	48	7	51	5	45	18	64	11	55	19	66	18	68	16		
68	13	72	20	84	20	77	22	76	30	86	32	75	32	93	42	92	41		
89	43	83	51	85	47	91	49	91	53	71	52	78	58	102	35	106	57		
92	57	79	62	85	59	88	64	84	56	98	68	79	55	70	61	87	68		
73	82	60	59	60	66	66	65	62	61	63	56	41	47	48	52	60	91		
35	1	18	1	24	3	27	3	27	7	31	9	25	10	33	8	35	8		
34	11	41	9	38	14	48	17	34	27	46	17	31	28	57	17	45	20		
60	28	47	29	54	49	66	41	72	34	66	35	46	56	57	36	81	42		
69	47	71	57	63	54	85	42	67	45	77	44	66	47	61	64	43	63		
69	73	58	63	61	69	68	75	61	47	60	55	52	78	54	77	45	113		
9	2	7	1	5	3	9	0	6	2	6	1	6	1	19	2	6	9		
18	3	13	5	25	5	15	11	9	4	14	14	13	10	22	8	36	23		
26	9	23	27	30	22	22	18	30	21	26	20	32	35	41	22	33	35		
43	35	52	43	39	35	44	35	55	27	48	50	61	44	44	45	47	67		
53	65	45	78	63	58	52	66	64	83	56	73	49	87	63	81	84	232		
1	1	0	0	0	2	0	3	3	1	1	2	0	5	1	1	3			
2	0	4	4	3	1	4	2	4	1	4	0	4	3	7	2	6	11		
6	4	6	5	6	9	7	11	13	2	11	10	12	3	25	10	10	15		
16	11	26	10	21	20	14	17	22	27	23	21	32	40	22	22	31	28		
27	31	20	32	44	55	33	53	41	53	42	66	44	64	54	84	88	200		
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	