Table A (web enhancement). Impact of the number of crossovers on the accuracy of population MAC estimates. Results are from a set of 500 replicate simulations.

	Number of crossovers				
	2	4	6	8	10
Average MAC	0.944	0.971	0.983	0.991	0.997
Average standard deviation	0.09	0.111	0.114	0.117	0.118
Smallest MAC value	0.6	0.7	0.767	0.812	0.81
Largest MAC value	1.25	1.2	1.2	1.15	1.14
Fraction of MAC estimates not within this percentage of population MAC:					
10%	0.34	0.23	0.16	0.10	0.06
15%	0.19	0.09	0.04	0.02	0.01
20%	0.10	0.03	0.01	0.00	0.00
25%	0.04	0.01	0.00	0.00	0.00

Assumptions used in these 500 replicates: population MAC = 1.0%, interindividual variability = 20% of population MAC, starting concentration = 0.5% inhaled anesthetic, incremental changes for inhaled anesthetic = 20% of starting concentration, machine error level = 5%, V-Q mismatch = 0.1%.

WEB ENHANCEMENTS

Table B (web enhancement). Impact of the increment size of concentration changes (percentage of starting concentration) on the resulting estimates of the population MAC, maximum, minimum, standard deviation, number of patients that are enrolled in a study, and the number of ambiguous responses. Results are average values of 500 replicates, values are shown for three representative starting concentrations.

	Increment size of concentration changes of inhaled anesthetic as percentage of starting concentration					
	10%			20%		
	Starting concentration			Starting concentration		
	0.5%	0.9%	1.5%	0.5%	0.9%	1.5%
MAC2	0.88	0.963	1.064	0.933	0.98	1.016
MAC4	0.918	0.976	1.041	0.955	0.986	1.008
MAC6	0.939	0.983	1.029	0.967	0.99	1.008
MAC8	0.952	0.987	1.023	0.976	0.993	1.004
MAC10	0.961	0.99	1.018	0.982	0.994	1.003
Max 2	1.125	1.26	1.5	1.3	1.35	1.35
Max4	1.1	1.238	1.35	1.2	1.35	1.35
Max6	1.125	1.155	1.3	1.167	1.17	1.25
Max8	1.094	1.148	1.256	1.15	1.193	1.2
Max10	1.085	1.134	1.23	1.13	1.206	1.2

WEB ENHANCEMENTS

Min2	0.525	0.765	0.675	0.55	0.72	0.6
Min4	0.613	0.765	0.75	0.65	0.72	0.75
Min6	0.692	0.84	0.8	0.767	0.81	0.75

Table B continued

Min8	0.725	0.844	0.863	0.788	0.81	0.75
Min10	0.75	0.819	0.87	0.81	0.828	0.78
SD2	0.07	0.07	0.106	0.091	0.115	0.136
SD4	0.083	0.092	0.133	0.11	0.138	0.167
SD6	0.086	0.096	0.139	0.112	0.144	0.183
SD8	0.087	0.099	0.14	0.114	0.148	0.187
SD10	0.088	0.101	0.139	0.116	0.149	0.188
N2	12.2	5.1	7.0	8.6	4.7	5.5
N4	18.0	10.3	11.9	13.7	9.4	9.9
N6	23.5	15.3	16.8	18.7	14.0	14.3
N8	28.9	20.4	21.6	23.7	18.7	18.7
N10	34.2	25.5	26.3	28.8	23.3	23.0
Ambig2	0.006	0.136	0.024	0.012	0.12	0.054

WEB ENHANCEMENTS

Ambig4	0.014	0.284	0.182	0.064	0.24	0.134
Ambig6	0.064	0.394	0.282	0.162	0.36	0.242
Ambig8	0.154	0.534	0.368	0.288	0.472	0.342
Ambig10	0.256	0.684	0.514	0.404	0.592	0.452

Assumptions used in these 500 replicates: population MAC = 1.0%, interindividual variability = 20% of population MAC, machine error level = 5%, V-Q mismatch = 0.01%.

MAC2, MAC4, MAC6, MAC8, MAC10 = estimated MAC for 2, 4, 6, 8, 10 crossovers; Max2, Max4, Max6, Max8, Max10 = highest estimated MAC for 2, 4, 6, 8, 10 crossovers; Min2, Min4, Min6, Min8, Min10 = lowest estimated MAC for 2, 4, 6, 8, 10 crossovers; SD2, SD4, SD6, SD8, SD10 = standard deviation for 2, 4, 6, 8, 10 crossovers; N2, N4, N6, N8, N10 = number of patients needed for 2, 4, 6, 8,10 crossovers; Ambig2, Ambig4, Ambig6, Ambig8, Ambig10 = number of observed ambiguous movement responses during an experiment (defined as effect site concentration being within 2% of the value of the individual MAC).

WEB ENHANCEMENTS

Table C (web enhancement). Impact of variability of individual MAC values on the resulting

estimates of the population MAC and the number of patients that are enrolled in a study. Except

for Max and Min, results are average values of 500 replicates, values are shown for two

representative starting concentrations.

	Interindividual Variability			
	0.1%		0.3%	
	Starting concentration		Starting concentration	
	0.5%	0.9%	0.5%	0.9%
MAC2	0.978	0.991	0.87	0.969
MAC4	0.987	0.993	0.914	0.985
MAC6	0.992	0.994	0.938	0.988
MAC8	0.995	0.996	0.953	0.992
MAC10	0.995	0.997	0.962	0.993
Max 2	1.15	1.17	1.3	1.35
Max4	1.125	1.17	1.225	1.35
Max6	1.1	1.14	1.2	1.29
Max8	1.1	1.125	1.188	1.238
Max10	1.09	1.098	1.19	1.26
Min2	0.8	0.81	0.45	0.54
Min4	0.85	0.855	0.625	0.675
Min6	0.883	0.87	0.65	0.72
Min8	0.9	0.878	0.687	0.742
Min10	0.91	0.882	0.73	0.738
SD2	0.065	0.081	0.108	0.126

WEB ENHANCEMENTS

SD4	0.075	0.098	0.133	0.154
SD6	0.078	0.105	0.14	0.165
SD8	0.079	0.108	0.143	0.172

Table C. continued

SD10	0.08	0.109	0.141	0.175
N2	8.8	4.4	8.1	4.8
N4	13.5	8.7	13.7	9.7
N6	18.0	13.1	19.0	14.5
N8	22.6	17.5	24.3	19.5
N10	27.3	21.8	29.4	24.4
Ambig2	0.000	0.174	0.022	0.094
Ambig4	0.022	0.350	0.062	0.176
Ambig6	0.240	0.500	0.122	0.302
Ambig8	0.404	0.666	0.210	0.400
Ambig10	0.630	0.852	0.304	0.500

Assumptions used in these 500 replicates: population MAC = 1.0%, incremental changes for inhaled anesthetic = 20% of starting concentration, machine error level = 5%, V-Q mismatch = 0.1%.

MAC2, MAC4, MAC6, MAC8, MAC10 = estimated MAC for 2, 4, 6, 8,10 crossovers; Max2, Max4, Max6, Max8, Max10 = highest estimated MAC for 2, 4, 6, 8,10 crossovers; Min2, Min4, Min6, Min8, Min10 = lowest estimated MAC for 2, 4, 6, 8,10 crossovers; SD2, SD4, SD6, SD8, SD10 = standard deviation for 2, 4, 6, 8,10 crossovers; N2, N4, N6, N8, N10 = number of patients needed for 2, 4, 6, 8,10 crossovers; Ambig2, Ambig4, Ambig6, Ambig8, Ambig10 =

WEB ENHANCEMENTS

number of observed ambiguous movement responses during an experiment (defined as effect site

concentration being within 2% of the value of the individual MAC).

WEB ENHANCEMENTS