

## Supplementary Material

### S.1.1. Sequence estimation for the simultaneous event-based model

Biomarker	Perturbed sequence
1	{{1}, {2}, {1,3}}
	{{2, 1}, {3}, {4}}
	{{2}, {3}, {4, 1}}
	{{2}, {3}, {4}, {1}}
2	{{1, 3, 2}, {4}}
	{{1, 3}, {2}, {4}}
	{{1, 3}, {4, 2}}
	{{1, 3}, {4}, {2}}
3	{{3}, {2}, {1}, {4}}
	{{2}, {3}, {1}, {4}}
	{{2}, {1}, {3}, {4}}
	{{2}, {1}, {4}, {3}}
4	{{4}, {2}, {1, 3}}
	{{2, 4}, {1, 3}}
	{{2}, {4}, {1, 3}}
	{{2}, {1, 3, 4}}

**Table S1.** Perturbations of the sequence  $(\{2\}, \{1, 3\}, \{4\})$ . For each perturbation, a biomarker is chosen at random (left-hand column) and replaced at any of the remaining valid positions, resulting in a perturbed sequence (right-hand column). These perturbations are used to propose sequences during greedy ascent and MCMC-based sequence estimation.