A clone deployment and selective harvest model and algorithms for seed orchards and clonal mixtures where candidates are related have been developed and applied. Candidates have known breeding values (different characters can be weighted) and relatedness (coancestry). The algorithms consider and are able to optimize average breeding value; loss by inbreeding depression and gene diversity (status number). Typically - and surprisingly - loss of gene diversity was a more important consideration than inbreeding depression loss. Some related clones in advanced generation seed orchards are often advantageous. The algorithms permit optimization of selective harvest in seed orchards where the clone representation is heterogeneous. Before applying the algorithms it is recommended to short-list candidates. If the desired status number is considerable lower than that of candidates, linear deployment of a short-list is near enough optimal and further optimization not needed. For establishing a Norway spruce seed orchard in Sweden, both growth and wood density could be considerably improved by the algorithms. Based on volume in a black spruce clonal trial series in Canada, deployment by those algorithms raised gain 7-25% (different scenarios) compared to truncation.