**JOINMAP 2.0 DEALS WITH ALL TYPES OF PLANT MAPPING POPULATIONS.**

Piet Stam, Department of Plant Breeding, Wageningen Agricultural Univer- sity, Wageningen, The Netherlands.

The JoinMap genetic mapping package [(P. Stam, The Plant Journal 3, 739 (1993)] has been upgraded (to JM 2.0) so as to cover virtually all types of plant mapping populations and marker types and to increase flexibility. Mapping populations now include F2, backcross, RI lines of any generation, doubled haploids from Fl and F2, haploid offspring of a single individual, any generation of an intercross following an F2, as well as crossbreeders. In the latter case the mapping population is the offspring of a mating between a single pair of heterozygous parents. JM 2.0 can deal with all types of segregation that may occur in crossbreeders, i.e. multiple allelism as well as dominance in case of two segregating alleles. The package has been reshaped so as to increase flexibility; it offers several options for data inspection. The main steps of map construction have been put in separate modules, i.e. (a) calculation of pairwise recombination estimates (together with LOD scores), (b) assignment of markers to linkage groups, stepping through LOD thresholds, and (c) construction of a linkage map. In the last phase (c) z map is built sequentially, by adding to the map one marker gene at a time, Markers that, at the first attempt of placement would cause a (user-set)decrease in overall fit, are put aside. This generally yields a "reliable hard core" map, which in a second round is completed with the markers that caused "trouble" when tried to map in the first round. Several features of the package (data format, setting parameter values and options, platforms) are briefly discussed.