Biomathematics and Statistics Scotland

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Biomathematics & Statistics Scotland (BioSS) is devoted to the application of statistics and mathematics in the biological sciences. Its core remit is to support the SEERAD programme of biological research, which is carried out within the SABRIs, SAC and RBGE. This is achieved through a dispersed group of statisticians, mathematics and computing experts based at BioSS centres in Edinburgh, Dundee, Aberdeen and Ayr. Over the last year, much effort has been spent on planning new programmes to meet our strategic priorities in bioinformatics and statistical genomics, systems modelling and risk. Work in bioinformatics was enhanced by an alliance with the Scottish Centre for Genome Technology and Informatics, initially focused on analysis of microarrays. Our programme on risk analysis is built on developing probabilistic methods for assessing food safety and covers several potential and known hazards, including mixtures of pesticide residues, zoonotic pathogens such as E. coli O157 and salmonella, GM crops and poor diet. New competitive core funding will allow expansion of our programmes in bioinformatics and systems modelling in 2001/2.

At SCRI, the development and application of statistical methods that recognize the importance of scale in ecological processes is being pursued in collaboration with staff from the Plants, Soils and Environment Division. These ideas are being applied in a number of important areas including the quantification of functional biodiversity in vegetation systems and the interaction between plant and microbial communities.

Work on the genetics of tetraploid species has progressed with the development of methodology for QTL mapping. This is an extension of the interval mapping method used for mapping QTLs in diploid species, but requires a novel step, namely the reconstruction of the genotypes along an entire chromosome for each offspring, and the location of crossovers. The methodology for linkage analysis and QTL mapping is currently being applied to 228 potato lines scored for more than 800 molecular markers and 40 traits (disease resistance, yield, processing quality, *etc.*), in collaboration with scientists at SCRI. In sequence analysis, an approximate Bayesian hypothesis test for discriminating between alternative DNA mosaic structures has been developed. Our work on Hidden Markov Models (HMMs) for detecting recombination is being expanded. The earlier approach estimated all the parameters of the model in a maximum likelihood sense with the EM algorithm. We are currently exploring a Bayesian approach, where parameters are sampled from the posterior distribution with Gibbs sampling and the Metropolis-Hastings algorithm.

BioSS has also contributed to two decision support packages being developed at SCRI. The Management Advisory Package for Potatoes (mappTM) enables growers to visualize the effect on profit margin of various management decisions relating to factors such as planting date, seed rate and harvest date. The Potato Cyst Nematode (PCN) package demonstrates the effectiveness of various control strategies on both yield and post-harvest PCN populations.