# In this issue

Sulphur isotopes in Himalayan rivers

Dissolved sulphate in river water is an important constituent of natural waters, the source of which could be from rock/mineral dissolution, oxidation of sulphide minerals, rainfall, groundwater input and pollution. The multi-sources of dissolved sulphate can be distinguished by their isotopic signatures. Being a major pollutant, dissolved sulpahte causes acidity of water systems and keeps trace elements (pollutants) in dissolution. Earlier, many publications on the Himalayan rivers showed high dissolved sulphate contents, but the sources were not identified. Chakrapani and Veizer (**page 500**) collected 30 water samples from the Alakananda–Bhagirathi rivers in the Himalayas and analysed them for dissolved sulphate concentrations and $\delta^{34}S$. Dissolved sulphate concentrations and $\delta^{34}S$ compositions show variations indicating multiple sources of dissolved sulphate in the waters. In the absence of significant point source of sulphate, the $\delta^{34}S$ values indicate dissolved sulphate to have been derived from dissolution of gypsum/anhydrite and oxidation of sulphides associated as disseminations with sedimentary rocks, such as shales and limestones.

Fault classification with incomplete measured data

Marwala and Chakraverty (**page 542**) propose a method to classify faults in
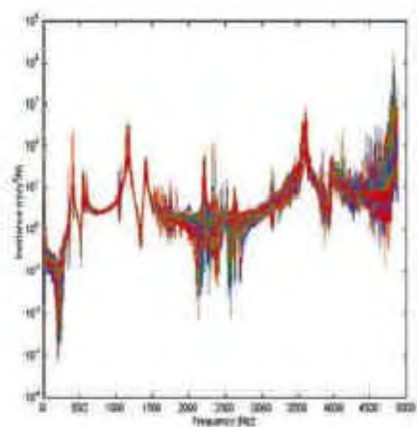
mechanical systems with incomplete data. The method uses autoassociative neural networks and genetic algorithms. The autoassociative neural networks are trained to recall the input data through a highly nonlinear autoassociative neural network mapping function. From the trained autoassociative neural network an error function with missing inputs as unknown variables is constructed. Genetic algorithm that is implemented through mutation, crossover and reproduction is used to solve for the missing input variables. The proposed method is tested on a fault classification problem in a population of cylindrical shells that are experimentally tested using vibration and modal analysis. It is observed that the proposed method is able to estimate single-missing-entries to the accuracy of 93% and two-missing-entries to the accuracy of 91%. When the estimated values were then used in the classification of faults in a population of cylindrical shells, fault classification accuracy of 94% was observed for single-missing-entry cases and 91% for two-missing-entry cases while the full database set is able to give classification accuracy of 96%.

Residue composition in proteins

Does the composition of amino acids in a non-redundant database of protein structures have a considerable dependence on any of the physicochemical properties of residues? Saha and Chakrabarti (**page 558**) find that there is a good inverse correlation with the residue size, given by the solvent accessible surface area of the residue in a model tripeptide. While many factors contribute to the occurrence of a given residue or its type at a particular position in a protein, the dependence of the overall distribution of amino acids on the size is also noticeable when applied to the protein repertoire of E. coli; there are plausible chemical reasons for the two residues, leucine and cysteine, showing the maximum deviation from the linear relationship. Such a relation does not exist if one calculates the composition taking into account the number of atoms each residue contributes to the

total count of protein atoms in the database. Although the chemical nature should be the main factor in determining the propensities of any two residues to interact with each other, the effect of size cannot be excluded when the residue-based composition is used in the calculation of the propensity values; however, size-normalized propensity values are obtained on using atom-based composition.

Genetic diversity study of Indian isolates of *Cercospora canescens*

Cercospora canescens (Ellis & Martin) is the principal pathogen causing leaf spotting and defoliation in several legumes including mungbean (*Vigna radiata*) and black gram (*Vigna mungo*), especially in humid tropical areas of Southeast Asia. A genetic diversity study was conducted by Joshi et al. (**page 564**) on C. canescens isolates obtained from different geographical locations. The polymorphism at the molecular level was studied by random amplified polymorphic DNA (RAPD) marker technique and variation in the internal transcribed spacer (ITS) region of
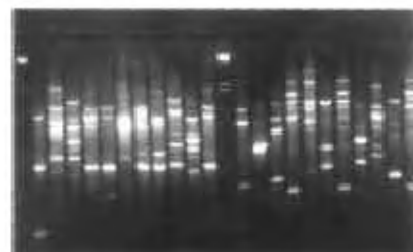
ribosomal DNA (rDNA). RAPD markers were found to be well suited for determining the genetic diversity and differentiation present in C. canescens isolates. Two important conclusions can be drawn from this study: Presence of considerable genetic variability among the isolates from the same host; and high level of similarity among isolates of different hosts from the same geographical location. These findings emphasize on the importance of considering the pathogen populations prevalent in a particular area in any resistance-breeding programme.