The structural analyses of microorganisms in soil present a far more complex problem than their functional analyses (CO₂ determination, ATP measurement etc.). Microbial communities of soils are extremely diverse, and it is assumed that with conventional microbiological cultivation techniques only about 1% of the indigenous species are recovered (Torsvik et al. 1990). Therefore, methods that require neither growth nor removal of cells from the soil matrix are needed. Microbial diversity and community structure may be best estimated by RNA analysis (Ward et al. 1990) or DNA extraction (Torsvik et al. 1990). Besides these techniques, the extraction and analysis of the fatty acids derived from phospholipids (PLFAs) and lipopolysaccharides (LPS; Vestal and White 1989; Tunlid and White 1992) are a promising approach to classify the structure of the microbial communities in soils. The measurement of the content of the phospholipids has also been used to estimate microbial biomass in sediments and soils (Smith et al. 1986; Baath et al. 1992; Korner and Laczko 1992; Zelles et al. 1992; Frostegard et al. 1993; Hill et al. 1993).

Phospholipids are found in membranes of all living cells, but not in the storage products of microorganisms (Kates 1964). Furthermore, membranes play an important role in the physiological conditions of microorganisms (Singer and Nicholson 1972). Phospholipids are actively metabolized during the growth of bacterial monocultures (White and Tucker 1969). A study of the degradation of labelled phosphatidylcholine in soils suggested a rapid turnover of microbial phospholipids (Tollefson and McKercher 1983).

The composition of total microbial fatty acids is of high taxonomic importance (Harwood and Russell 1984; Ratledge and Wilkinson 1988). Its quantitative analysis can provide taxonomic information at the species (O’Donnell et al. 1985) and at subspecies level (Mukwaya and Welch 1989). A classification of soil microorganisms can be achieved by subdividing the fatty acids according to their
chain structure, degree of saturation and substitution (Zelles et al. 1992; Zelles and Bai 1993). The phylogenetic classification of bacteria according to their “natural” relationship (Balows et al. 1992) supports the assumption that the pathways of fatty acid synthesis in taxonomically related groups are similar. Thus, the fatty acid profiles of unculturable microorganisms can be based on the fatty acid profile of the cultivable relatives. There is a great amount of data concerning the fatty acids of different taxonomic groups that have been obtained from microorganisms cultivated under controlled laboratory conditions (Harwood and Russell 1984; Ratledge and Wilkinson 1988).

A rough grouping can be made among prokaryotes on the basis of lipid composition (Lechevalier and Lechevalier 1988):

a) Archaebacteria whose alkyl chains are ether-linked to glycerol (Langworthy et al. 1982)
b) Anaerobic bacteria, containing sphingolipids and/or plasmalogs which are largely absent from aerobic bacteria
c) Cyanobacteria (and also eukaryotes) whose lipids contain polyunsaturated fatty acids
d) Gram-negative bacteria whose lipids contain abundant hydroxylated fatty acids
e) Gram-positive bacteria whose lipids contain large amounts of branched fatty acids (O’Leary and Wilkinson 1988; Kaneda 1991)

By using the above-listed differences, populations in a microbial community can be identified by specific “signature” PLFAs. For example, Gram-positive bacteria characteristically contain odd-chain methyl-branched (e.g. iso- and anteiso-branched) fatty acids (O’Leary and Wilkinson 1988; Kaneda 1991). Many actinomycetes contain methyl-branched tuberculostearic acid (10Me18:0; Kroppenstedt 1985). The Bacillus species mainly contain monounsaturated fatty acids with the unsaturation on Δ-5 or Δ-10 (Harwood and Russell 1984), and Thiobacillus species contain methoxy, cyclopropyl and α-hydroxy-cyclopropyl fatty acids as indicators (Kerger et al. 1986).

The unique outer membrane of Gram-negative cells is mainly composed of LPS polymers consisting of lipid A, a core polysaccharide, and an O-specific side chain (Wilkinson 1988). In general, lipid A consists of a β 1,6-linked D-glucosamine