We develop a flexible model for the analysis and clustering of complete or sparse longitudinal data. The model combines functional principal component analysis and model-based clustering. The functional modelling is based on splines. The main data groups are modelled as arising from clusters in the space of spline coefficients (the factors). The clusters are modelled by a mixture of Student's t-distributions whose degrees of freedom are unknown. The model is embedded into a Bayesian framework. The MAP estimators are found with the EM algorithm. Our main applications are to gene expression and clinical data.