**POURIA RAMAZI**,
*Machine-learning methods for modeling biological processes*

Although traditional models used to predict biological processes from underlying covariates have a record of success, they also suffer from limitations: typically, (1) they cannot handle highly correlated covariates, (2) they cannot make predictions when one or more covariates are missing, and (3) they do not provide a "primary" set of covariates, which are sufficient to make accurate predictions, and specify which other "secondary" covariates can help to make an educated prediction when the values of some primary covariates are missing. I will show how Bayesian Belief Networks (BBN) provide a very useful structure for analyzing factors governing biological processes, and this approach overcomes the typical limitations posed by traditional models. Things you will learn in the minicourse are: * How to preprocess a dataset for the use of BBN's, including discretization of continuous variables, * How to properly partition the dataset into train and test, * How to choose the score function, e.g., BIC, AIC, AUC, for evaluation, * How to learn, fully from data and without any human expert interference, a BBN that scores highest on the training dataset (using the bnstruct package in R), * How to construct other types of BBN's, such as Naive Bayes (using the bnlearn package in R), * How to decide on the 'best BBN', * How to properly interpret a BBN by its conditional probability tables (using the bnlearn package in R),