Assessing the effect of miRNAs on protein expression

- Oslo2 cohort (n = 283 tumors)
- Expression of 421 miRNAs
- Expression of 105 matched mRNAs and proteins

**Univariate modeling**
Modeling the effect of individual miRNAs on protein expression

\[ \log P = \alpha + \beta \log M_k + \gamma \log E + \epsilon \]

**Multivariate modeling**
Modeling the joint effect of several miRNAs on protein expression

\[ \log P = \alpha + \beta_1 \log M_1 + \cdots + \beta_{421} \log M_{421} + \gamma \log E + \epsilon \]

- Interactome map representing all direct and indirect associations between the expression of miRNA and proteins
- Cell line functional assessment validating associations between miRNAs and proteins
- Predicted patient-specific effect of all miRNAs combined on protein expression
- Potentially direct miRNA-mRNA target interactions using *in silico* predictions

Validation on two independent breast cancer data sets
- 348 miRNAs and 34 proteins overlapping
- Comparison of estimated effects of miRNA on protein
- Predicted vs. measured protein