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

Predicted patient-specific effect of
all miRNAs combined on protein
expression

Cell line functional
assessment validating
associations between
miRNAs and proteins

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