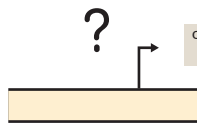


1. Design Reporters

unknown regulatory sites



obtain sequence
from database

ACTGGAATT...

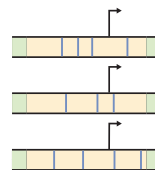


computationally design
promoter variants

GCTGGTATT...
ACGGGAATA...
ACTTCAACT...

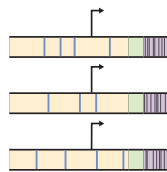
add primer pairs

order oligo pool



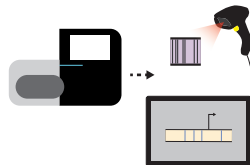
2. Library Cloning

add random barcode

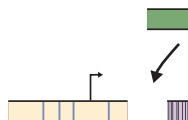


sequencing

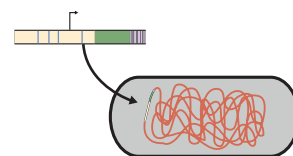
barcode mapping



add reporter gene

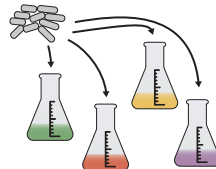


integrate reporters into genome

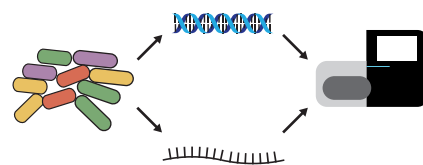


3. Growth and Sequencing

grow library in
various growth conditions



targeted sequencing on
gDNA and RNA



4. Identify Binding Sites

compute mutual information

low mutual information

ATAG

high mutual information

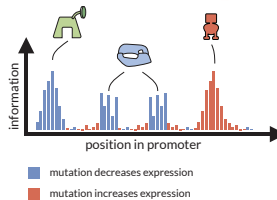
ATAG

ATTG

ACAG

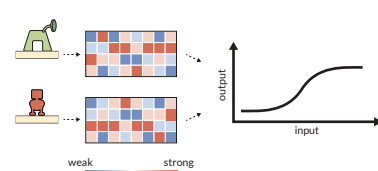
obtain information
footprint

identify binding sites



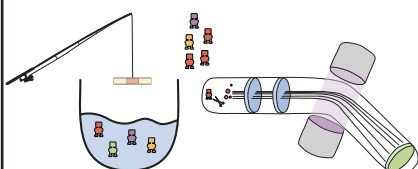
compute energy
matrices

fit thermodynamic models
for input/output functions

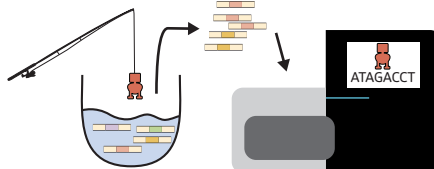


5. Identify Transcription Factors

DNA chromatography &
mass spectrometry



in vitro binding assay



knockout strains

