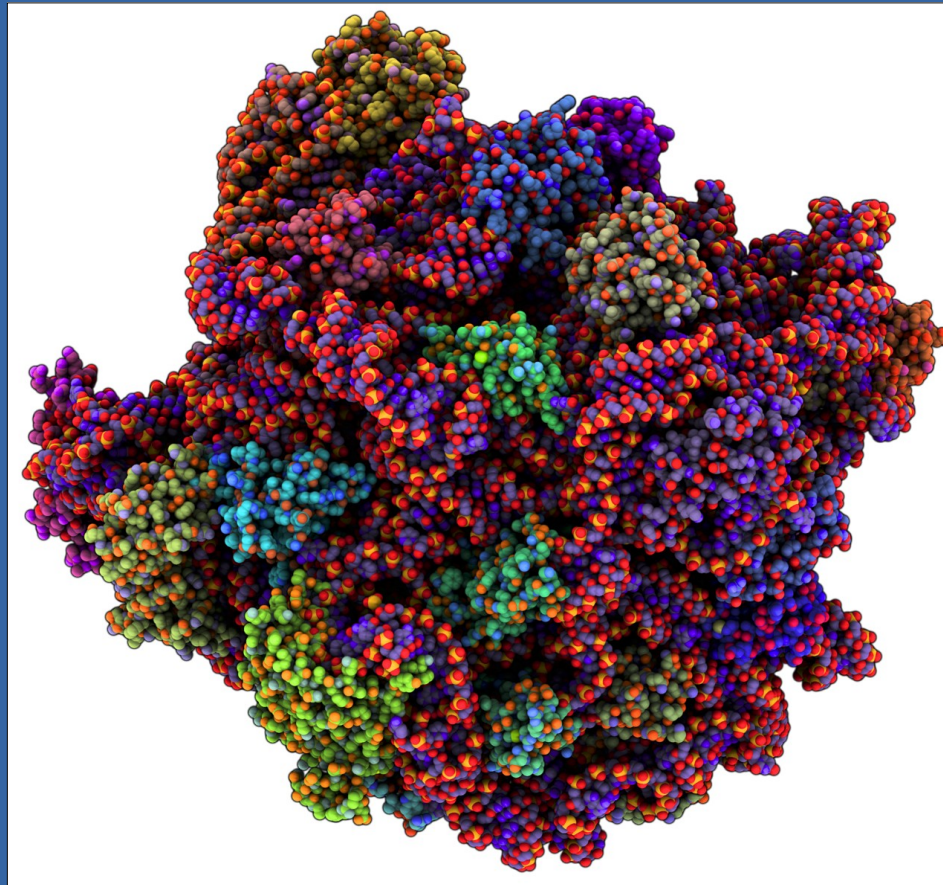


Background



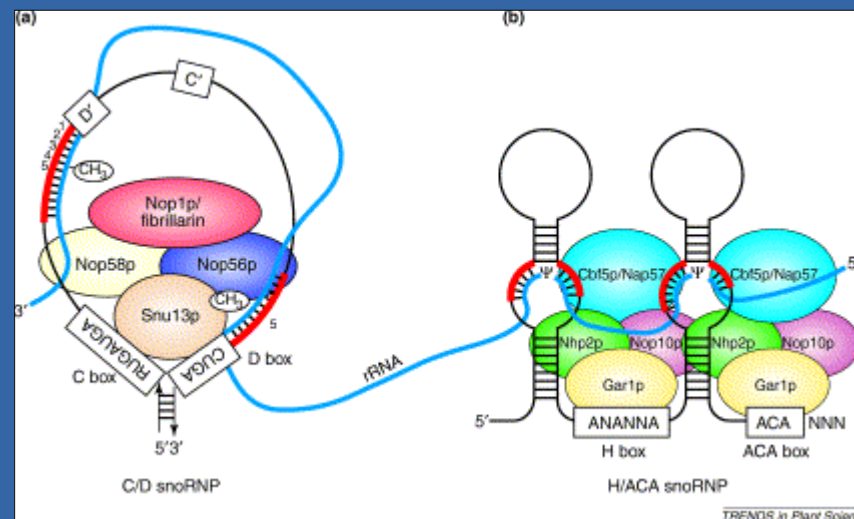
Background



Prader-Willi Syndrome

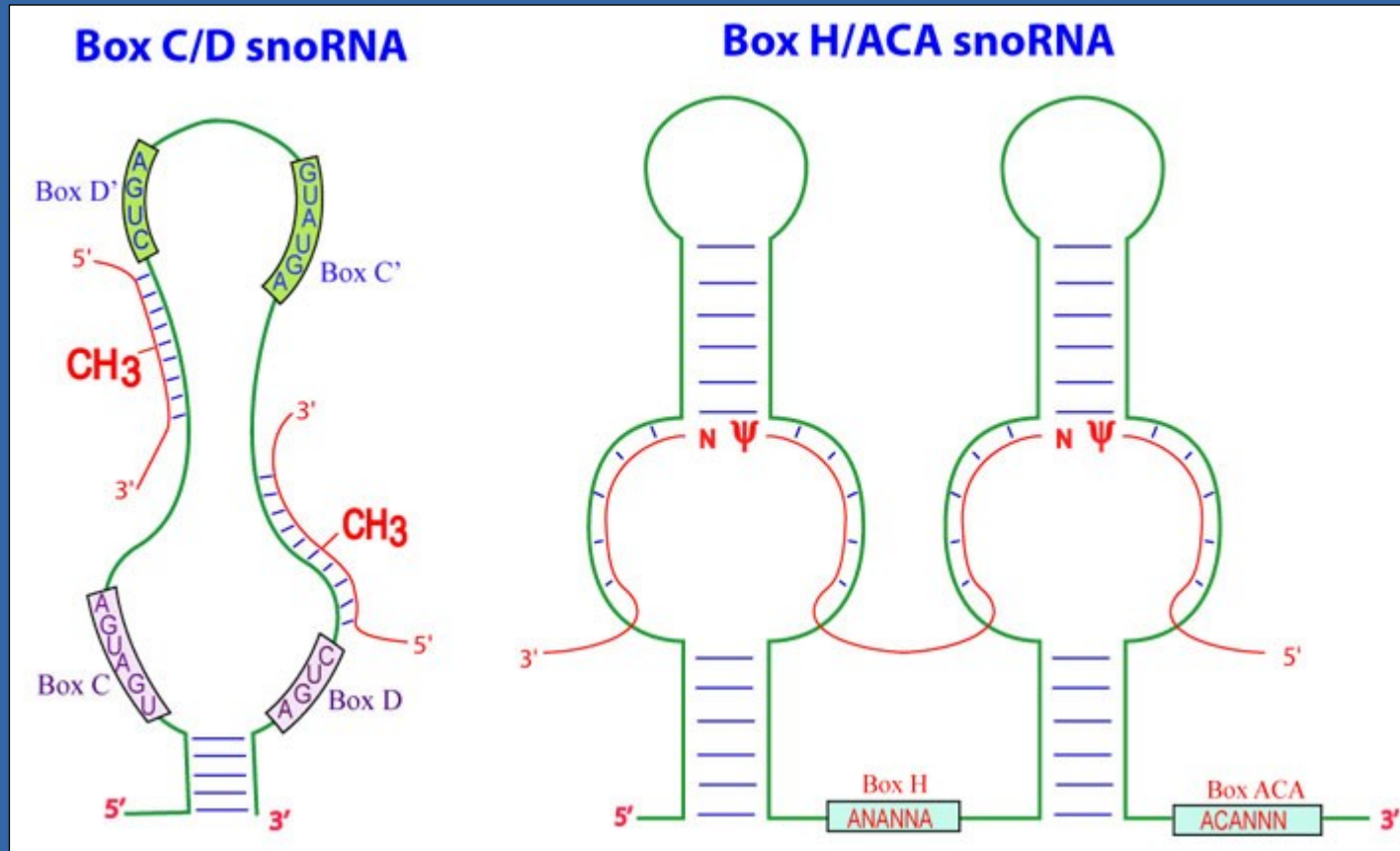
Skryabin BV et al 2007

Background



John W.S Brown et al 2002

Background



Cbox: RUGAUGA
Dbox: CUGA

Hbox: ANANNA
Tail: ACA

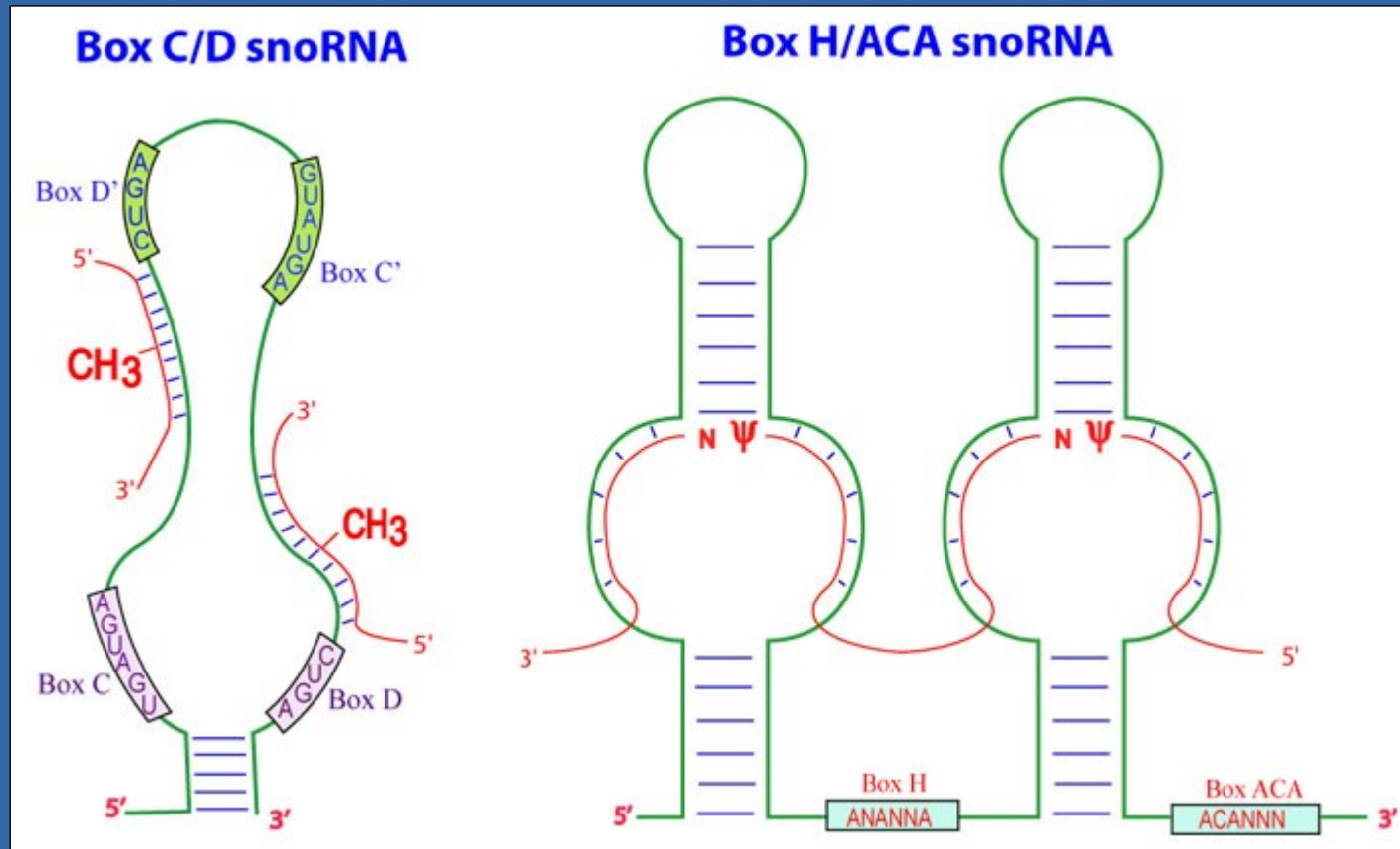
Source: <http://biochem.ncsu.edu>

Folding HACA Motif Example

[illegible]

VS

Background



Cbox: RUGAUGA
Dbox: CUGA

Hbox: ANANNA
Tail: ACA

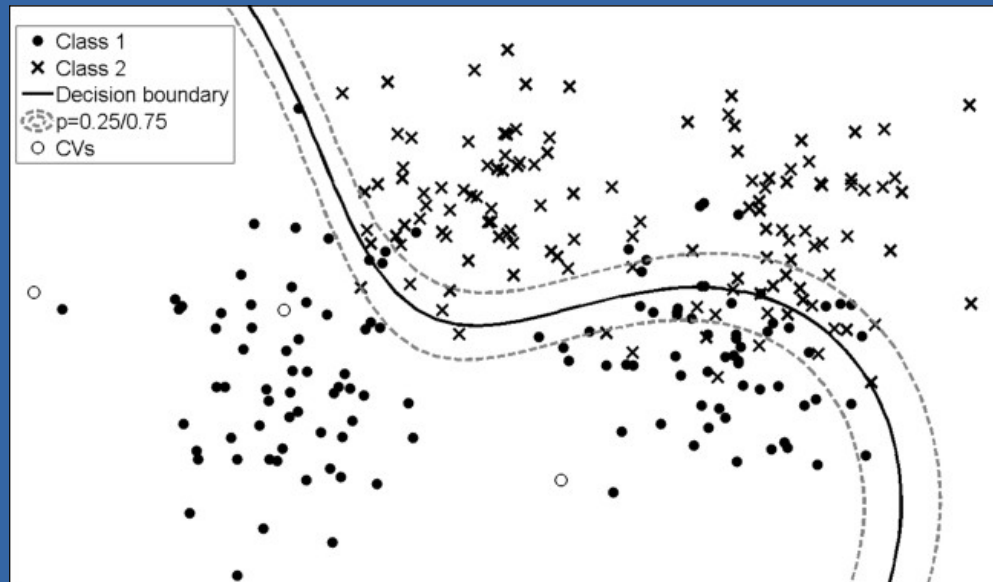
Source: <http://biochem.ncsu.edu>

1D Motifs as a Feature

Hbox	+	-
AGAGAA	76	27
AGAGCA	65	25
AAAGCA	65	21
AGAGGA	63	28
AGAGUA	61	17
AUAGAA	61	17
ACAGCA	58	24
ACAGAA	53	28
AGAUUA	51	28

Cbox	+	-
AUGAUGA	366	10
GUGAUGA	238	37
CUGAUGA	92	24
UUGAUGA	84	28
CUGAAGA	70	23
AUGAUGU	57	7
CUGAUGC	57	12
AUGAAGA	45	10
AUGAUGG	43	19

Methods



Kernel Methods

- SVM
- CRUM

Objectives

- Crossfold validation of current snoRNA CRUM
- Add folding data as a feature for crum
- Rewrite crum training program
- Compare crum-snoRNA classifier with existing methods
- Create web interface for easy DNA/RNA feature selection so users can generate their own models

Questions?



The secret of all victory lies in the organization of the non-obvious.

-Marcus Aurelius