

pH-modulated Watson-Crick duplex - quadruplex equilibria of guanine-rich and cytosine-rich DNA sequences upstream of the *c-kit* transcription initiation site

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Outline

- Introduction
 - G-quadruplex structures at the *c-kit* promoter site
 - The cytosine-rich complementary strand
- Dealing with spectroscopic multivariate data
- Results
 - Solution equilibria of the guanine-rich region
 - Acid-base properties
 - Thermal stability
 - Solution equilibria of the cytosine-rich region
 - Acid-base properties
 - Thermal stability
 - Competition Watson-Crick duplex – secondary structures

G-quadruplex structures at the *c-kit* oncogene

The *c-kit* gene encodes a receptor tyrosine kinase involved in cell proliferation

c-kit activity is elevated in gastrointestinal stromal tumors, and its therapeutic inhibition by small molecules such as imatinib, is clinically validated

Two G-quadruplex-forming regions near the transcription initiation site:

5'-AGG GAG GGC GCT GGG AGG AGG G-3', 87 nucleotides upstream of the transcription start site

It has been deeply studied and its structure resolved [Todd, 2007; Phan, 2005; Rankin, 2005]

5'-CGG GCG GGC GCG AGG GAG GGG-3', 140 nucleotides upstream of the transcription activation site

Fernando et al. *Biochem.* **2006**, 45, 7854-7860:
predominant parallel G-quadruplex structure

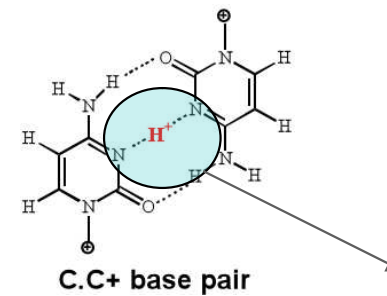
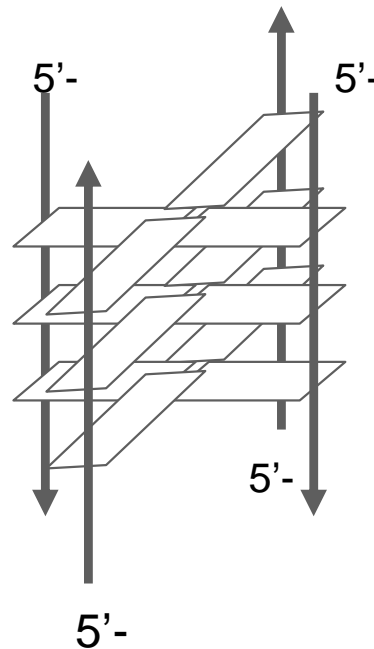
The cytosine-rich complementary strand

The sequence 5'-CGG GCG GGC GCG AGG GAG GGG-3' has shown to form a G-quadruplex...

... however, this sequence is not isolated *in vivo*, and the **complementary C-rich strand** is also present:

ckitC1 5'-CCC CTC CCT CGC GCC CGC CCG-3'

C-rich strands can form stable structures known as *i*-motifs:



Protonation at N3 is required!

Objective

We will study the competition equilibria between these two sequences:

ckitG1	5'-CGG GCG GGC GCG AGG GAG GGG-3'
ckitC1	5'-CCC CTC CCT CGC GCC CGC CCG-3'

duplex? formation of G-quadruplex and i-motif? a mixture?

“Solution equilibria”:

- how does pH affect to the structures formed by these sequences?
- how do these structures behave in front of a temperature increase?
- can we quantify each species or conformation in a mixture?

Tools:

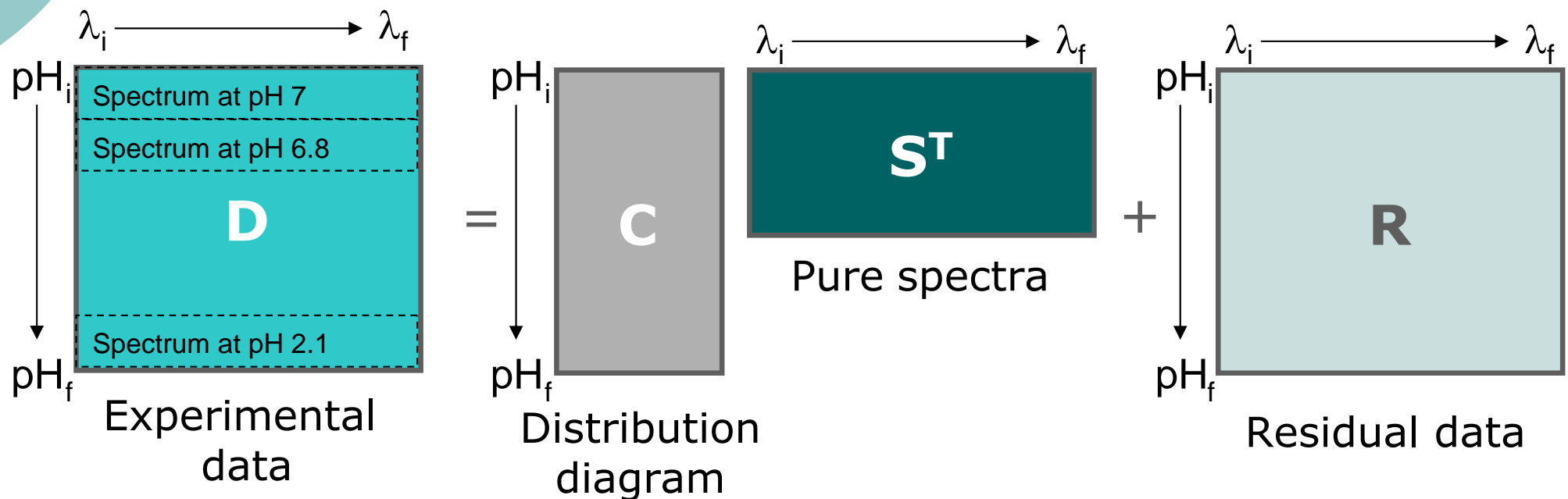
- experimental procedures: pH titrations, melting experiments, mole-ratio studies
- spectroscopic techniques: CD and molecular absorption
- multivariate data analysis methods

Multivariate data analysis: theory

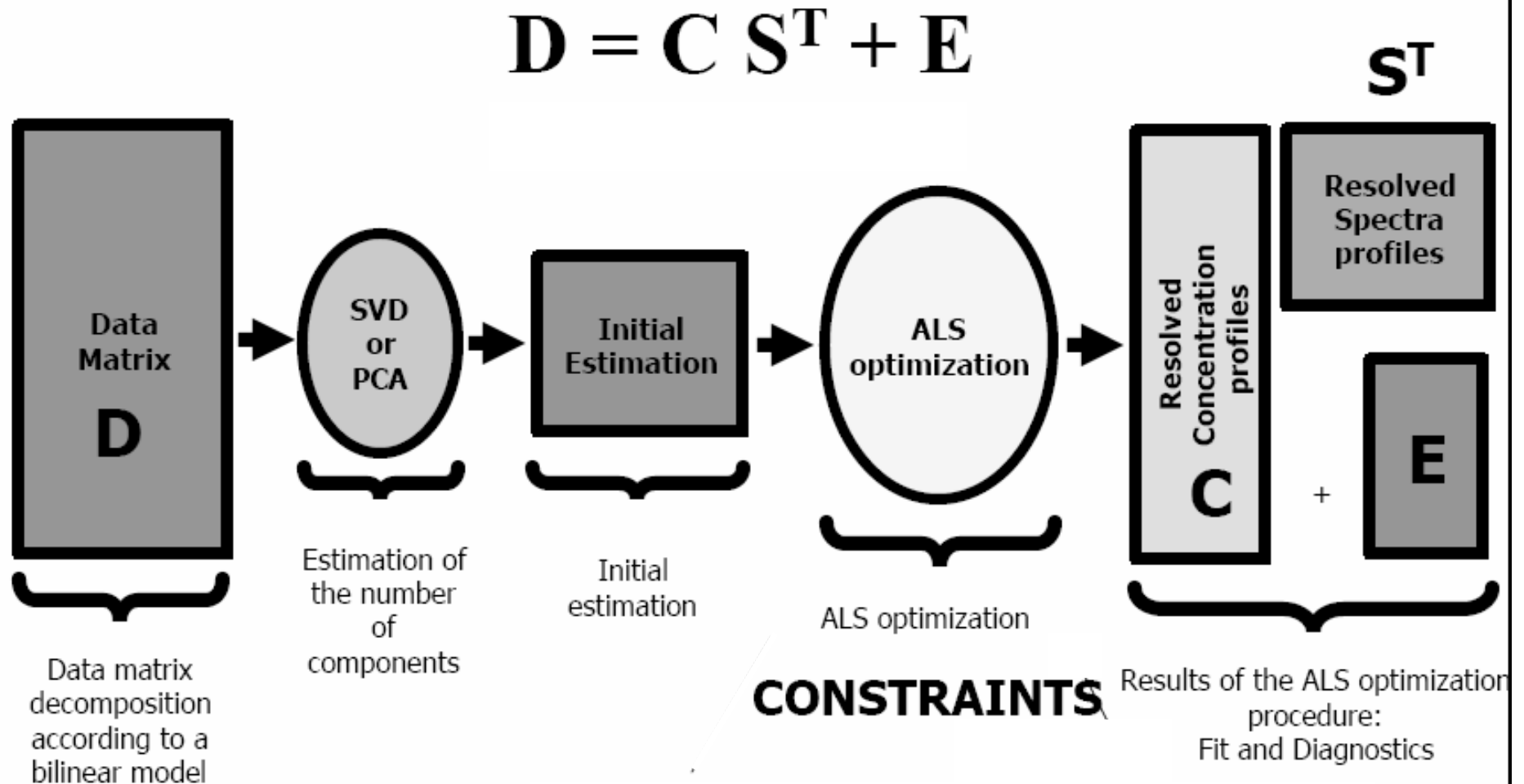
The well-known Beer-Lambert law for a single wavelength... $A_\lambda = c \varepsilon_\lambda$

... is now applied to the whole spectrum: $D = CS^T + R$

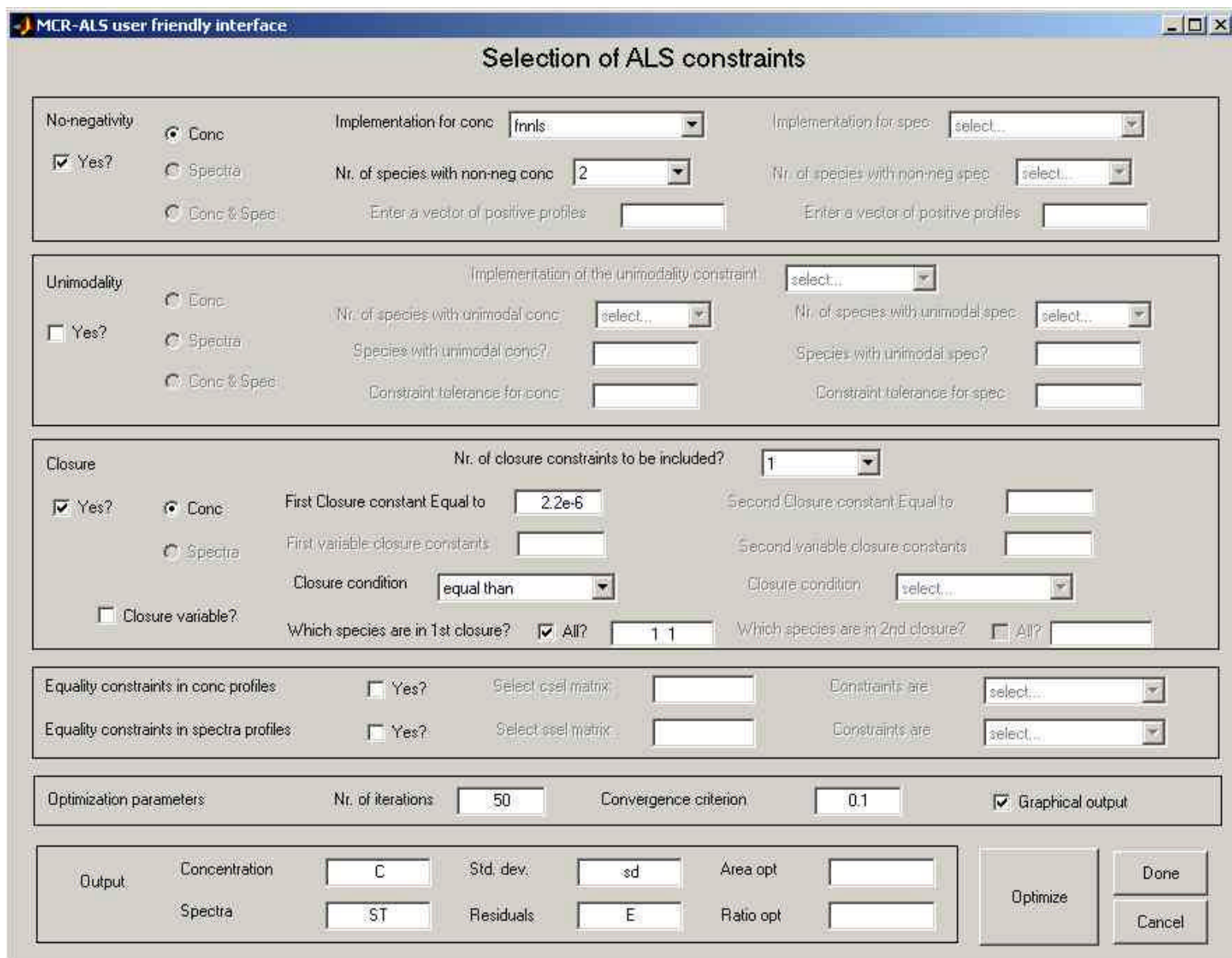
In a graphical form:



Multivariate data analysis: theory



MCR-ALS in practice (1)



MCR-ALS user friendly interface

Selection of ALS constraints

No-negativity

Yes? No?

Conc Spectra Conc & Spec

Implementation for conc: Implementation for spec:

Nr. of species with non-neg conc: Nr. of species with non-neg spec:

Enter a vector of positive profiles: Enter a vector of positive profiles:

Unimodality

Yes? No?

Conc Spectra Conc & Spec

Implementation of the unimodality constraint:

Nr. of species with unimodal conc: Nr. of species with unimodal spec:

Species with unimodal conc?: Species with unimodal spec?:

Constraint tolerance for conc: Constraint tolerance for spec:

Closure

Yes? No?

Conc Spectra

Nr. of closure constraints to be included?:

First Closure constant Equal to: Second Closure constant Equal to:

First variable closure constants: Second variable closure constants:

Closure condition: Closure condition:

Closure variable?

Which species are in 1st closure? All? Which species are in 2nd closure? All?

Equality constraints in conc profiles Yes? No?

Select csel matrix: Constraints are:

Equality constraints in spectra profiles Yes? No?

Select csel matrix: Constraints are:

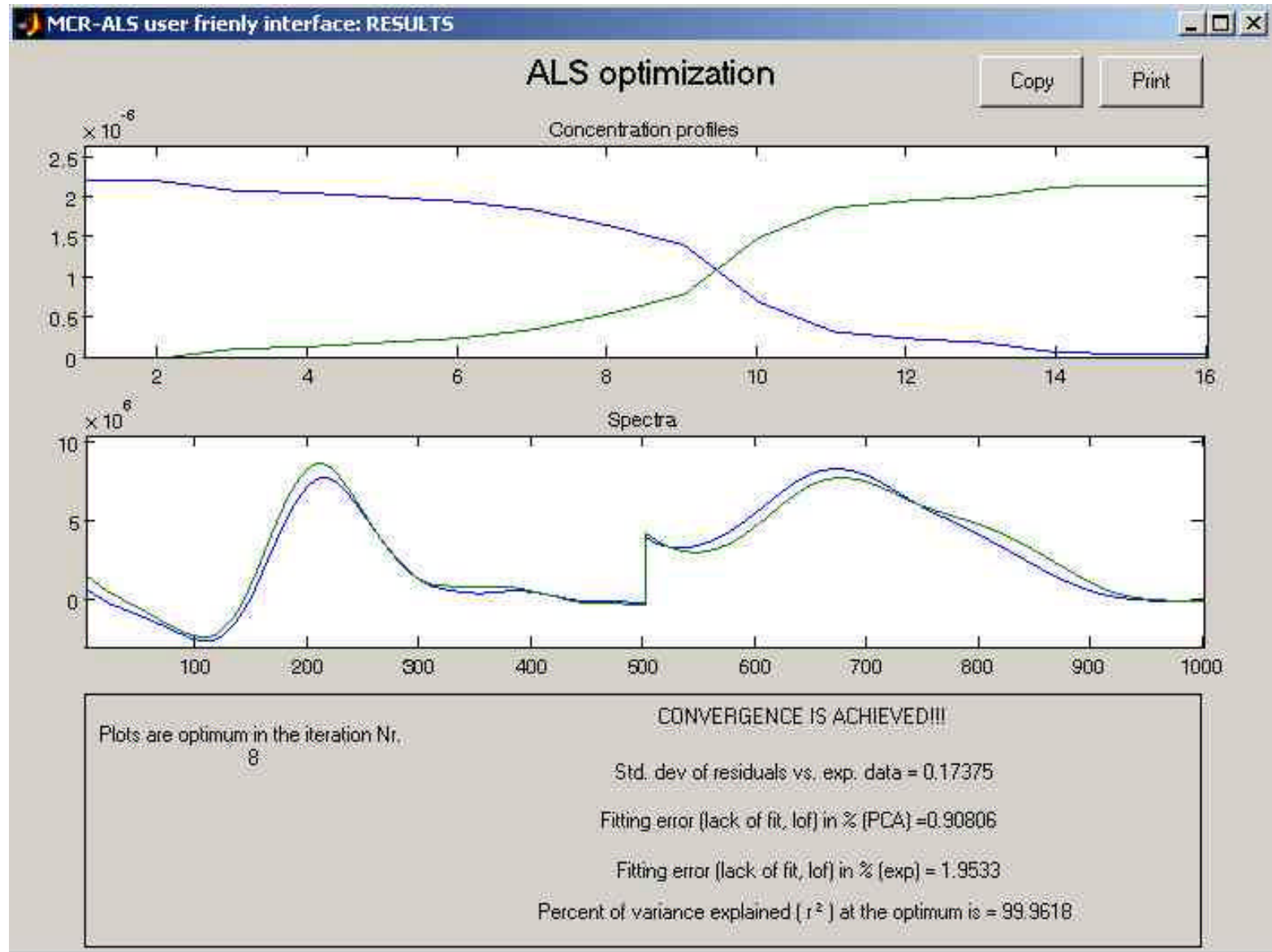
Optimization parameters

Nr. of iterations: Convergence criterion: Graphical output

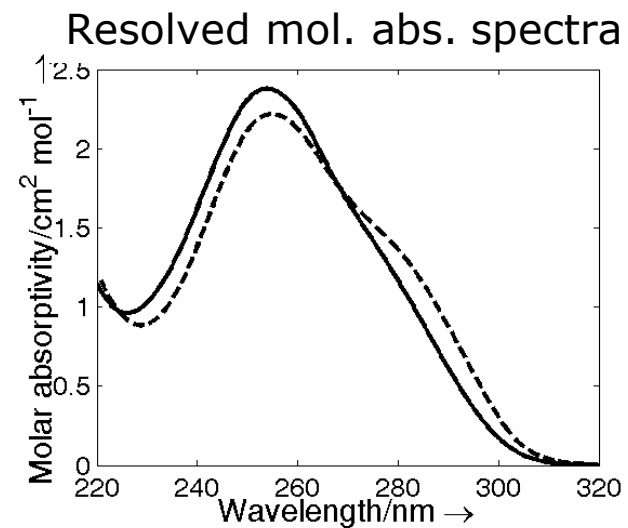
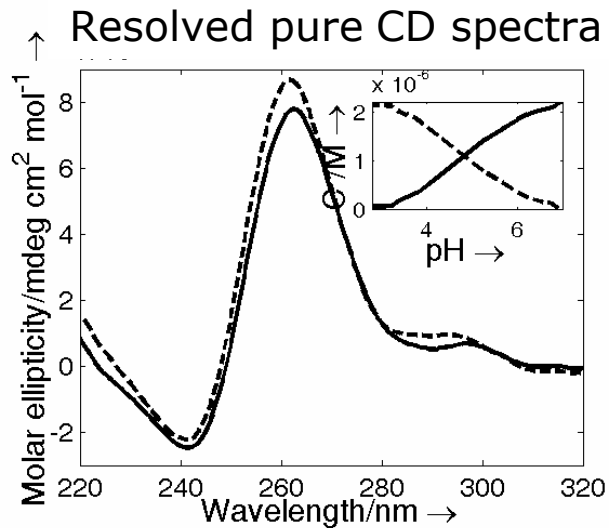
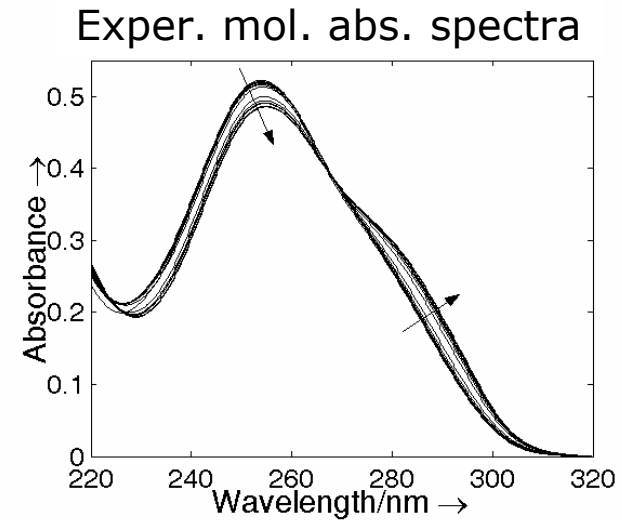
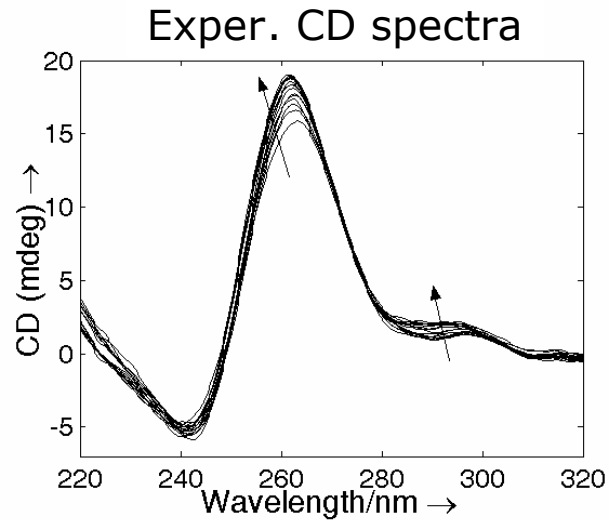
Output

Concentration	<input type="text" value="C"/>	Std. dev.	<input type="text" value="sd"/>	Area opt	<input type="text"/>
Spectra	<input type="text" value="ST"/>	Residuals	<input type="text" value="E"/>	Ratio opt	<input type="text"/>

MCR-ALS in practice (2)

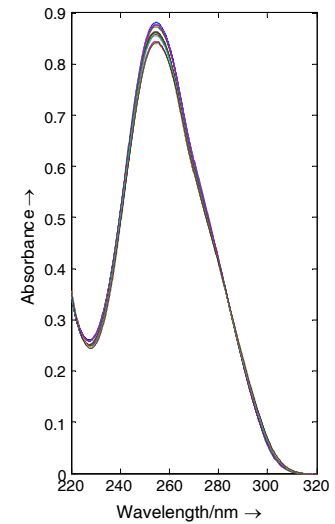
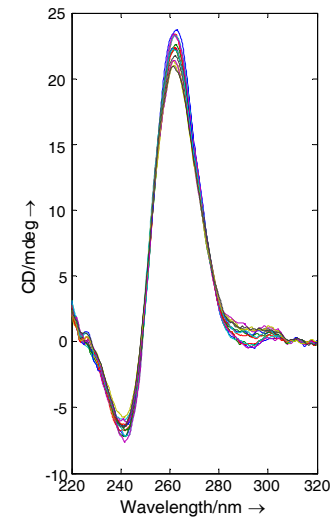
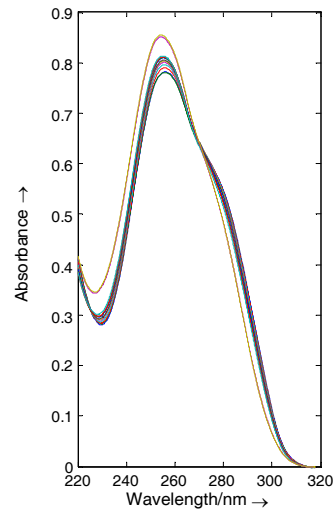
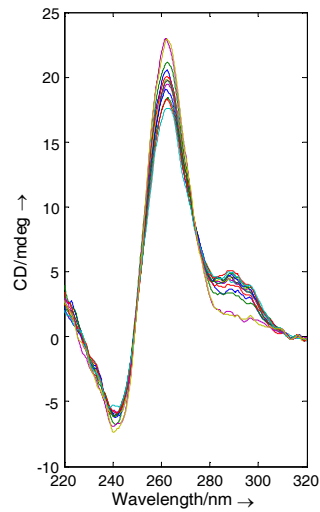


ckitG1: acid-base properties



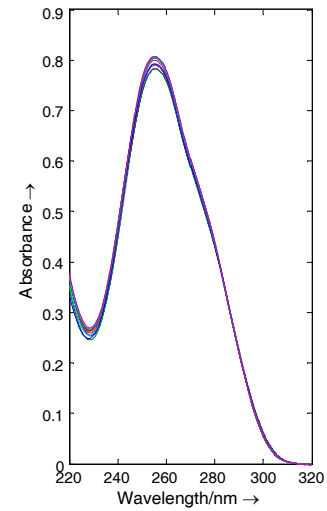
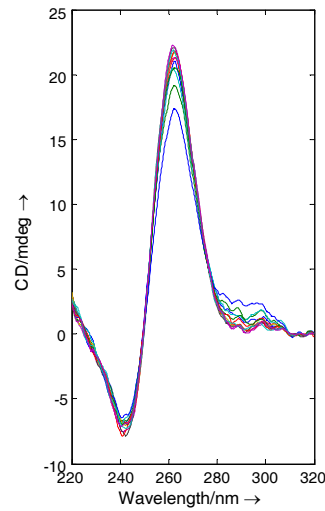
Titration of a ckitG1 sample with HCl, 1 mM Mg²⁺, 150 mM ionic strength with KCl

ckitG1-related sequences: acid-base properties



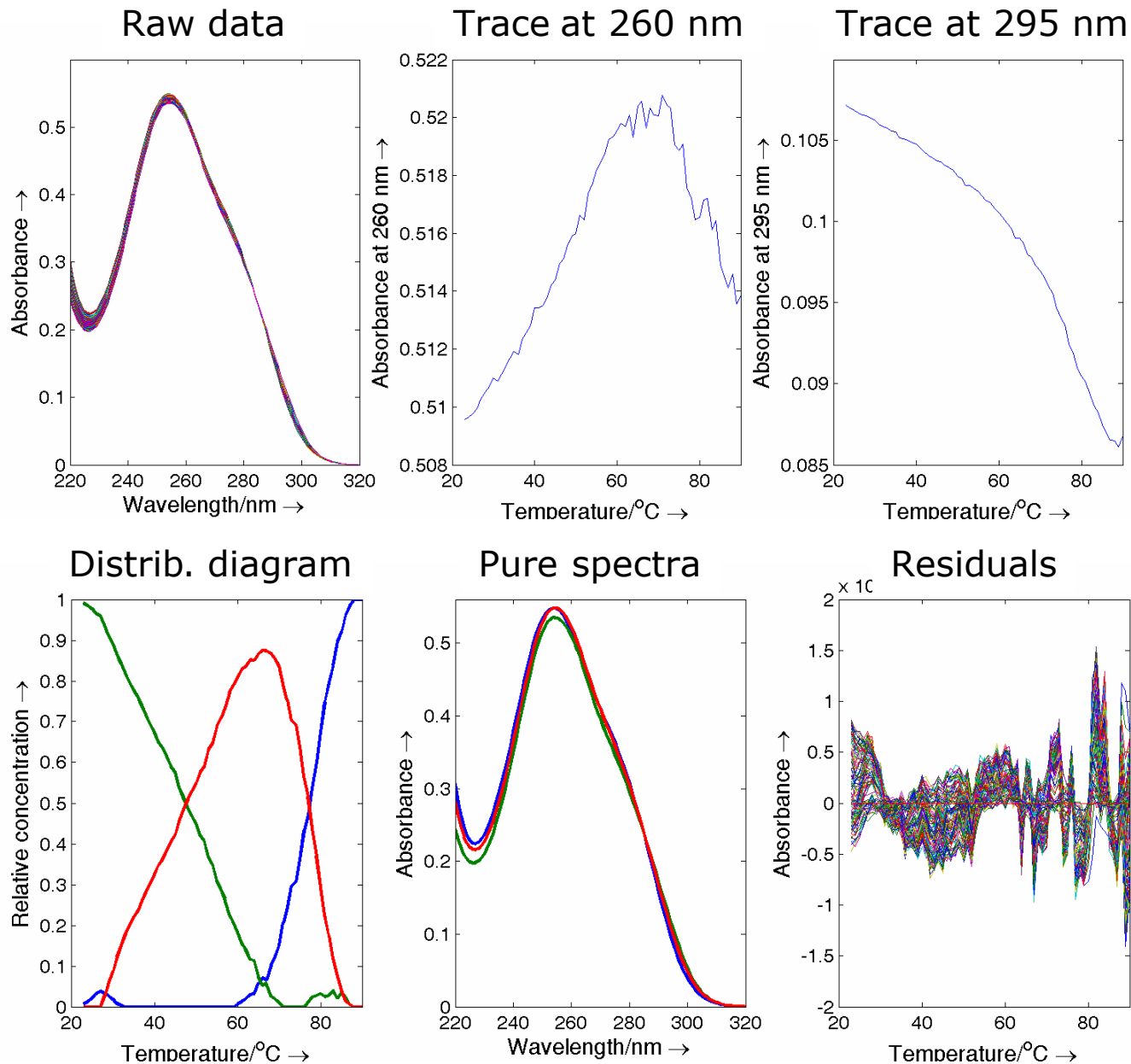
5'-CGG GCG GGC GCG TGG GTG GGG-3'

5'-TGG GTG GGT GTG TGG GTG GGG-3'



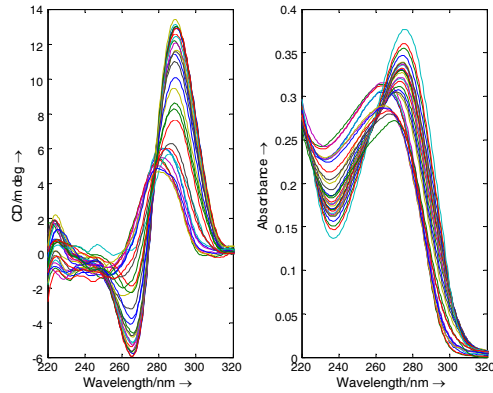
5'-TGG GTG GGT GTG AGG GAG GGG-3'

ckitG1: melting properties



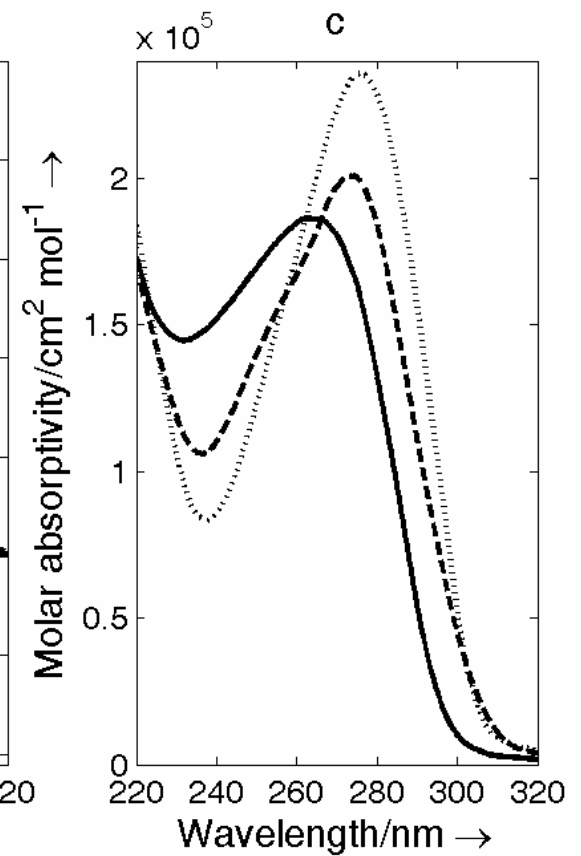
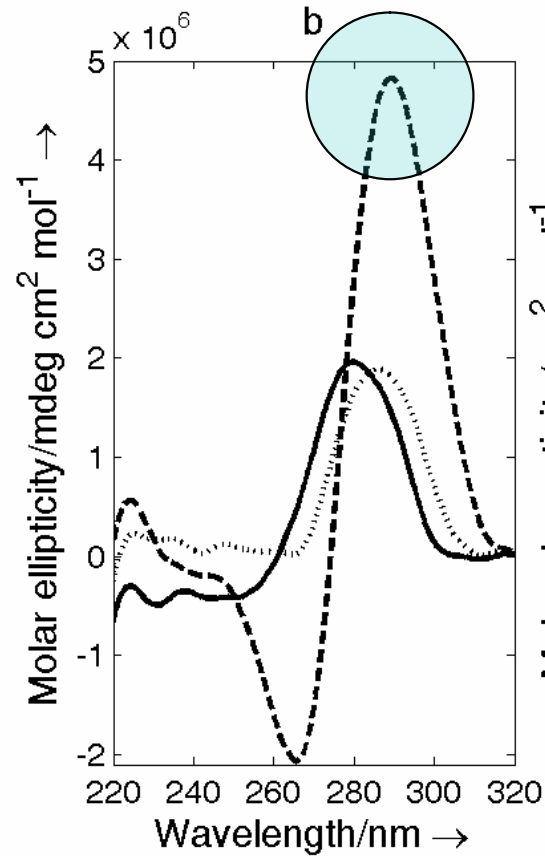
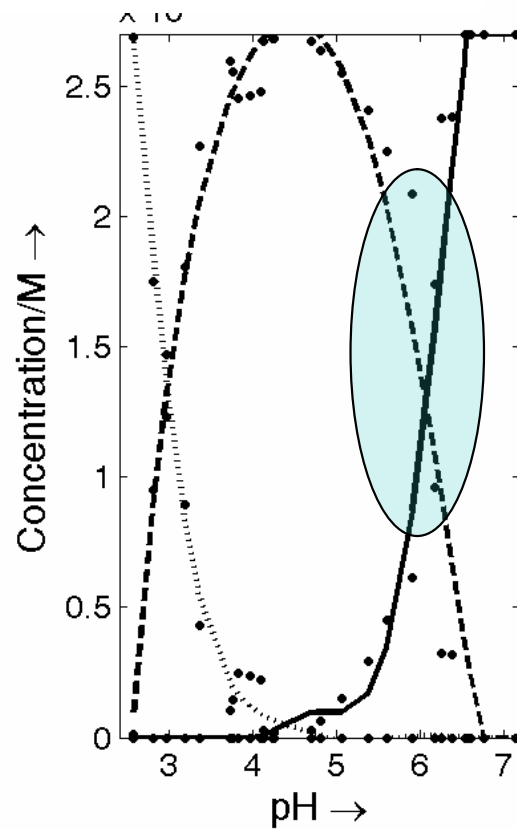
Melting of a
ckitG1
sample, 1 mM
Mg²⁺, pH 6.0,
150 mM ionic
strength with
KCl

c-kitC1: acid-base properties



Titration of a ckitC1 sample with HCl, 1 mM Mg²⁺,
150 mM ionic strength with KCl

Formation of i-motif at pH < 7
is reflected around 290 nm

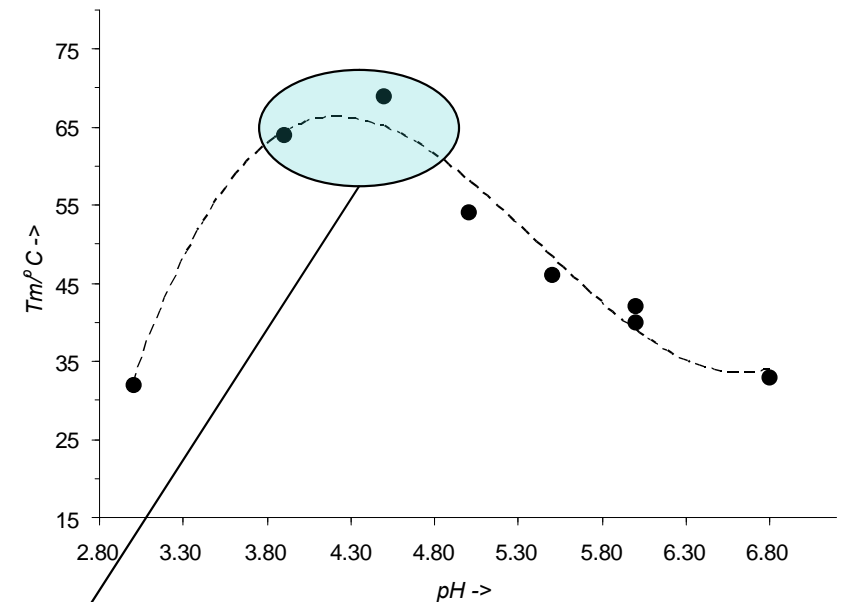


ckitC1: melting studies

Melting experiments have been carried out from pH 7 to pH 3

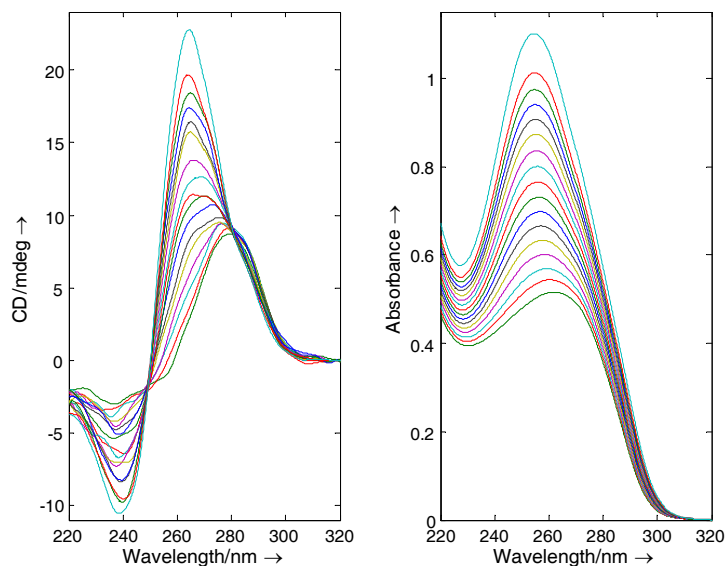
Results of Van't Hoff analysis:

pH	T _m (°C)	ΔG ⁰ at 20 °C (kcal mol ⁻¹)	ΔH ⁰ (kcal mol ⁻¹)	ΔS ⁰ (cal K ⁻¹ mol ⁻¹)
4.0	64	-5.5	-49	-146
4.5	69	-7.7	-54	-156
5.0	54	-3.9	-45	-139
5.5	47	-3.5	-47	-147
6.0	41	-2.7	-52	-167
6.8	33	-1.4	-47	-152

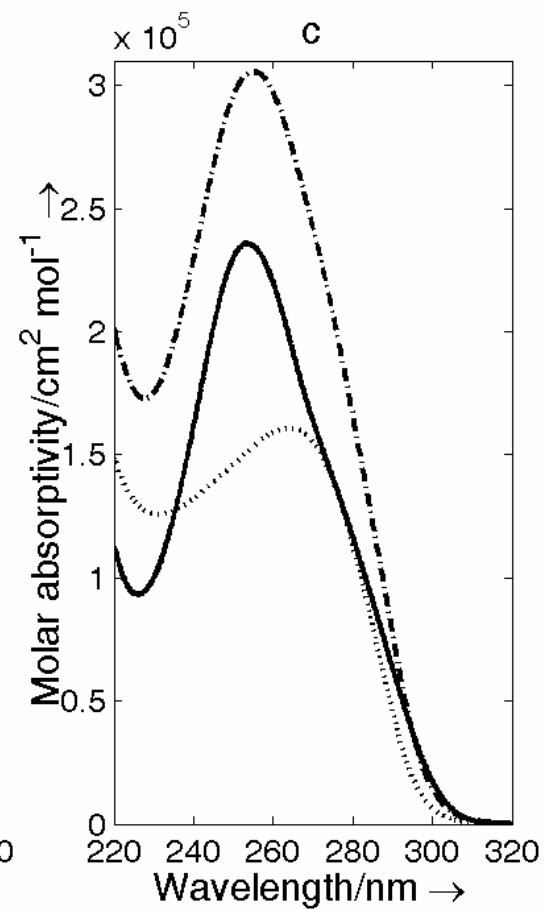
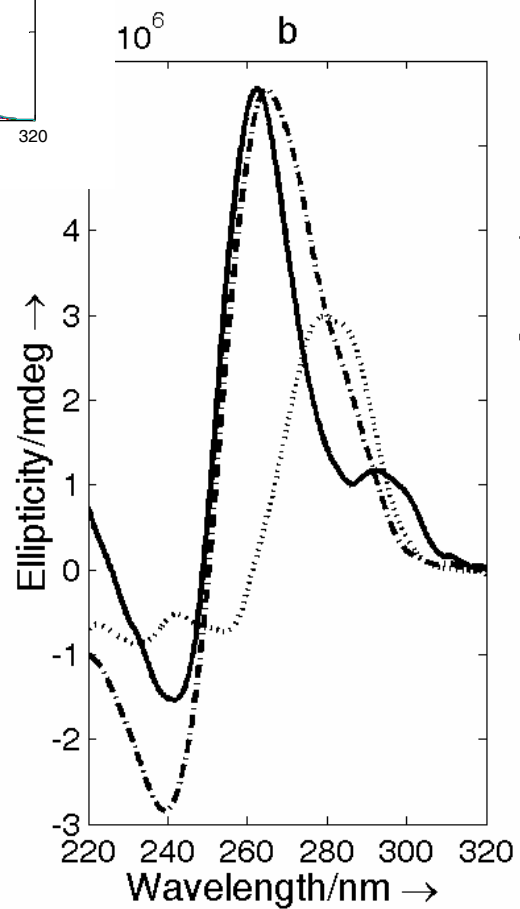
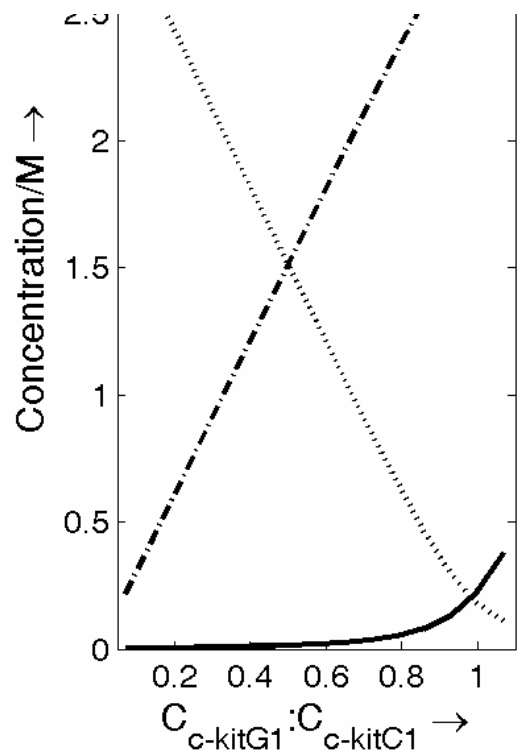


At pH ~ 4.3, T_m reaches a maximum

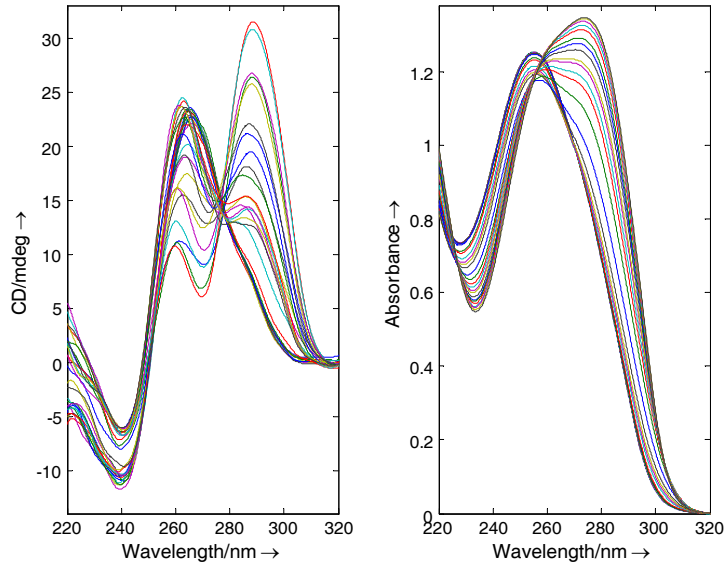
Competition: mole-ratio study



Titration of a ckitC1 mixture with a ckitG1 stock solution, pH 7.1, 1 mM Mg²⁺, 150 mM ionic strength with KCl

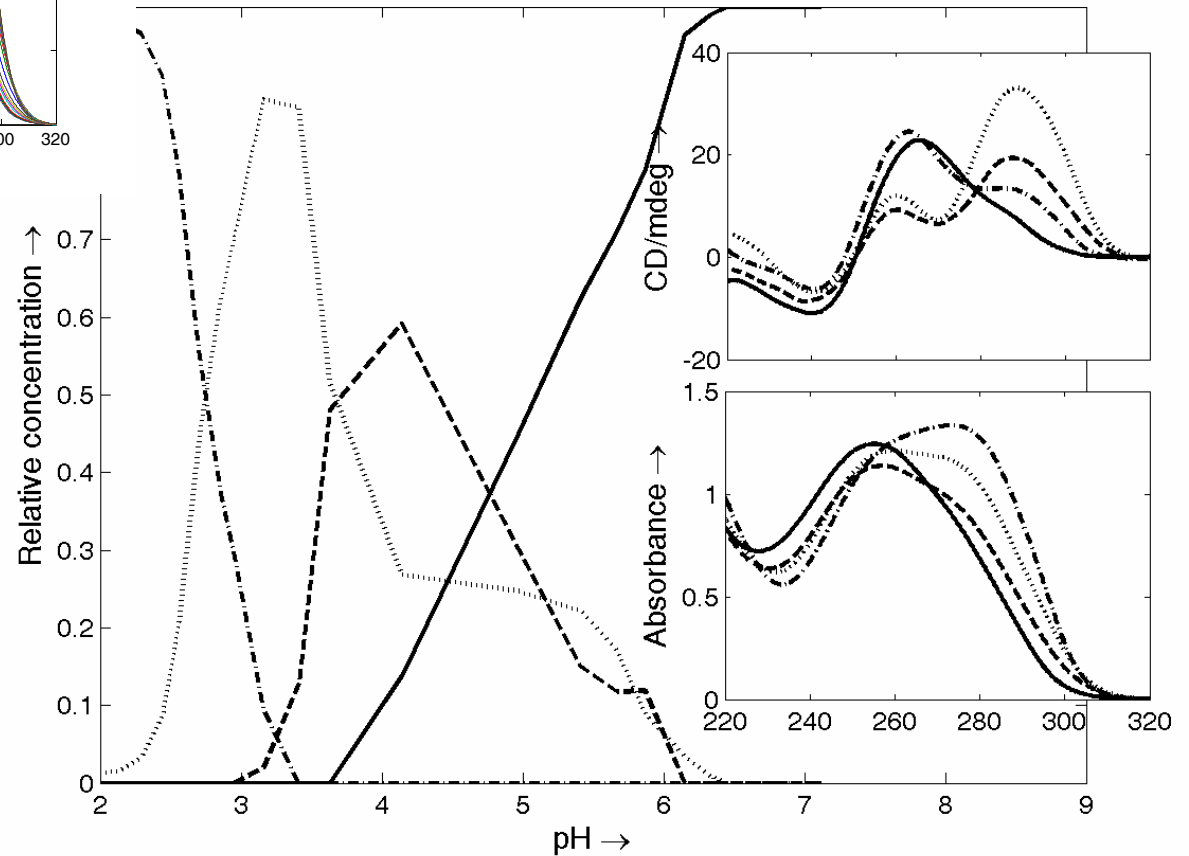


Competition: acid-base study



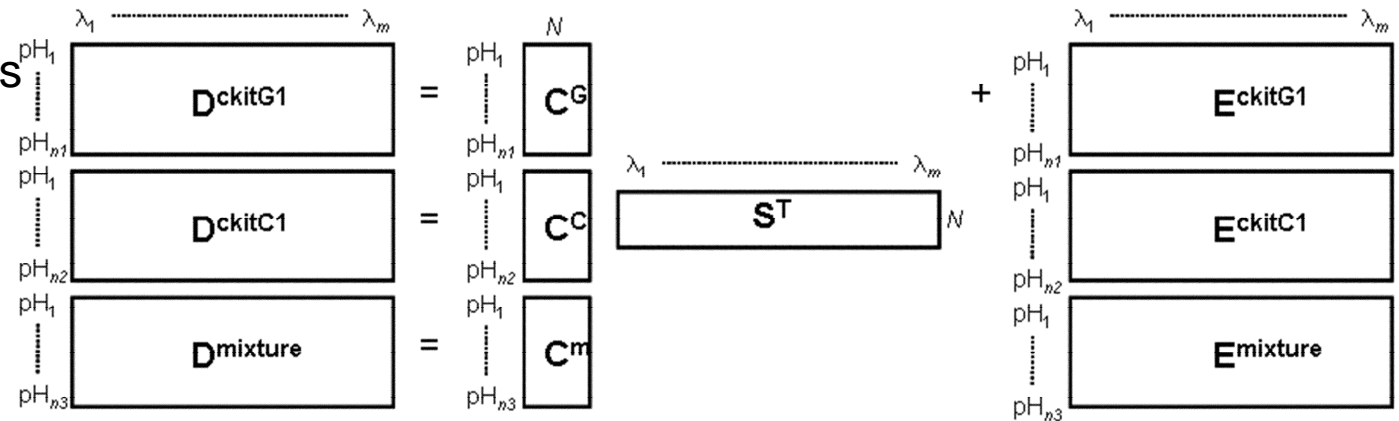
Here, only spectra recorded along the acid-base titration of a 1:1 mixture have been analyzed

4 species, which are not easy to be explained!

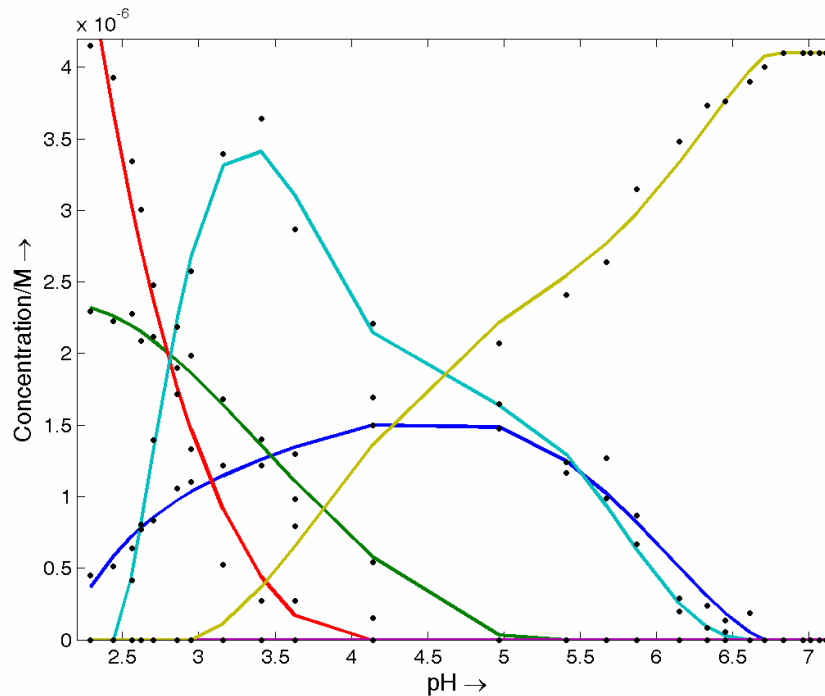


Competition: acid-base study

Now, three data sets have been simultaneously analyzed:



And the results can be explained in a easiest way:



Legend:

Watson-Crick duplex

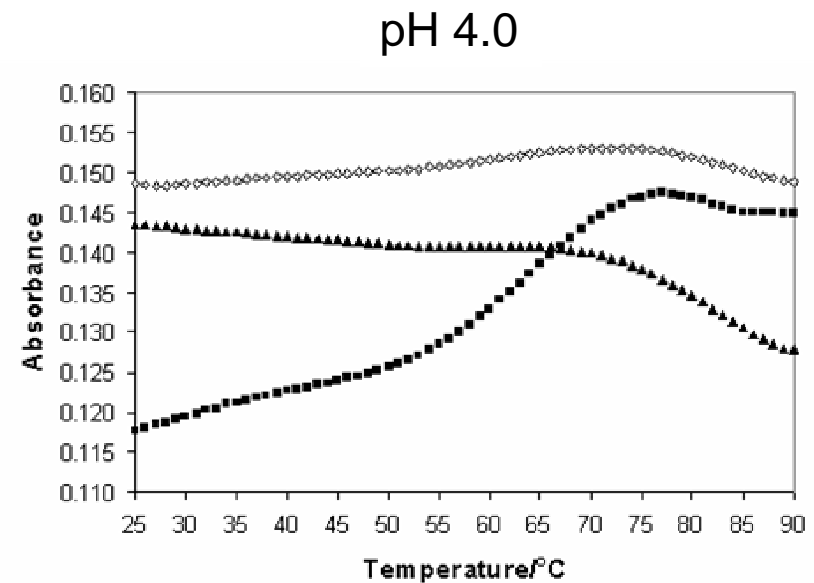
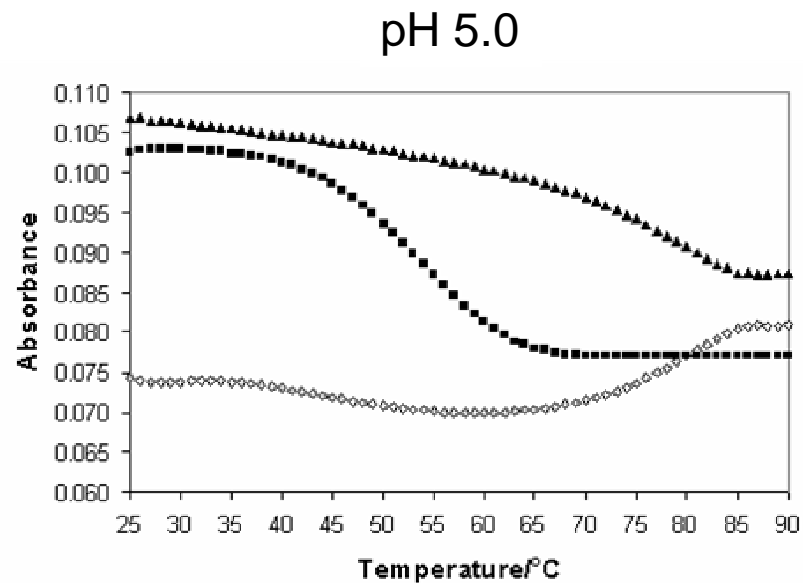
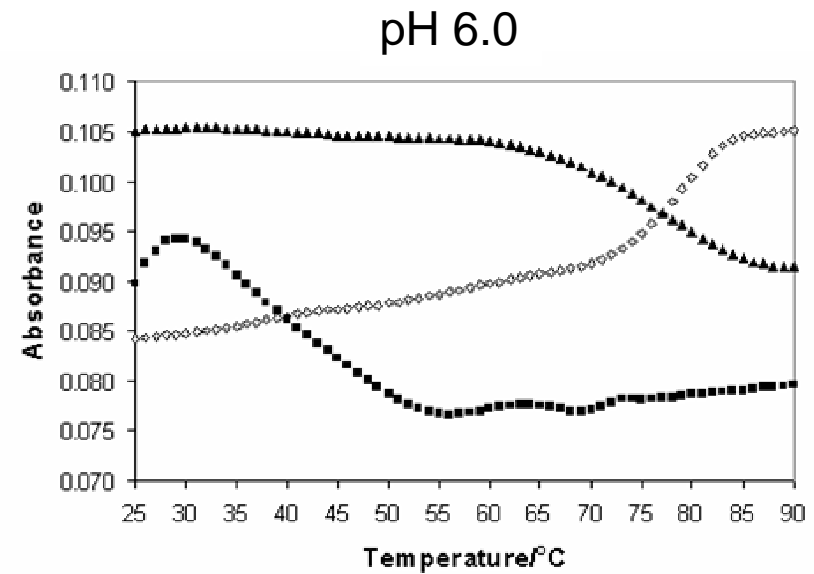
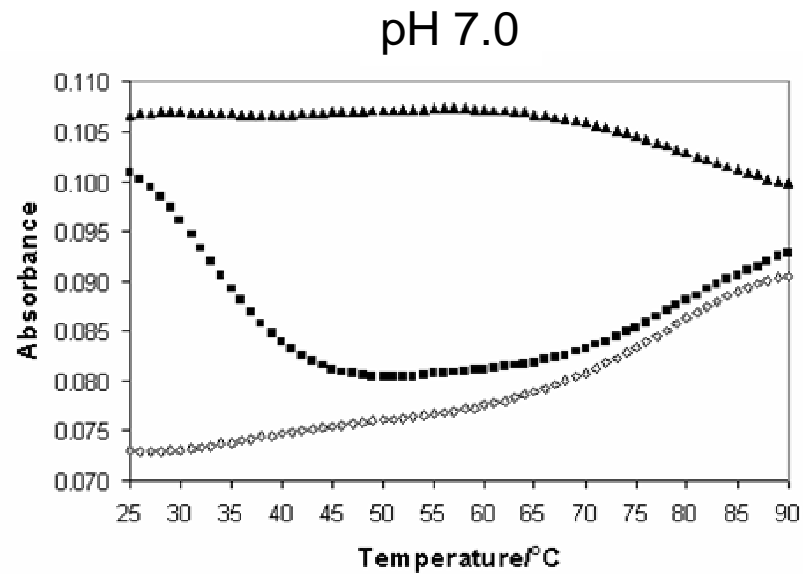
ckitC1 i-motif

protonated ckitC1

neutral ckitG1 quadr.

protonated ckitG1 quadr.

Competition: melting studies



▲: ckitG1; ■: ckitC1; □: ckitG1:ckitC1 1:1 mixture



Conclusions and future work

- ckitG1 sequence forms a G-quadruplex structure throughout the pH range 3 – 7
- An increase of stability is observed at low pH which has been associated to the reduction of repulsive interaction of phosphates
- ckitC1 sequence forms just one *i*-motif structure in the pH range 2- 7
- Stability of the *i*-motif structure is higher at pH ~ 4.3
- Watson-Crick duplex is the predominant structure at pH higher than 5, being practically the only one at pH 7.0
 - Effect of Mg²⁺ ions?
 - Effect of polyamines?
 - Crowding conditions?



Acknowledgments

- Funded projects BFU2004-02048/BMC and CTQ2006-15052-C02-01/BQU from the Ministerio de Educación y Ciencia
- Scientific-Technical Services UB
- Nicolas Roucou (IUT, Lannion, France)



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Thank you!!

More info at: www.ub.es/gesq/dna