

CATCH-U-DNA

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FETOPEN MEETING at Valencia

- Marc Meléndez Schofield
- Adolfo Vazquez-Quesada
- Raul Pérez Peláez
- Proteins in collab with Ivan Korotin and Sergei Karavasov, Queen Mary University (London)

Objectives

- M30. QCM analysis of liposome-DNA complex
- M20. Molecular dynamics simulations QCM for streptavidin under GHz flow.

M30. QCM analysis of liposome-DNA complex

- Theoretical understanding of dissipation and frequency shifts.
- Ways to increase the acoustic ratio
- Predictions at higher frequencies (up to 135MHz)

Setup and relevant parameters

Liposome

Radius. $R = [15-100] \text{ nm}$

Bending rigidity. $\kappa_{\text{LIPO}} \sim [10-100] k_B T$

lipid phase ($T-T_m$) (gel / fluid)

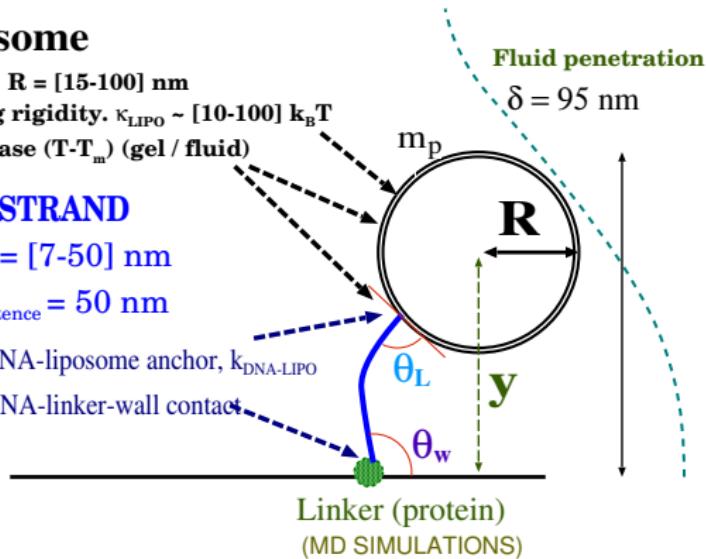
DNA-STRAND

$L_{\text{DNA}} = [7-50] \text{ nm}$

$\lambda_{\text{persistence}} = 50 \text{ nm}$

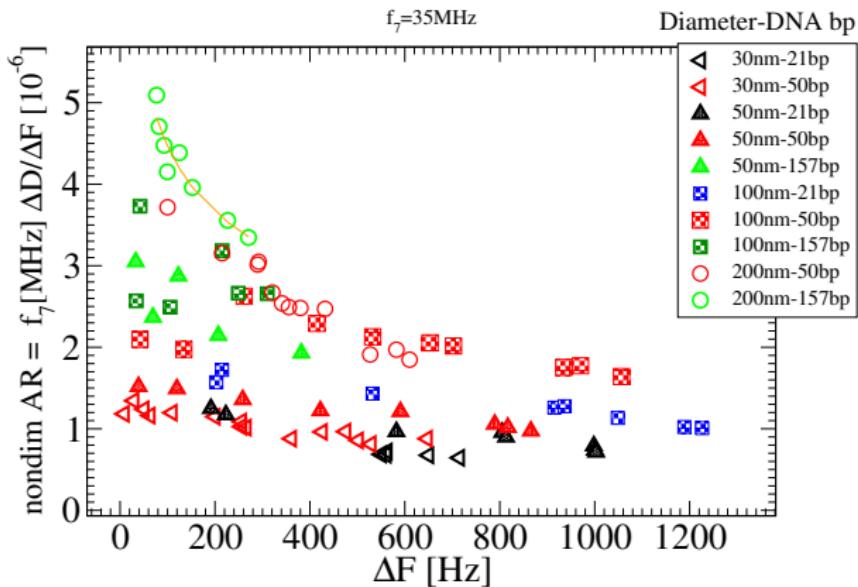
θ_L : Stiffness of the DNA-liposome anchor, $k_{\text{DNA-LIPO}}$

θ_w : Stiffness of the DNA-linker-wall contact



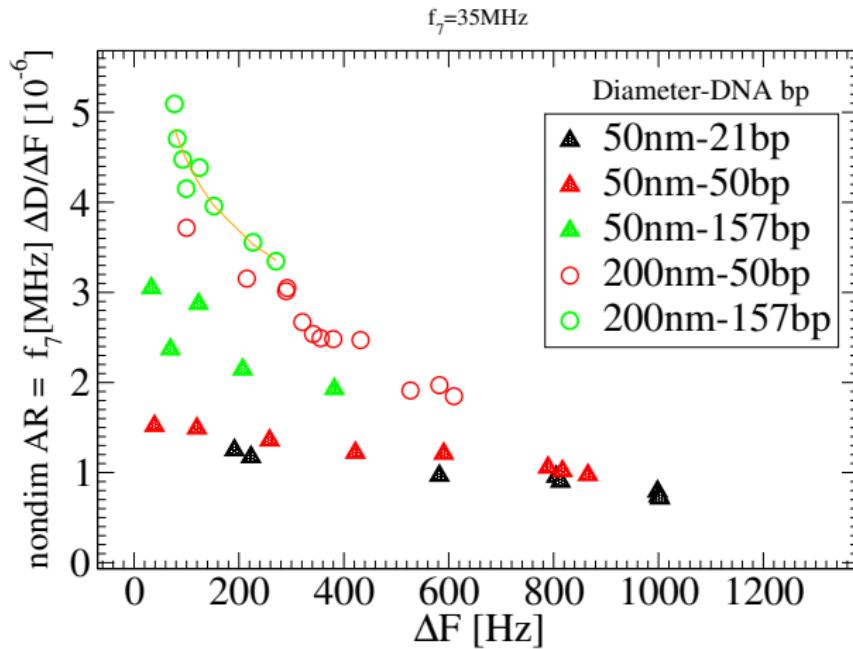
Experimental acoustic ratio

AR_{exp} is the value of $\Delta D / \Delta f$ at the limit $\Delta f \rightarrow 0$ (very low coverage).



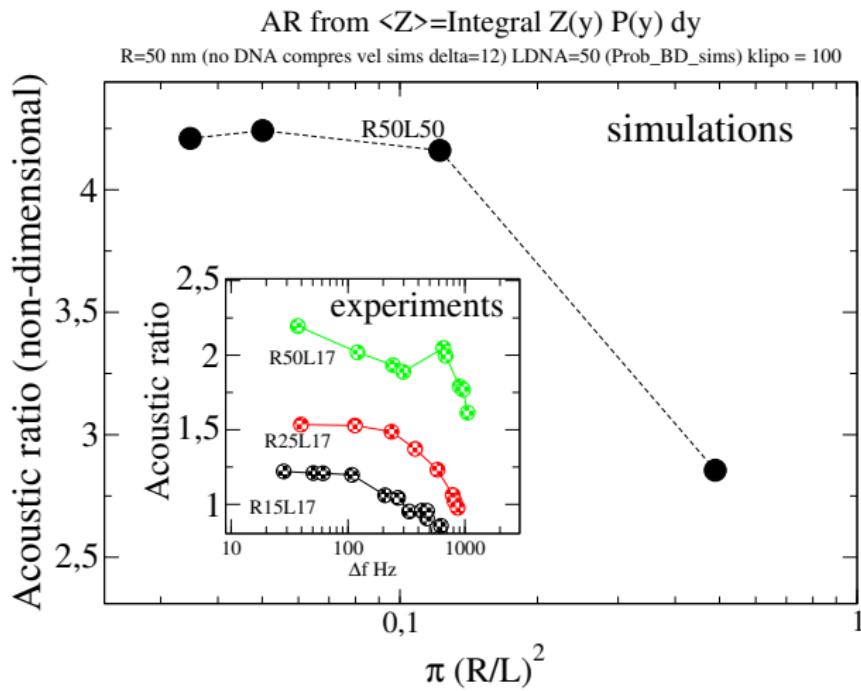
Outlook

Observed values of Δf are larger for smaller DNA strands.



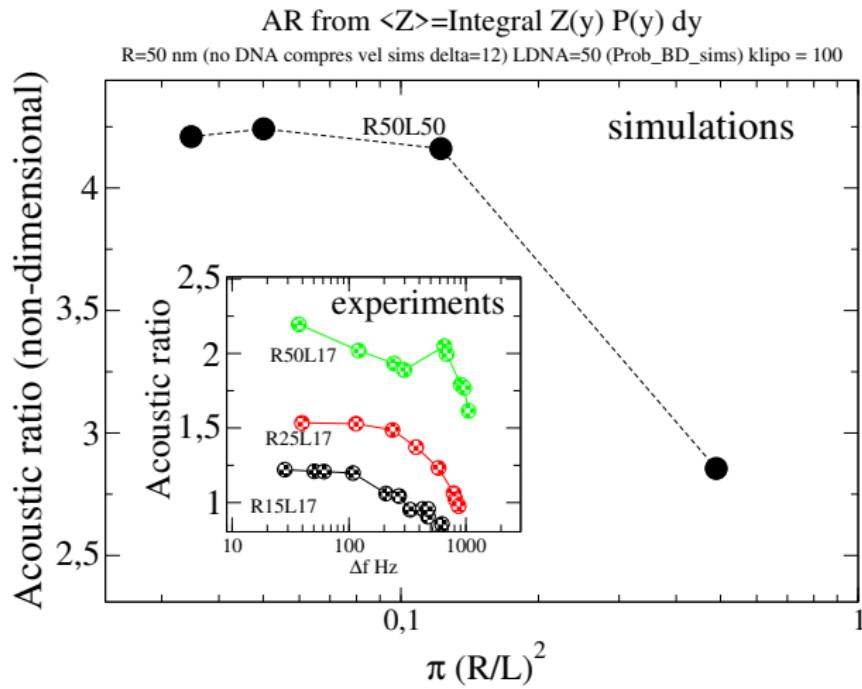
Outlook

Simulations: AR converges for large boxes ("small concentration").



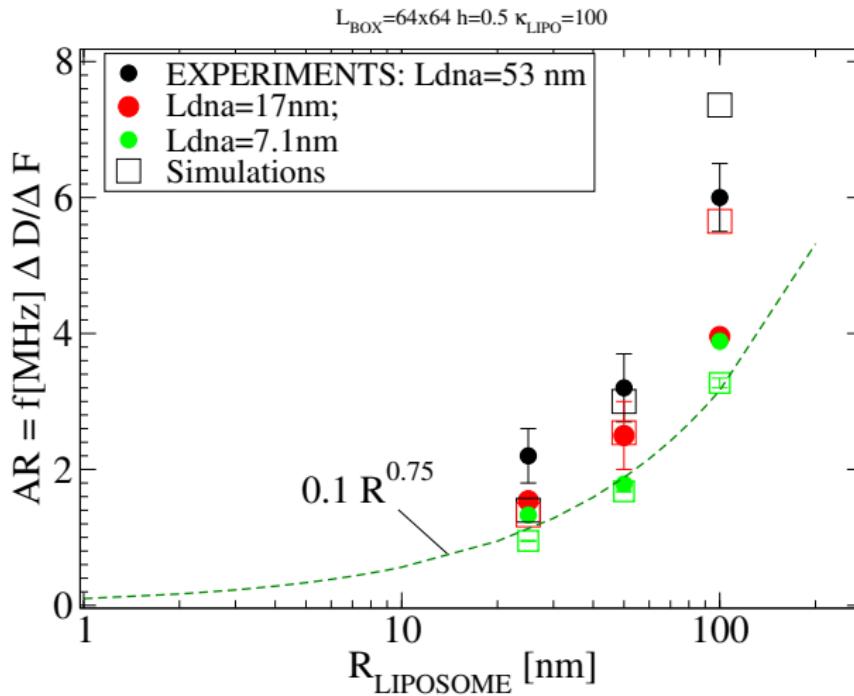
Outlook

Objective of simulations: Relate Δf and AR with liposome surface fraction ϕ .



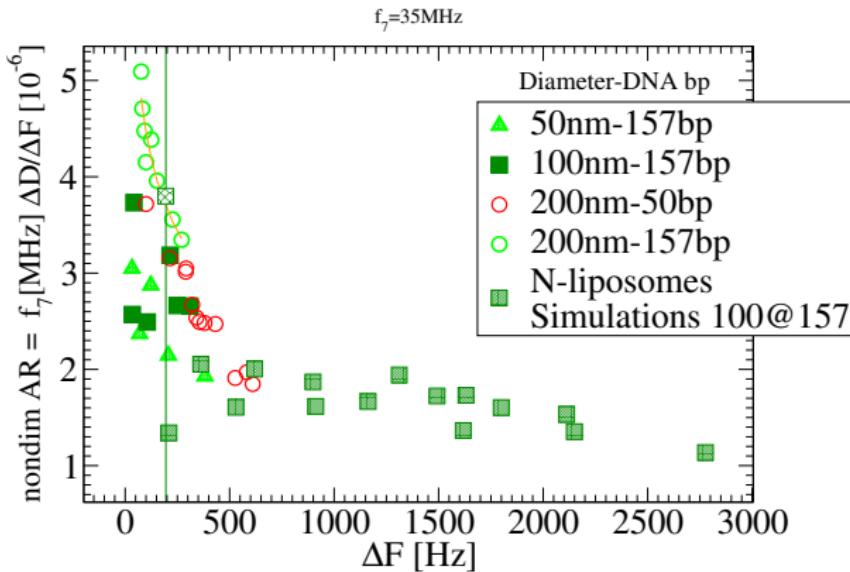
Acoustic ratio: comparison with experiments

Achieved: relatively good **quantitative** agreement with experiments
(POPC lipids).



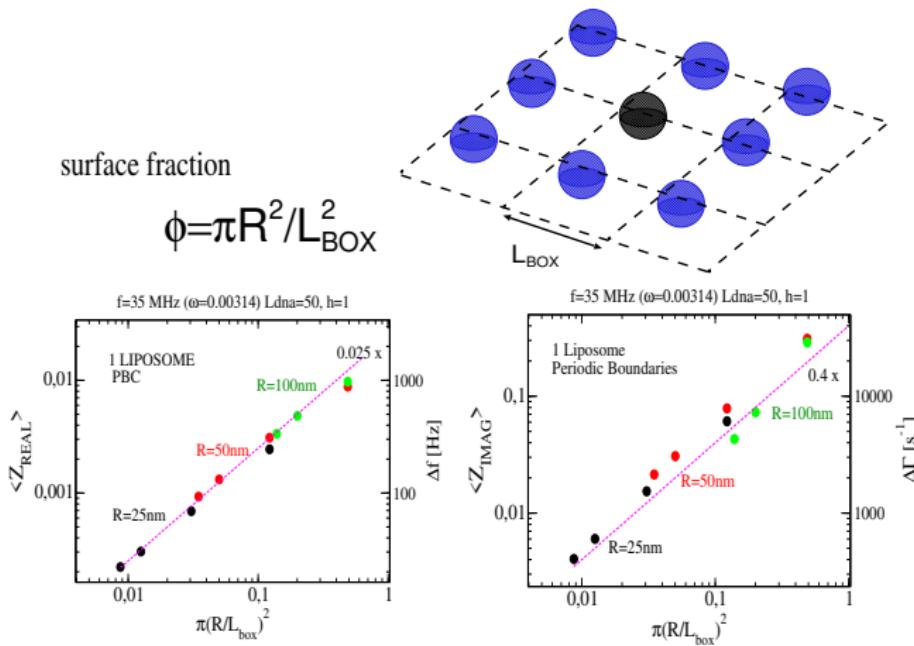
Acoustic ratio: comparison with experiments

Soon: theoretical prediction of lipid coverage from Δf and AR



Frequency shift dependence with liposome concentration

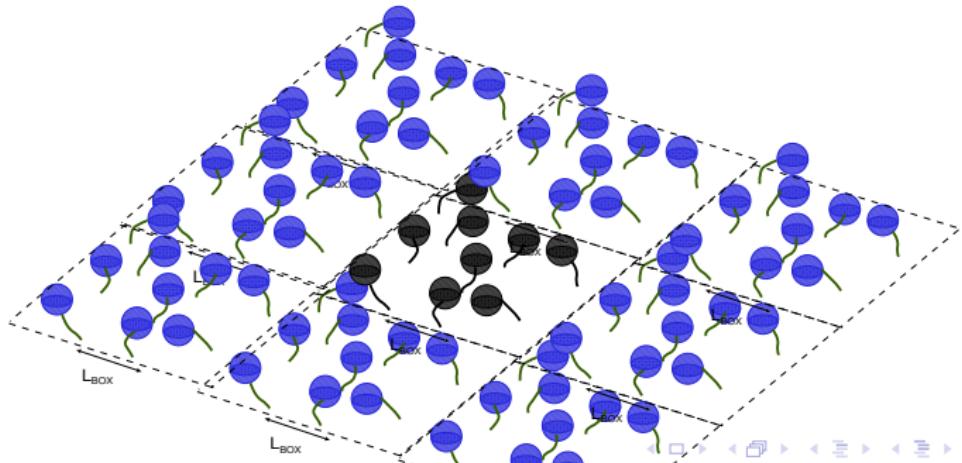
ONE LIPOSOME in a periodic box: hydrodynamic interaction with its own images



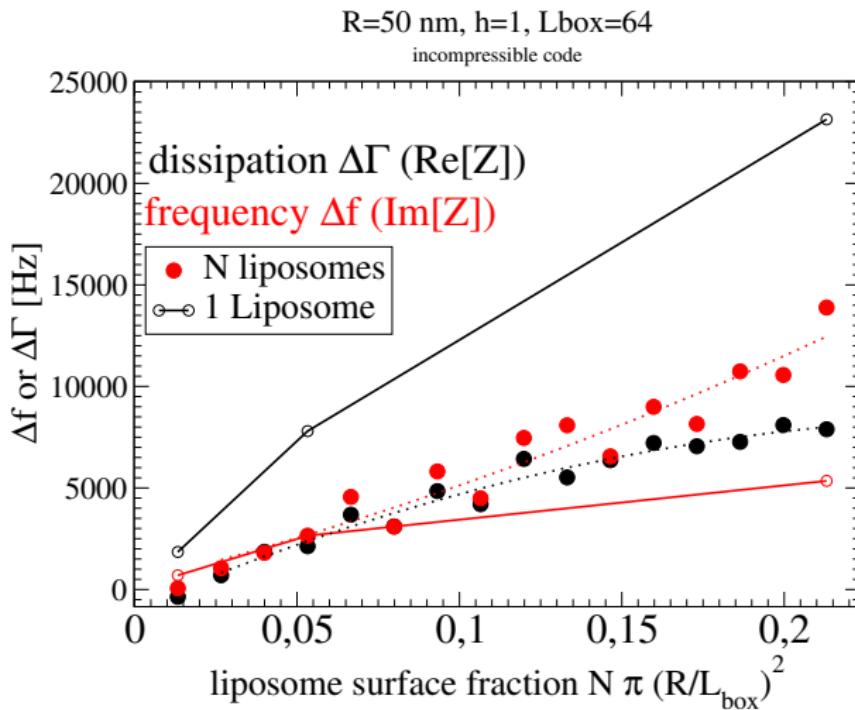
N LIPOSOMES in PBC: hydrodynamic interactions between randomly distributed liposomes

number of liposomes in primary box $N = [1, 16]$

surface fraction $\phi = N \pi R^2 / L_{\text{BOX}}^2$

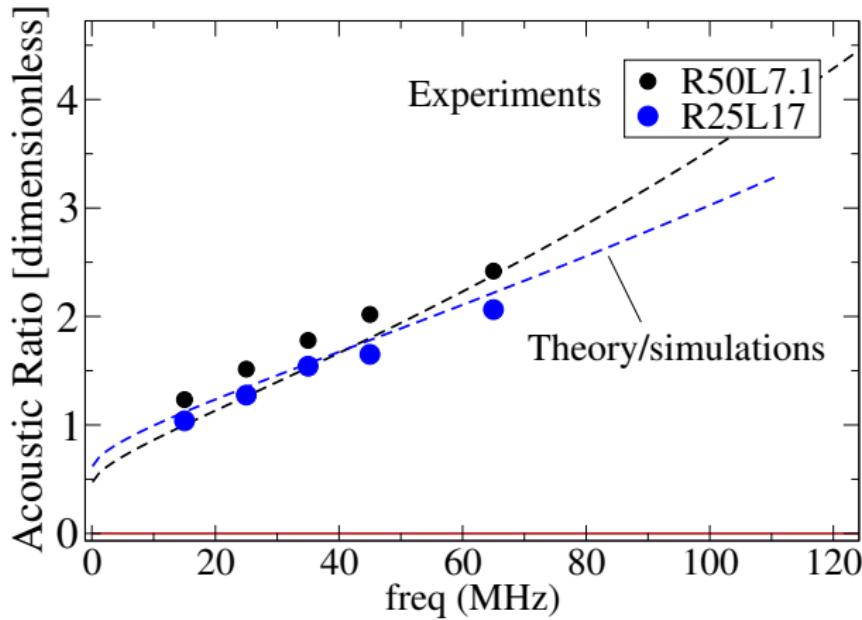


N LIPOSOMES in PBC: hydrodynamic interactions between randomly distributed liposomes



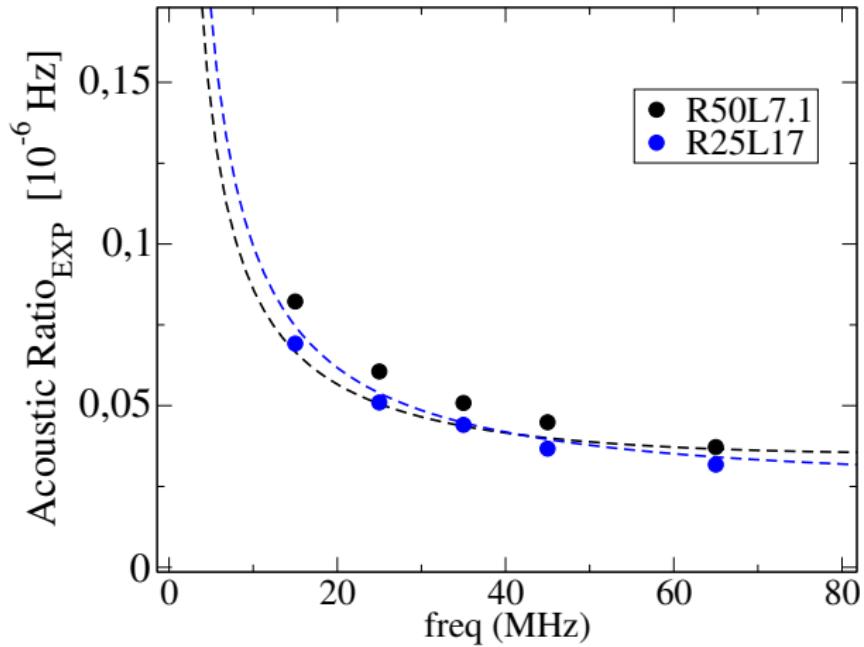
Prediction at higher QCM frequencies

Achieved: AR at different frequencies



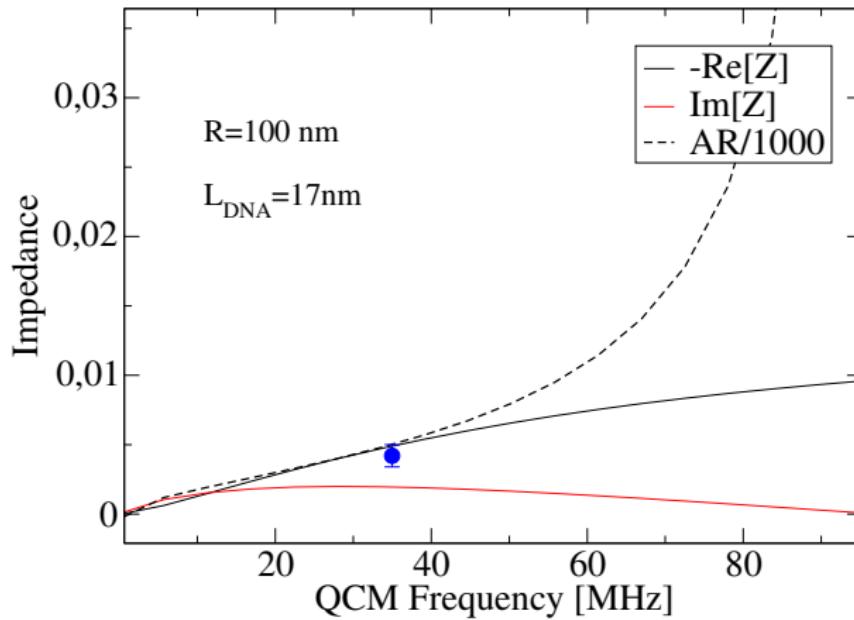
Prediction at higher QCM frequencies

Achieved: AR at different frequencies



Prediction at higher QCM frequencies

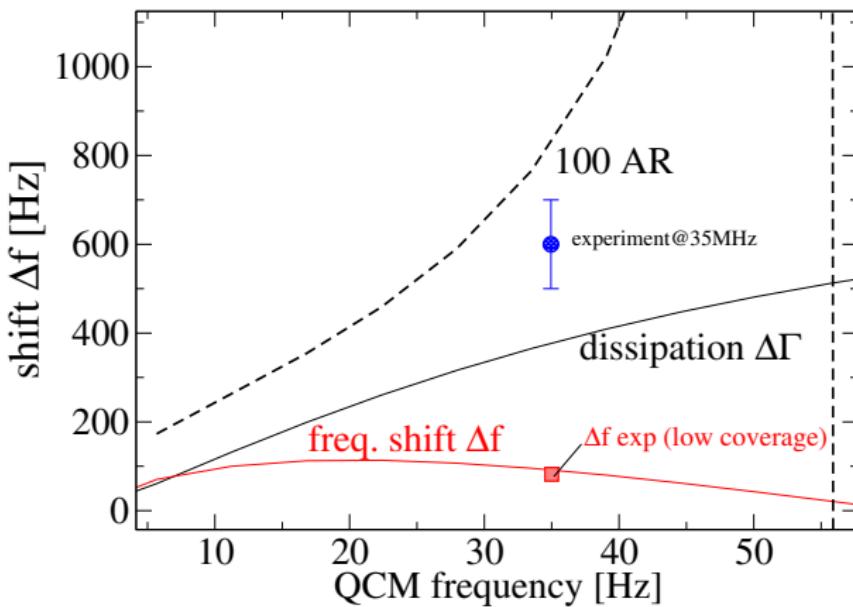
Prediction: Divergence of AR for the largest liposomes $R = 100\text{nm}$



Prediction at higher QCM frequencies

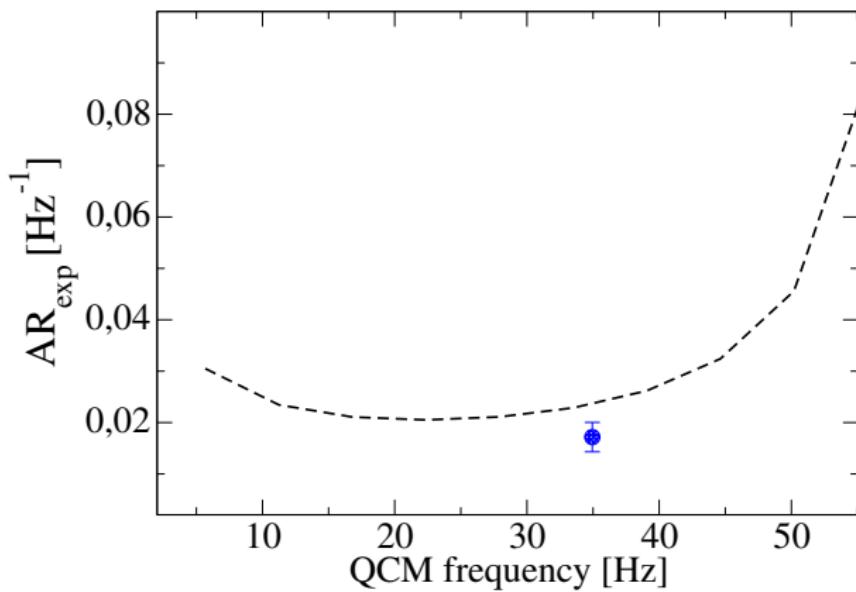
Prediction: Divergence of AR for the largest liposomes $R = 100\text{nm}$

$R=100\text{nm} L_{\text{DNA}}=50\text{nm (157bp)}$

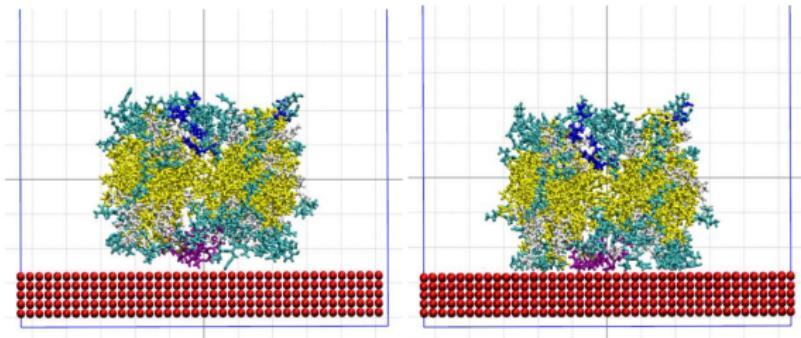


Prediction at higher QCM frequencies

$R=100\text{nm}$ $L_{\text{DNA}}=50\text{nm}$ (157bp)

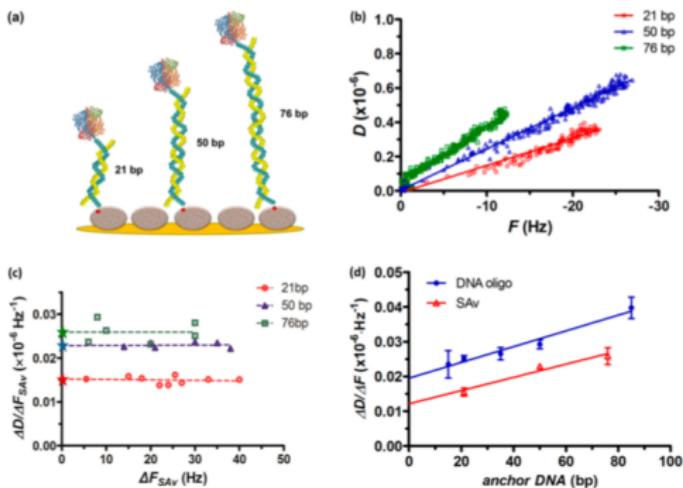


Molecular simulations of streptavidin close/adsorbed to the resonator surface



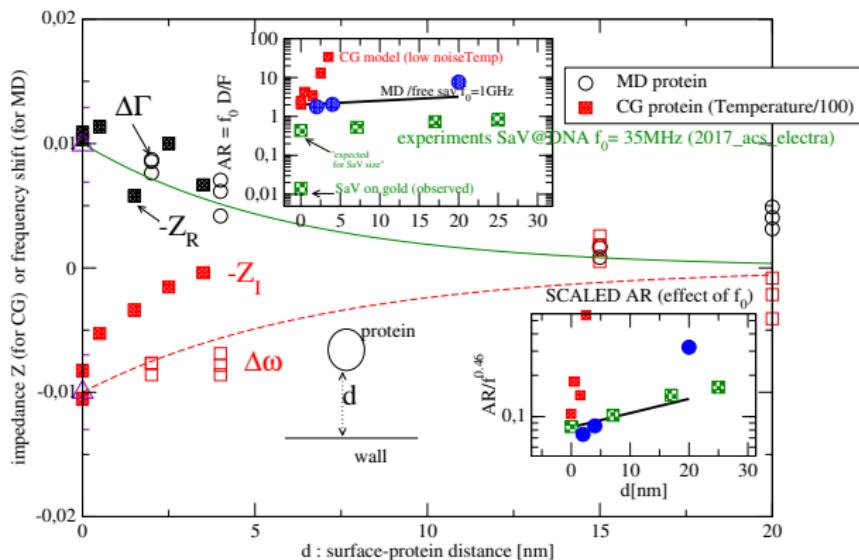
Molecular simulations of streptavidin close/adsorbed to the resonator surface

Chemistry



) Schematic representation of the 21, 50, and 76bp DNA anchors used to achieve SAv binding through a single point
(b) typical D versus F plots of SAv ($20 \mu\text{g/mL}$) obtained for each one of the three DNAs;
(c) plot of SAv ac
ing surface coverage (indicated by ΔF) for each DNA anchor;
(d) plot of the acoustic ratio of SAv (red) and 47b
the DNA anchor length.

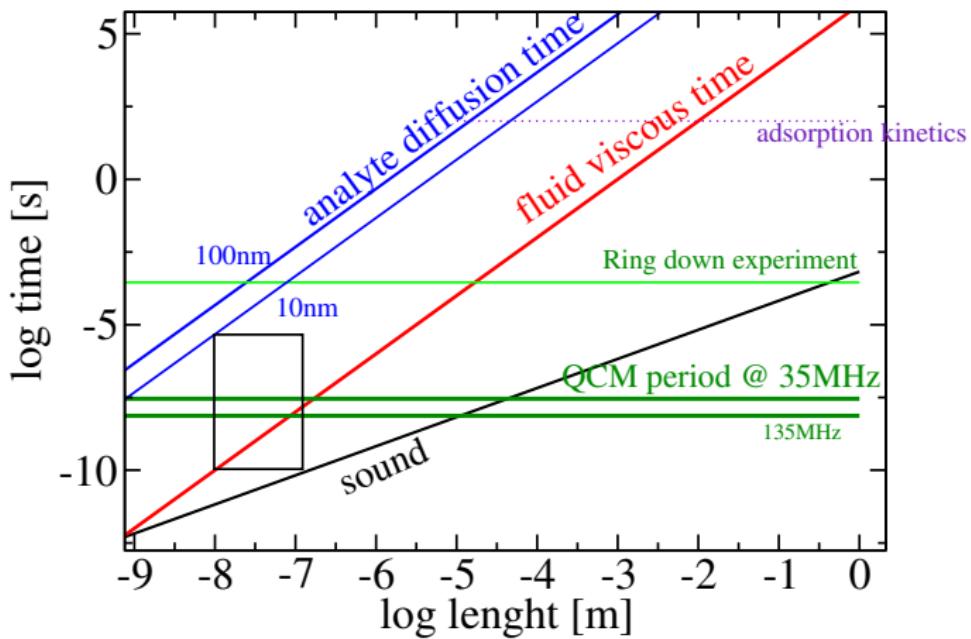
Molecular simulations of streptavidin close/adsorbed to the resonator surface



- Reproduce the experimental acoustic ratio ✓
- Predict QCM response at higher frequencies ✓
 - Divergence of AR induced by hydrodynamics (feasible for $R = 100\text{nm}$)
- Predict the relation between lipid coverage and Δf and $\Delta \Gamma$ (Soon)
- Effect of **liposome bending rigidity** ✓
 - Number of carbons in lipid chains (quantitative analysis yet to be done)
 - Membrane in fluid/gel phase (microscopic relation with the **stiffness of the DNA-Liposome link?**)
- Propose ways to increase the dissipation and the AR
 - Increase the liposome height \implies increase AR (electric fields?, modifying ph?)
 - Numerical estimation of coverage $\Delta f(\phi)$ permits calibration with larger impedance complex \implies (working with smaller DNA strands)
 - Other ideas ready to be tested

Time scales and mapping with experimental units

Time and lenght scales



Units

Code reference unit lenght: $\ell = 7.917\text{nm}$

Magnitude	Simulation	International Units
Lenght	1	7.917nm
Kin. viscosity	0.226	$10^{-6}\text{m}^2/\text{s}$
fluid density	1	10^3kg/m^3
sound velocity	2.68	$1.5 \times 10^3\text{m/s}$
QCM frequency	$0.003145/(2\pi)$	35MHz
$k_B T$	6.6×10^{-5}	$4 \times 10^{-21}\text{J}$

Basic definitions

Phasor

$$x(t) = x_R \cos(\omega t) + x_I \sin(\omega t)$$

$$x(t) = \hat{x} \exp[-i\omega t]$$

$$\hat{x} \equiv x_R + i x_I$$

- **Resonator position (Ring down)**

$$x(t) = \Delta x \exp[-\Gamma t] \cos(2\pi f t + \phi)$$

- Angular frequency $\omega = 2\pi f$
- Decay rate Γ
- **Phasor**

$$x(t) = \operatorname{Re} [\hat{x} \exp[-i(\omega - i\Gamma)t]]$$

- Complex frequency $\tilde{\omega} = \omega - i\Gamma$
- Dissipation

$$D = \frac{\Gamma}{\pi f} = \frac{2\Gamma}{\omega}$$

- Reference state: (R)

$$x_R(t) = \operatorname{Re}[\hat{x}_R \exp[-i(\omega_R - i\Gamma_R)t]]$$

- Loaded state: (A)

$$x_A(t) = \operatorname{Re}[\hat{x}_A \exp[-i(\omega_A - i\Gamma_A)t]]$$

- Complex frequency shift

$$\Delta\tilde{\omega} = \tilde{\omega}_A - \tilde{\omega}_R$$

- Shifts

$$F \equiv \Delta f = f_A - f_R \quad (1)$$

$$\Delta\Gamma = \Gamma_A - \Gamma_R \quad (2)$$

$$D \equiv \Delta D = D_A - D_R \quad (3)$$

Acoustic ratio: two definitions

$$\text{AR} \equiv -\frac{2\Delta\Gamma}{\Delta\omega} \text{ No dimensions} \quad (4)$$

$$\text{AR}_{exp} \equiv \frac{D}{(-F)} \times 10^{-6} = \frac{1}{f_0[\text{MHz}]} \frac{2\Delta\Gamma}{\Delta\omega} [10^{-6}\text{Hz}^{-1}] \quad (5)$$

$$\boxed{\text{AR}_{exp} = \frac{\text{AR}}{f_0[\text{MHz}]}}$$

Impedance

Impedance = stress at the wall / wall velocity

- Total stress at the wall: $\hat{\sigma}_{tot} = \sigma_A + \sigma_R$
- Analyte's impedance:

$$Z_A = \frac{\hat{\sigma}_A}{\hat{v}_{wall}} = \frac{\hat{\sigma}_{tot} - \hat{\sigma}_R}{\hat{v}_{wall}}$$

- Impedances sum up:

$$Z_A = Z_{tot} - Z_R$$

Reference load	Reference impedance
Simple fluid	$Z_R = -\mathcal{Z}_f(1 - i)$

Simple fluid impedance (modulus)

$$\mathcal{Z}_f \equiv \frac{\eta}{\delta} \tag{6}$$

$$\delta = \left(\frac{2\eta}{\rho\omega} \right)^{1/2} \text{ penetration lenght} \tag{7}$$

The Small Load Approximation (SLA)

- If the resonator “mass” (per area) is much larger than that of any other load..

$$m_Q \gg m_{Fluid} = \rho\delta$$

$$m_Q \gg m_{Load}$$

- Then.. the impedance is proportional to the complex frequency shift:

$$\frac{\Delta f}{f_0} = -\frac{Z_{Im}}{\pi Z_Q}$$

$$\frac{\Delta \Gamma}{f_0} = -\frac{2Z_{Re}}{Z_Q}$$

with **Unloaded resonator impedance**

$$Z_Q = (C\rho_Q)^{1/2} \approx 8.8 * 10^6 \text{kg/(m}^2\text{s})(\approx 15.745 \text{ Simulation Units})$$

C is the quartz elastic modulus and ρ_Q its density.

The Small Load Approximation (SLA)

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$$m_Q \gg m_{Fluid} = \rho\delta$$

$$m_Q \gg m_{Load}$$

- Then.. the impedance is proportional to the complex frequency shift:

Acoustic Ratio

$$AR = \frac{\Delta\Gamma}{\pi\Delta\omega} = -\frac{2Z_{Re}}{Z_{Im}}$$

Impedance analysis

$$Z = -\frac{\sigma}{\hat{v}_w} = -\frac{\sigma}{i\omega \hat{x}}$$

- Imposing the wall motion: $x(t) = x_0 \cos(\omega t)$ or $\hat{x} = x_0 \in \mathcal{R}$
- Imposing the wall stress: $\sigma_{ext}(t) = \sigma_e \cos(\omega t)$ or $\hat{\sigma}_e \in \mathcal{R}$

Simple analytic models: impedance

$$Z = \frac{\hat{\sigma}}{\hat{v}_0}$$

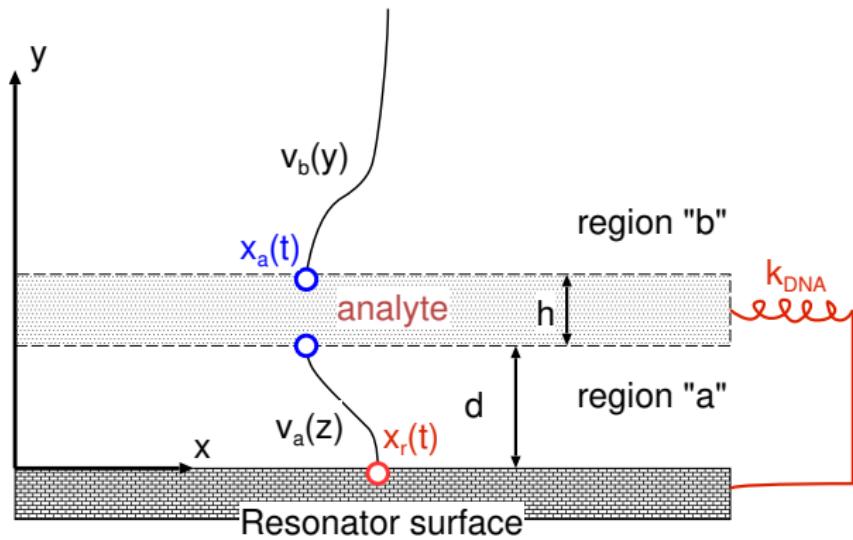
- ① Impose the wall velocity $\hat{v}_0 = -i\omega x_0$
- ② Solve (or model) the stress at the wall, as a function of the analyte motion: $\hat{\sigma} = \hat{\sigma}(\hat{x}_a)$
- ③ Solve the analyte motion:

$$-im_a\omega^2\hat{x}_a = F_f(\hat{x}_a, x_0) - k_{DNA}(\hat{x}_a - x_0) \quad (8)$$

with

- F_f : Fluid force on the analyte
- k_{DNA} : effective spring for the DNA (could be complex)

Plane model



$$-im_a\omega^2\hat{x}_a = F_f(\hat{x}_a, x_0) - k_{DNA}(\hat{x}_a - x_0)$$

- Mass per unit surface: $m_a = \rho_a h$
- Fluid force (per unit area):

$$F_f = \eta \left(\frac{\partial v}{\partial y} \right)_{y=d+h} - \eta \left(\frac{\partial v}{\partial y} \right)_{y=d}$$

- Fluid

$$\frac{\partial v}{\partial t} = \nu \frac{\partial^2 v}{\partial z^2}$$

$$v(0, t) = \frac{dx_r}{dt}$$

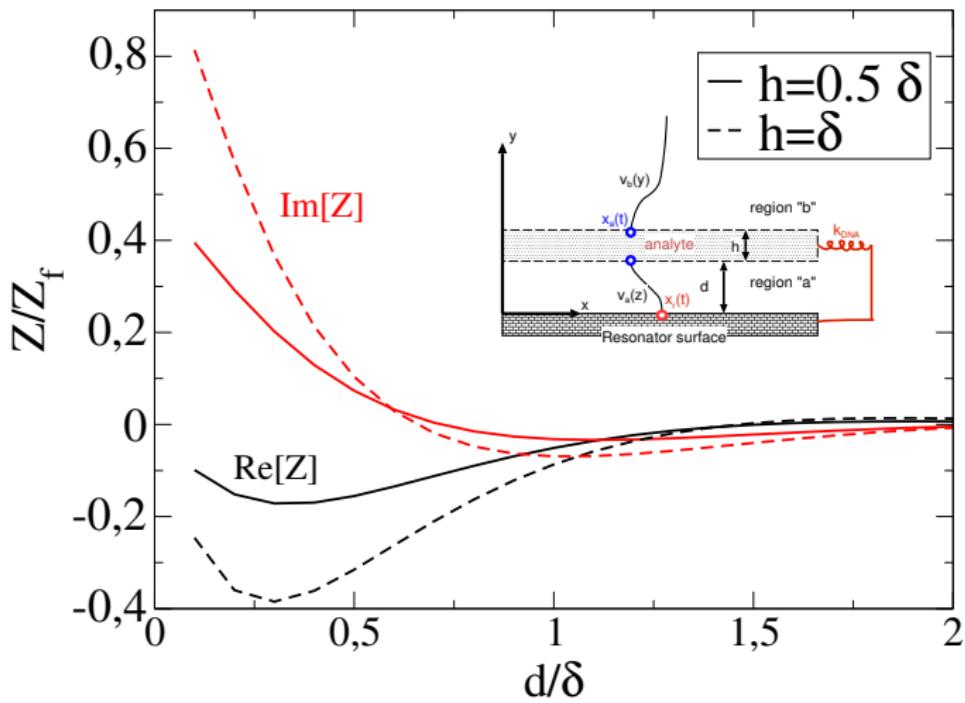
$$v(d, t) = \frac{dx_a}{dt}$$

$$v(d + h, t) = \frac{dx_a}{dt}$$

$$v(\infty, t) = 0$$

Analytical results

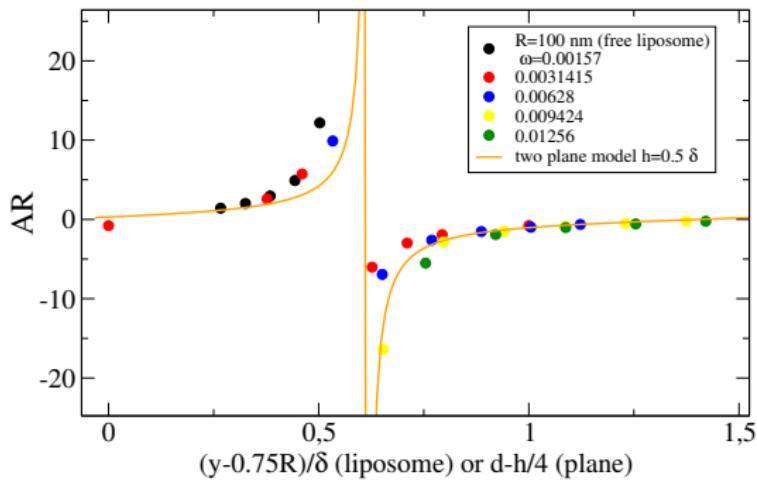
Plane model



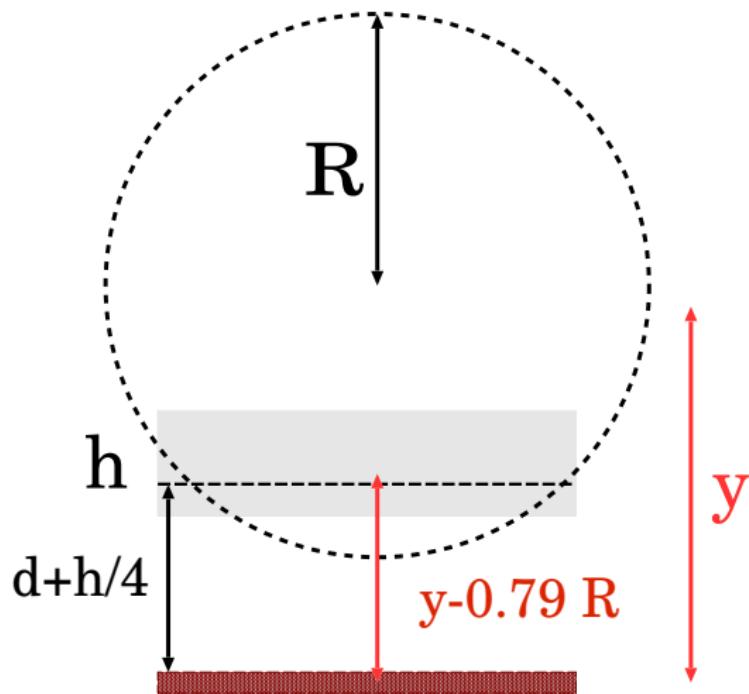
Analytical results

Zero crossing of $\text{Im}[Z]$ leads to AR divergence at some height y_c .

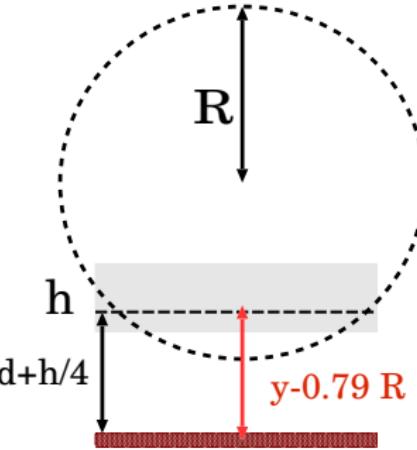
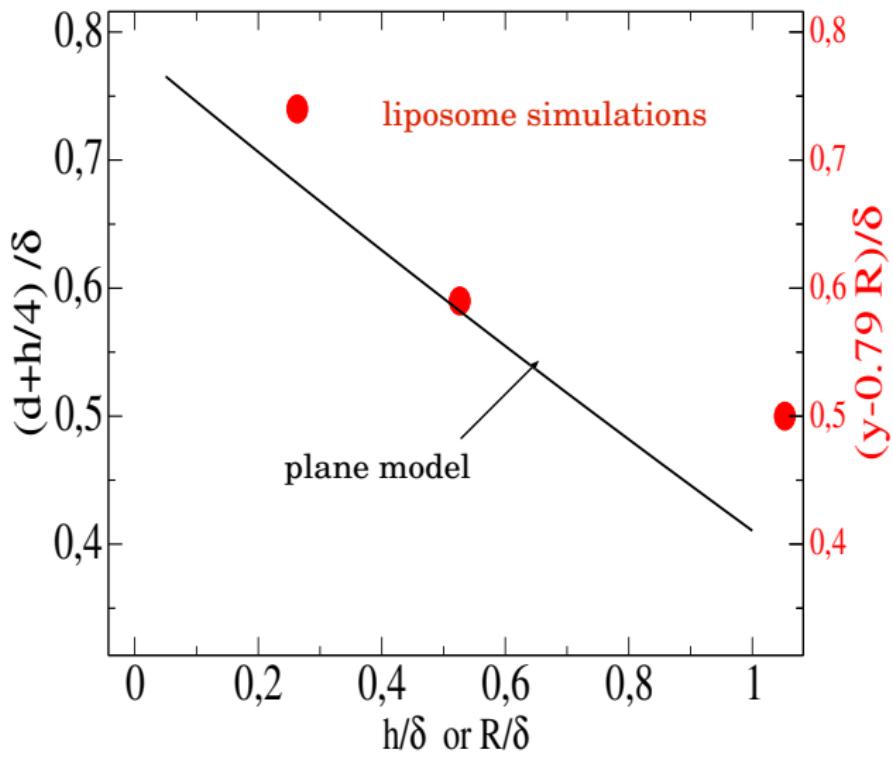
Plane model



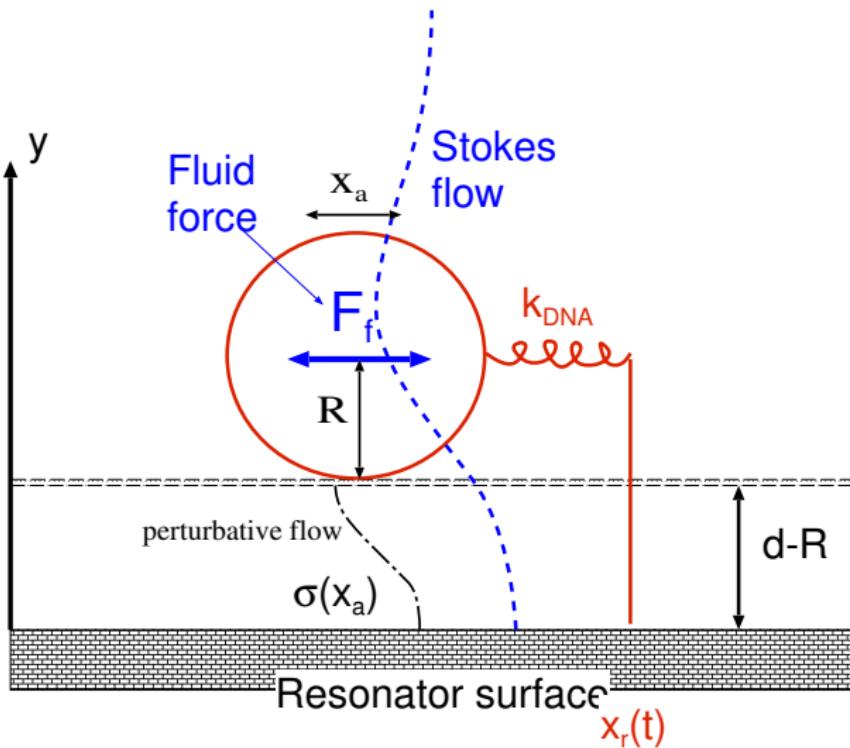
Height y_c for the zero crossing of $\text{Im}[Z]$ (divergence of AR)



Height y_c for the zero crossing of $\text{Im}[Z]$ (divergence of AR)



Sphere-Plane model



Sphere-Plane model

- Analyte mass: $m_a = (4/3)\pi\rho_a R^3$
- Fluid force (Mazur and Bedeaux 1979)

with $\alpha = \frac{(1-i)}{\delta}$ and $\hat{u} = -i\omega\hat{x}_a$ analyte velocity

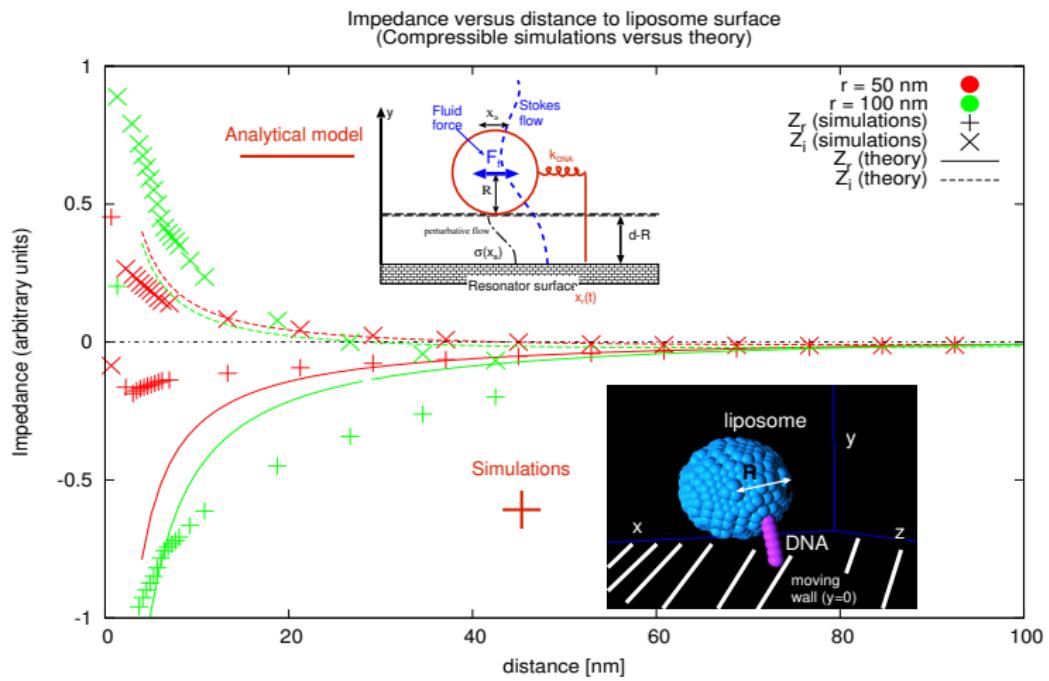
$$\frac{F_f(\omega)}{6\pi\eta R} = [1 + \alpha R(\hat{v}_s - \hat{u}) + (1/3)(\alpha R)^2(\hat{v}_v - \hat{u}) - (2/9)(\alpha R)^2\hat{u}]$$

$$\hat{v}_s = \frac{1}{4\pi R^2} \oint \hat{v}(\mathbf{r}) d^2\mathbf{r} \text{ Surface average}$$

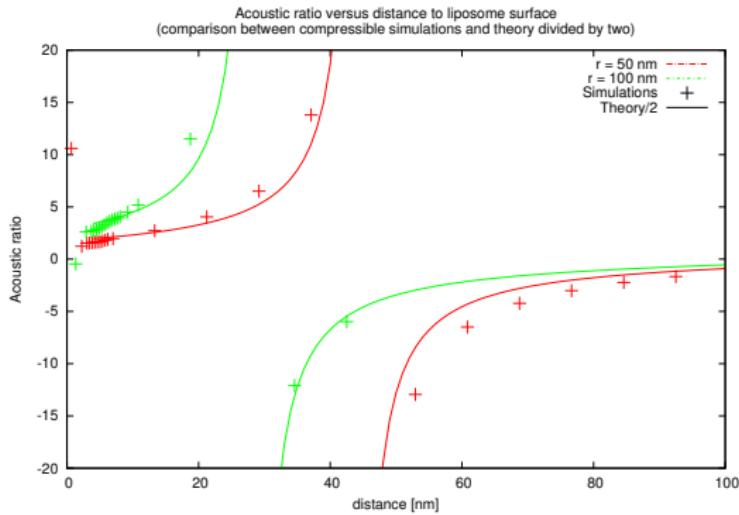
$$\hat{v}_v = \frac{3}{4\pi R^3} \int \hat{v}(\mathbf{r}) d^3\mathbf{r} \text{ Volume average}$$

$$\hat{v}(y) = -i\omega x_0 \exp[-\alpha y] \text{ Stokes base flow}$$

Sphere-Plane model



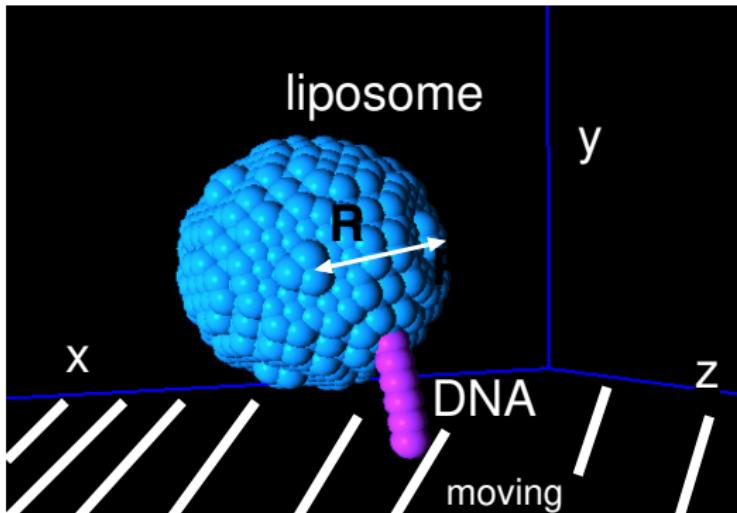
Sphere-Plane model



Simulations of QCM dynamics of free liposomes

- Immersed boundary method: mesh size h
- Compressible fluid (sound velocity of water).
- Resolution: number of cells per penetration layer. $N_\delta = \delta/h \geq 12$
- Numerical evaluation of the wall stress (second order accurate).

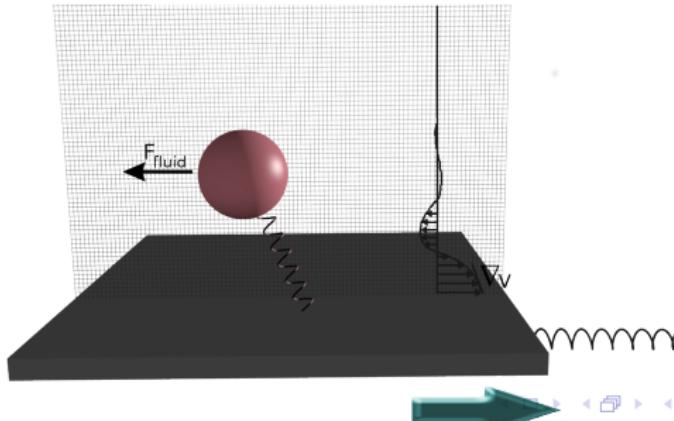
$$\sigma = \eta \left(\frac{\partial v_x}{\partial y} \right)_{y=0}$$



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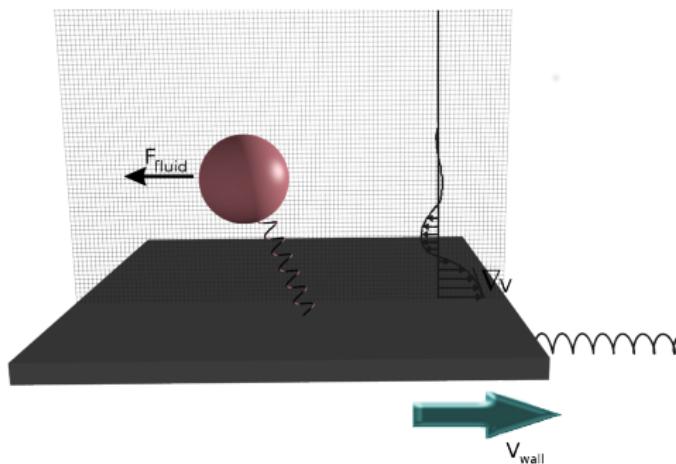
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Simulations of QCM dynamics of free liposomes

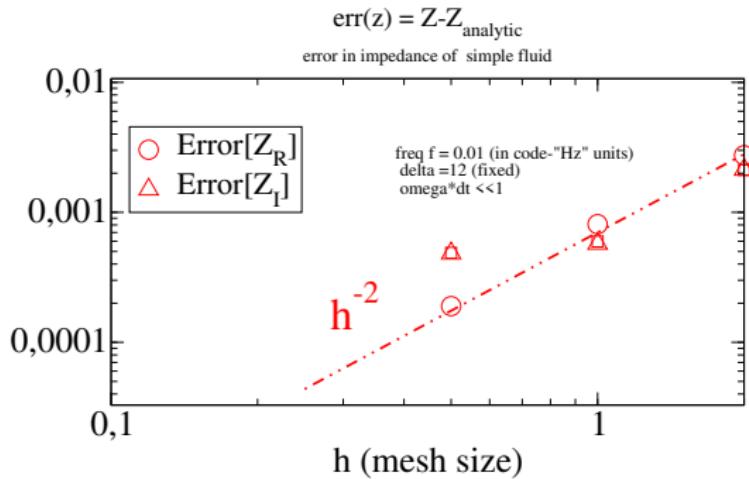
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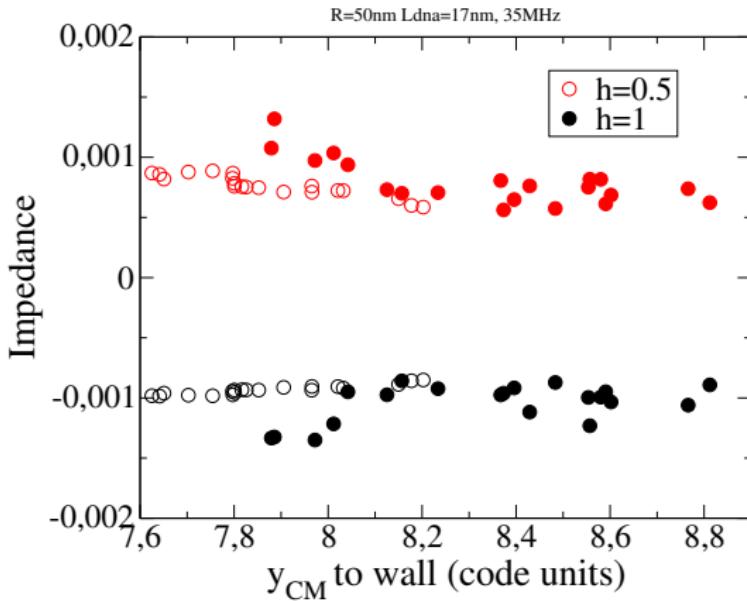
Simulations of QCM dynamics of free liposomes

- Convergence tested for simple fluid and liposome.



Simulations of QCM dynamics of free liposomes

- Double resolution needed for liposomes close to the wall.
 $h = 0.5\ell = 3.95\text{nm}$



Coarse-grained model: some movies

1GHz

Coarse-grained model: some movies

1GHz

CODE PARAMETERS

$\delta = \sqrt{\frac{2\eta}{\rho\omega}}$	6, 6.9282, 8.48528, 12 , 16.9706 (47.5, 54.9, 67.2, 95.0 , 134.4 nm)
Radius R	3.16, 6.32, 9.0, 12.63 (25, 50, 75, 100 nm)
DNA length L_{DNA}	0.88, 2.15, 6.32 (7, 17, 50 nm) (or without DNA)
Box length $L_x = L_y$	8, 16, 24, 32, 60, 64 (63.3, 126.0, 190.0, 253.0, 475.0, 506.0 nm)
Box length L_z	64 (506 nm)
Liposome thickness	1.26 (10 nm)
Cell size h	0.5, 1.0, 2.0 (0.06, 0.13, 0.25 nm)
DNA rigidity	$k_{DNA}^{spring} = 100$ $k_{DNA}^{spring} = 63.16$
Liposome rigidity	$k_{Lipo}^{spring} = 1, 10, 20, 100, 300, 1000$
Type of oscillations	Forcing wall Imposing velocity
Angular frequency ω	between 0.0005 and 0.0157

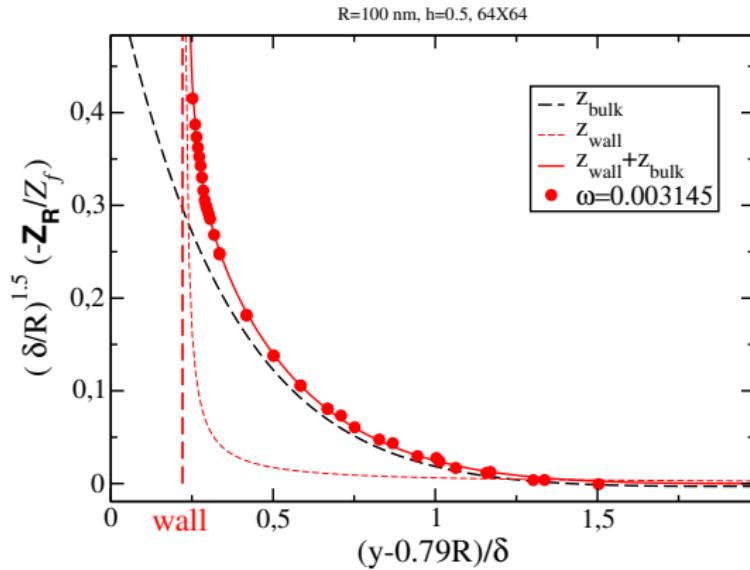
TABLE I. Parameters of the model.

COLOR CODE

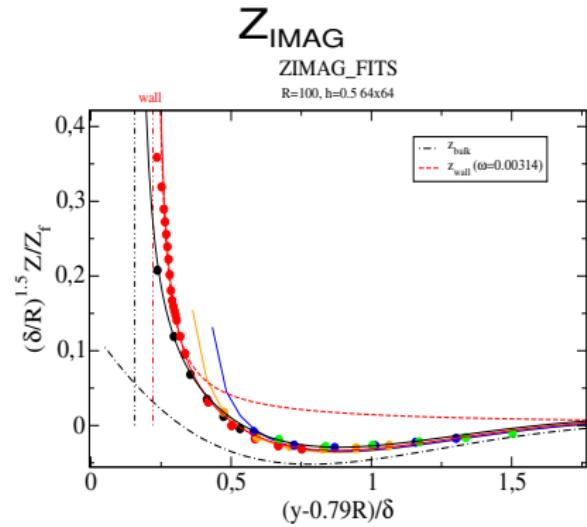
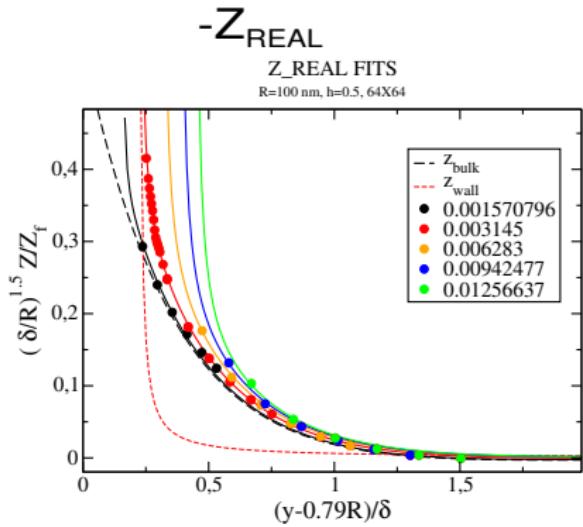
	ω	f [MHz]	δ [nm]
• BLACK	0.0015708	17.5	134.4
• RED	0.0031416	35	95
• GREEN	0.0062832	70	67.2
• BLUE	0.0094248	105	54.8
• YELLOW	0.0125664	140	47.5

Free liposomes (without DNA)

Impedance scaling with y far from wall

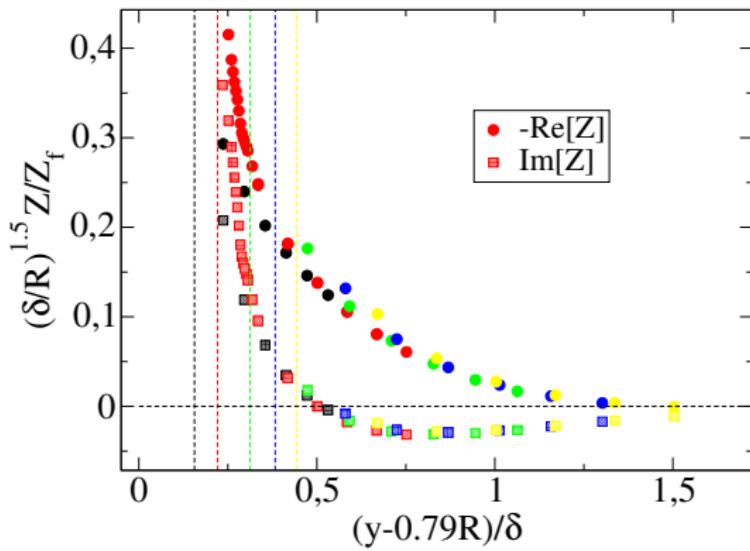


Free liposomes (without DNA)



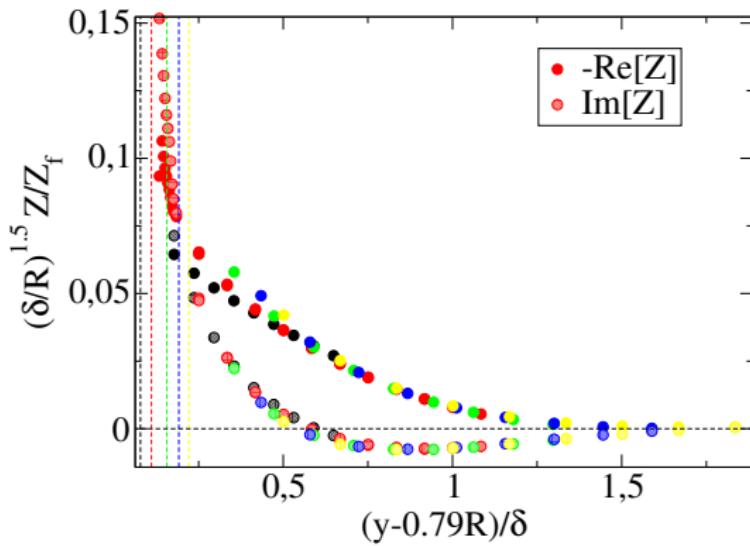
Free liposomes (without DNA)

R=100nm h=0.5 64x64



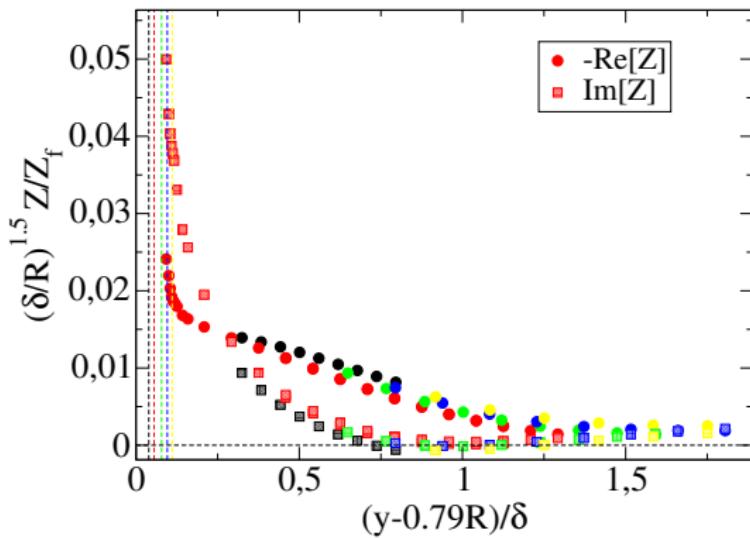
Free liposomes (without DNA)

R=50nm h=0.5 64x64



Free liposomes (without DNA)

R=25nm h=0.5 64x64

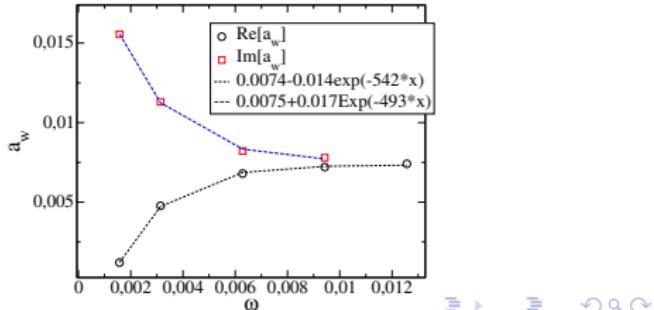


Free liposomes (without DNA)

Fits to $Z = Z(y)$, impedance relation with liposome height above surface y

$$\begin{aligned}Z(y) &= \left(\frac{R}{\delta}\right)^{1.5} \left[z_w \left(\frac{y - R}{\delta} \right) + z_b \left(\frac{y - 0.79R}{\delta} \right) \right] \\z_w(\xi) &= \frac{a_w(\omega)}{\xi} \\z_b(\xi) &= ae^{-b\xi} \cos(c\xi + d)\end{aligned}$$

	$Re[z_b]$	$Im[z_b]$
a	3.51646	0.21900
b	2.20985	1.54217
c	0.115397	1.99065
d	1.40748	0.92781



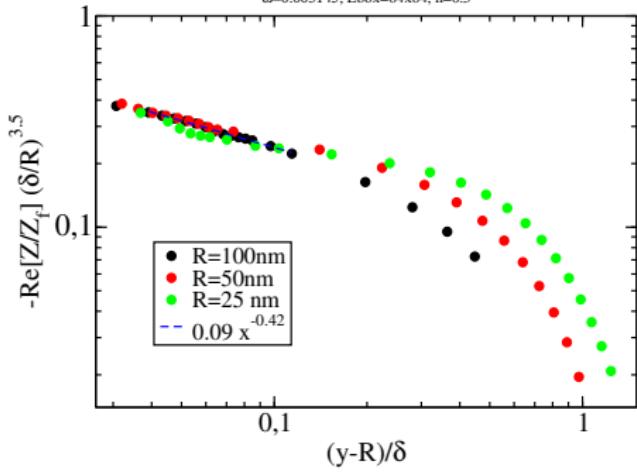
Free liposomes (without DNA)

Scaling near the wall

$$AR = -\frac{2Z_R}{Z_I} \sim R^{0.75} \text{ observed in experiments}$$

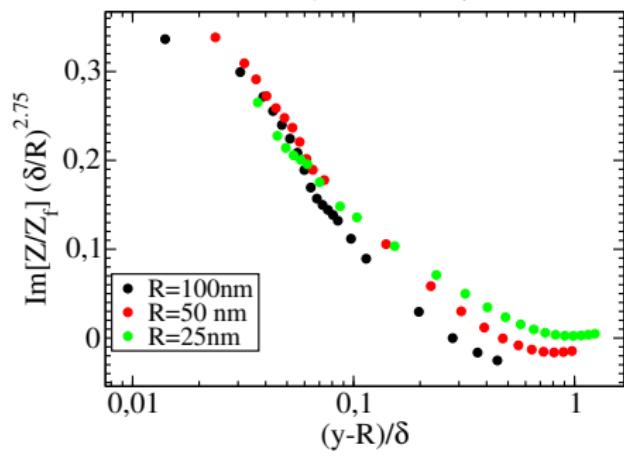
Real part

$\omega=0.003145$, Lbox=64x64, h=0.5



Imaginary part

$\omega=0.00314$, Lbox=64x64, h=0.5



Effect of DNA strand

- Z_{LIPO} . DNA constraints liposome motion and alters the perturbative flow,
 - Fluid velocity

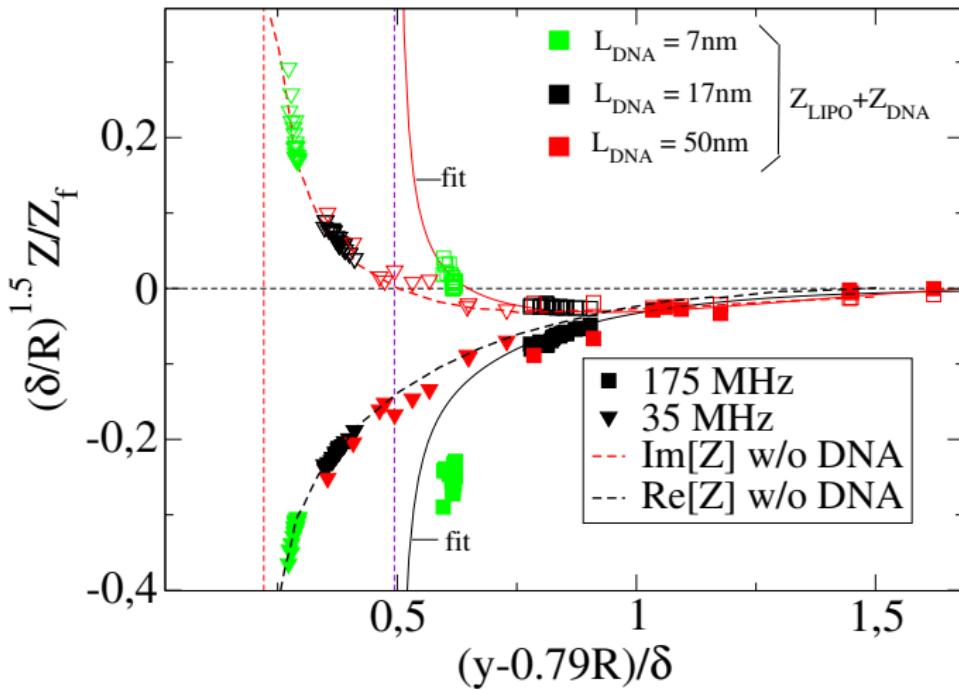
$$v = v_{\text{base}} + v_{\text{perturbation}}$$

$$\sigma = \eta \left(\frac{\partial v_{\text{perturbation}}}{\partial z} \right)_{\text{wall}}$$

- Z_{DNA} : DNA explicit stress on the surface.

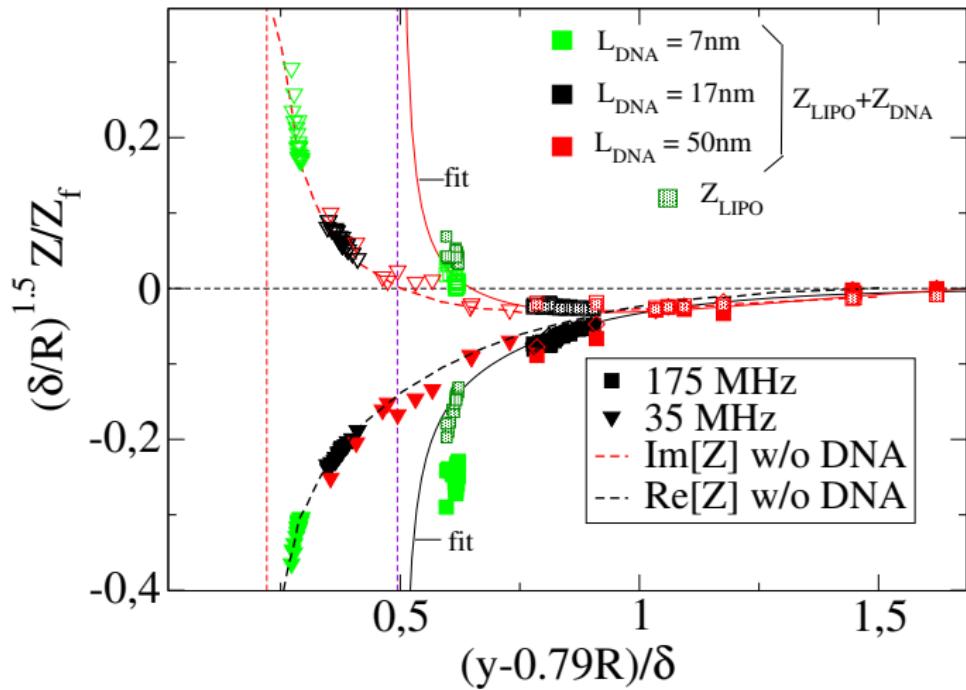
Effect of DNA strand on the impedance

$R=100\text{nm}$ $h=0.5$ 64×64

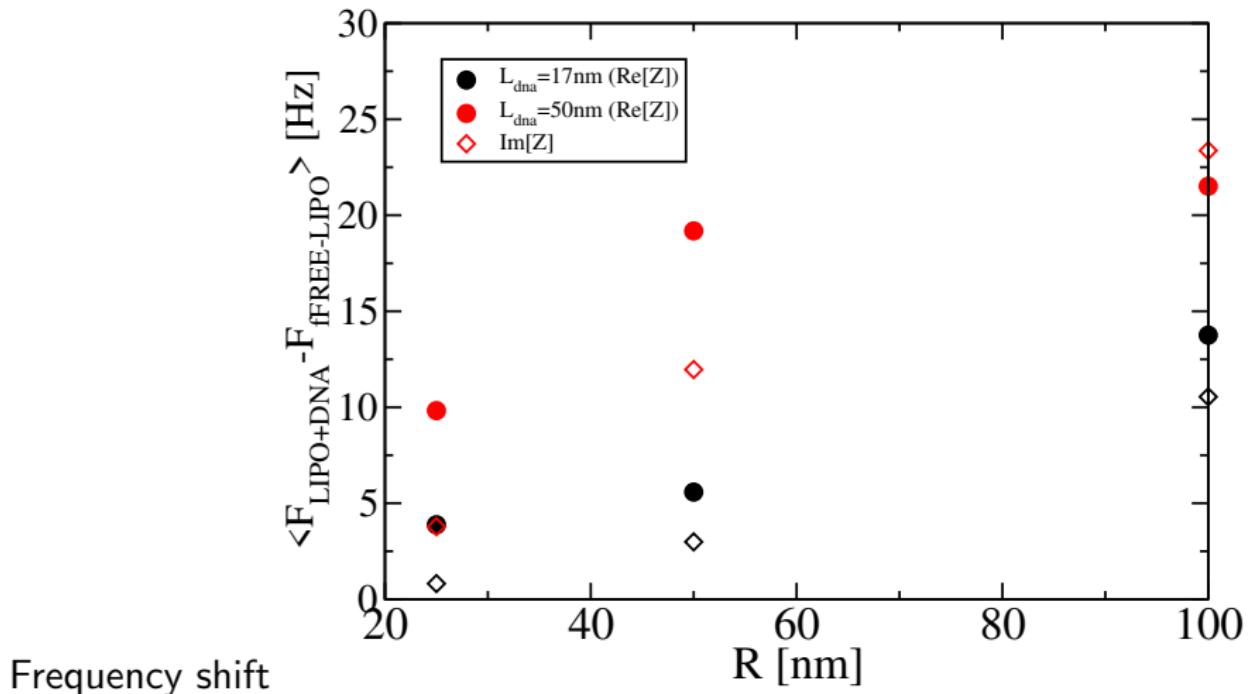


Effect of DNA strand on the impedance

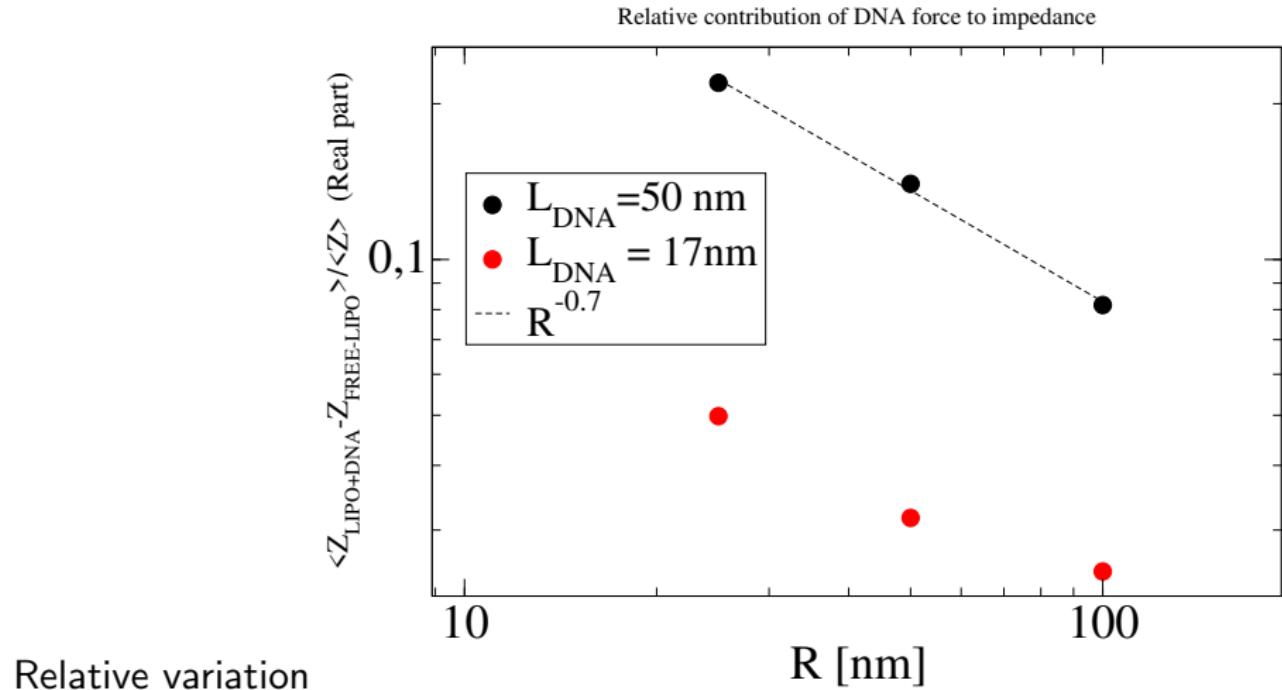
$R=100\text{nm}$ $h=0.5$ 64×64



Effect of DNA strand on the frequency shift and impedance

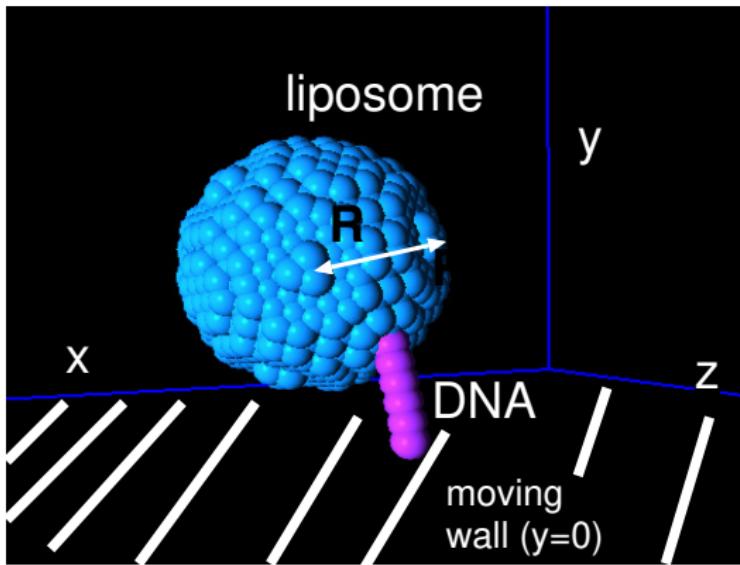


Effect of DNA strand on the frequency shift and impedance



Bending rigidity of the liposome

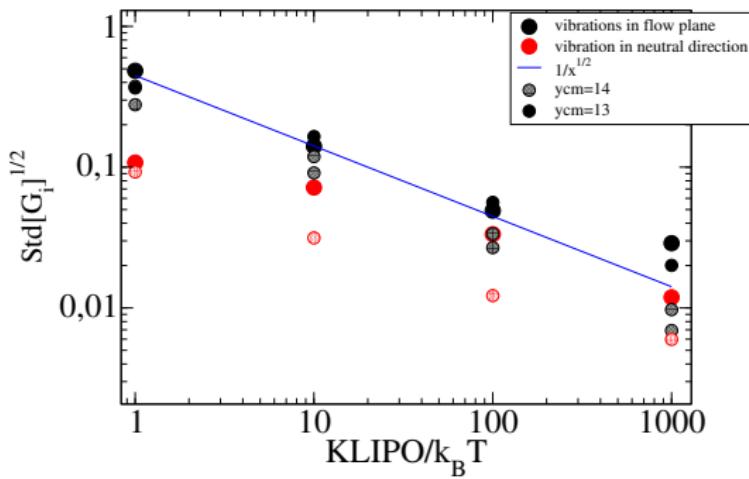
- Modelled using the elastic network model: spring between neighbours liposome beads κ_{LIPO} (the effective κ_{BEND} needs to be calibrated)



Bending rigidity of the liposome

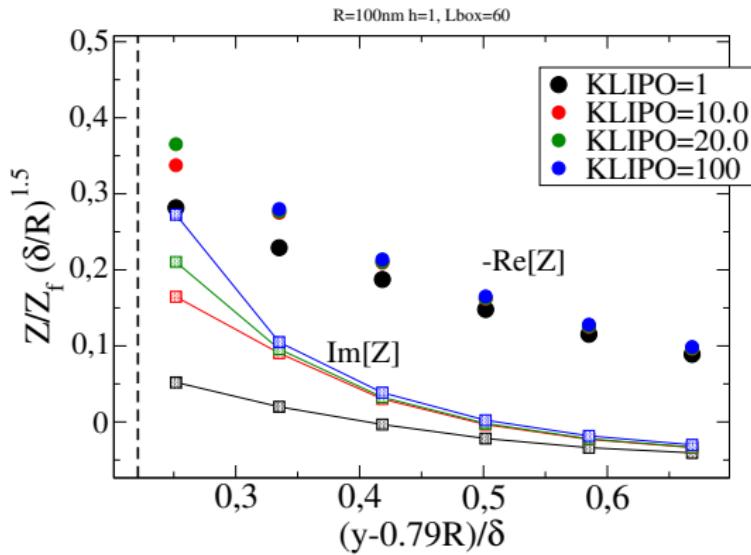
- The liposome membrane vibrates more easily as $\downarrow \kappa_{\text{LIPO}}$
 $\downarrow \kappa_{\text{LIPO}} \implies \downarrow \text{impedance}(Z)$

Fluctuations of eigenvalues of liposome gyration tensor (prism)
noDNA Lbox=32, h=1, R=100nm y= ?



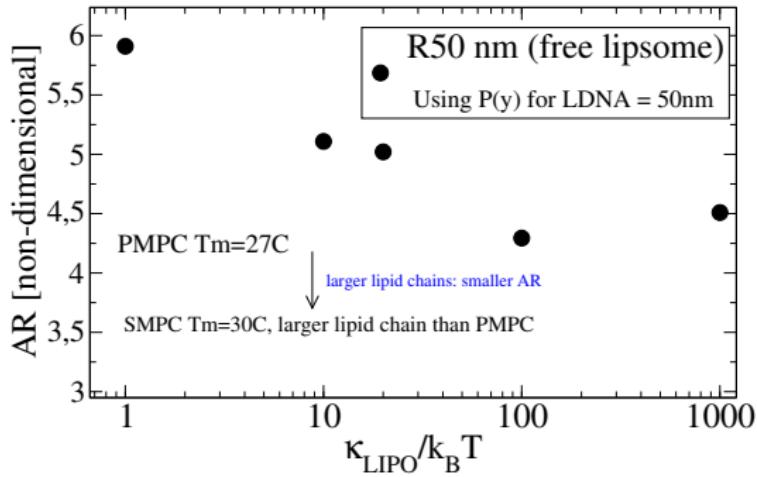
Bending rigidity of the liposome

- But as $\uparrow \kappa_{\text{LIPO}}$ frequency shift $Im[Z]$ increases more than dissipation $-Re[Z]$.



Bending rigidity of the liposome

- **Fact:** Liposome bending rigidity increases with lipid length.
- **Experiments:** AR decreases with lipid length (for similar T_m).
- **Theory and experiments in qualitative agreement**

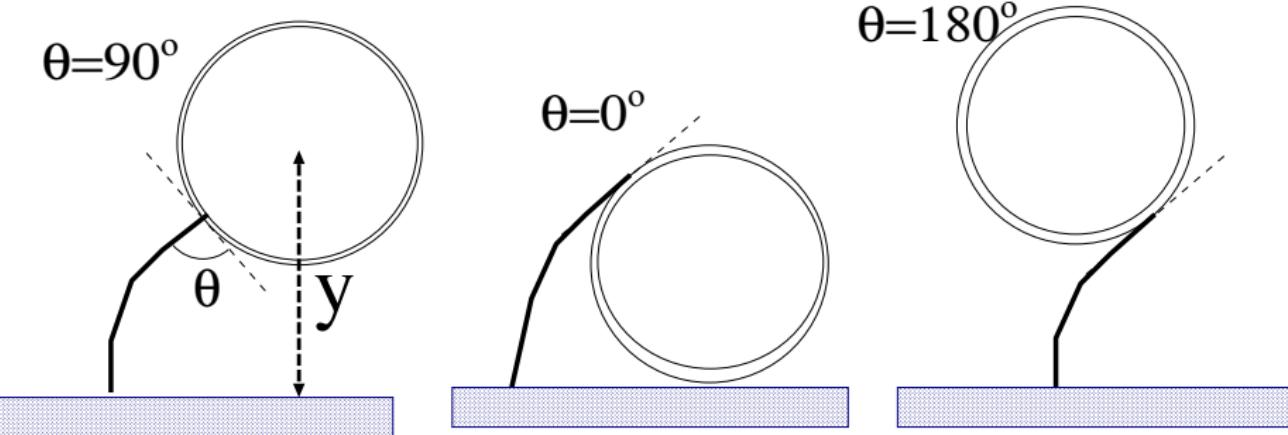


DNA-LIPOSOME molecular link

DNA-Liposome link affects the liposome height y above the surface, $P(y)$.

Modelled by bending energy $\kappa_{\text{DNA-LIPO}}$

$$P_\theta(\theta) = \exp[-\kappa_{\text{DNA-LIPO}} (\theta - 90^\circ)^2]$$

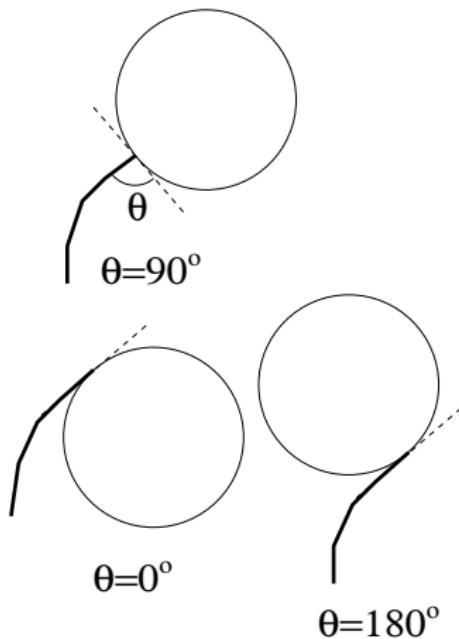
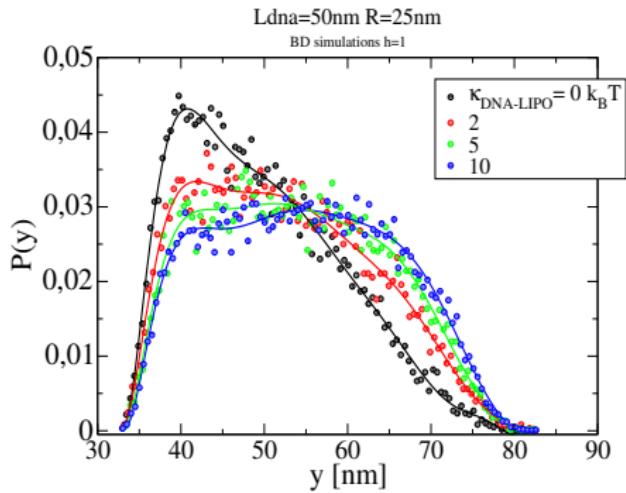


$$\kappa_{\text{DNA-LIPO}} \gg k_B T$$

$$\kappa_{\text{DNA-LIPO}} \sim 0 k_B T$$

DNA-LIPOSOME molecular link

DNA-Liposome link affects the liposome height y above the surface, $P(y)$.
Modelled by bending energy $\kappa_{\text{DNA-LIPO}}$

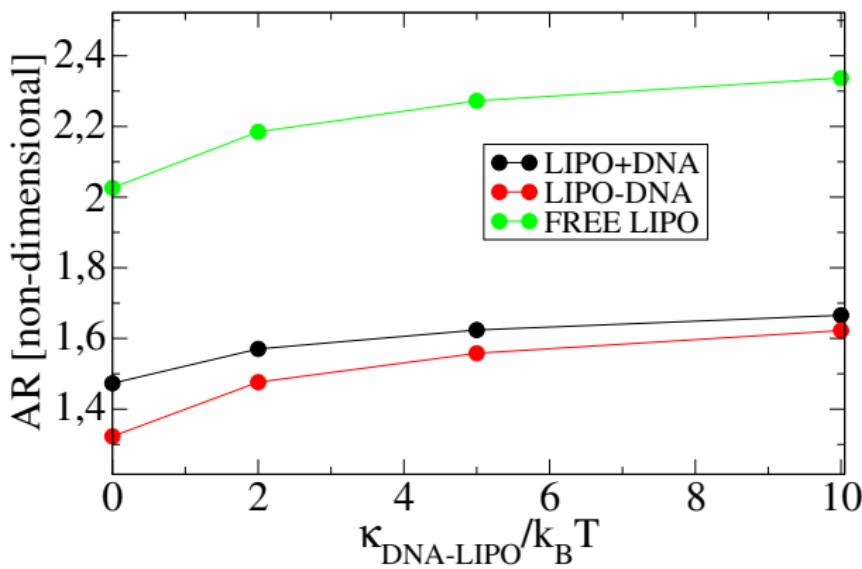


DNA-LIPOSOME molecular link

DNA-Liposome link affects the liposome height y above the surface, $P(y)$.

AR saturates at large κ_{DNALIPO}

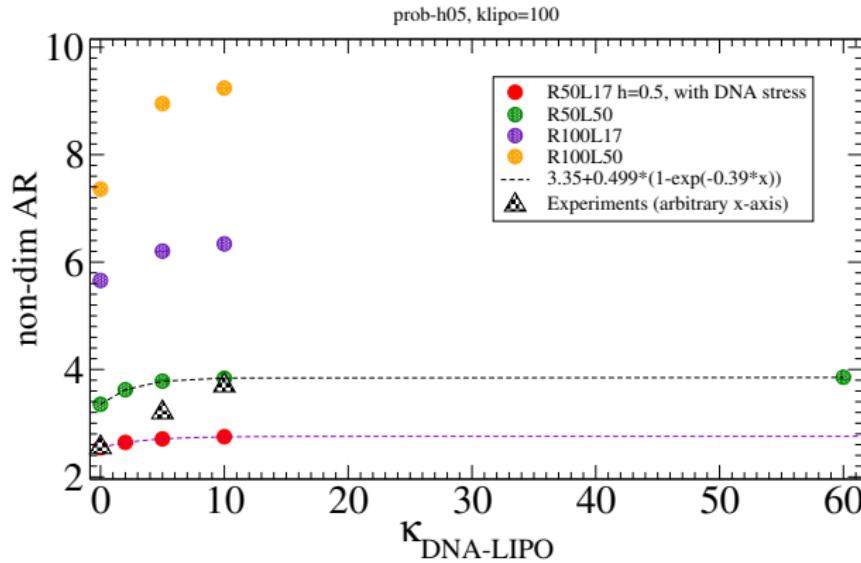
$R=25\text{nm}$, $h=0.5$, $L_{\text{box}}=64$, $L_{\text{DNA}}=50\text{nm}$



DNA-LIPOSOME molecular link

DNA-Liposome link affects the liposome height y above the surface, $P(y)$.

Just qualitative agreement with experiments; AR increases with $(T - T_m)$
(larger in gellified lipid phase)



- Reproduce the experimental acoustic ratio ✓
- Predict QCM response at higher frequencies ✓
 - Divergence of AR induced by hydrodynamics (feasible for $R = 100\text{nm}$)
- Predict the relation between lipid coverage and Δf and $\Delta \Gamma$ (Soon)
- Effect of **liposome bending rigidity** ✓
 - Number of carbons in lipid chains (quantitative analysis yet to be done)
 - Membrane in fluid/gel phase (microscopic relation with the **stiffness of the DNA-Liposome link?**)
- Propose ways to increase the dissipation and the AR
 - Increase the liposome height \implies increase AR (electric fields?, modifying ph?)
 - Numerical estimation of coverage $\Delta f(\phi)$ permits calibration with larger impedance complex \implies (working with smaller DNA strands)
 - Other ideas ready to be tested

Thanks for your attention