Myocardial Blood Flow:
The Science

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Disclosures

- Siemens – Research Funding and Speaker Honorarium

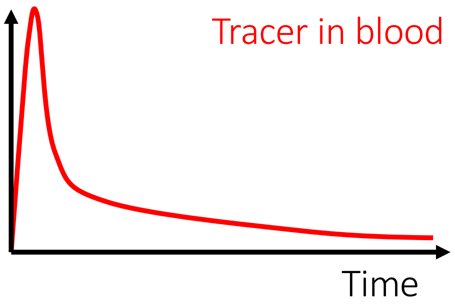
MBF : the principle

- Myocardial Blood Flow is the absolute measurement of tracer flow from the blood into the myocardium
- Both quantities are measured from the PET images

Available tracer

Tracer circulating in the blood

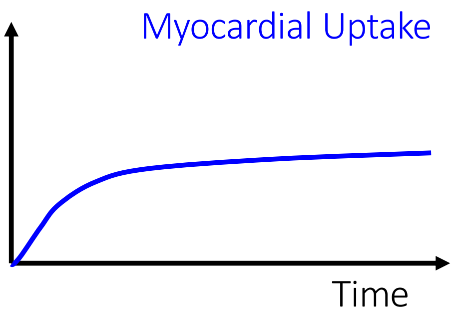
(referred to as the **Blood Input**)



Myocardial uptake

Tracer in the myocardium

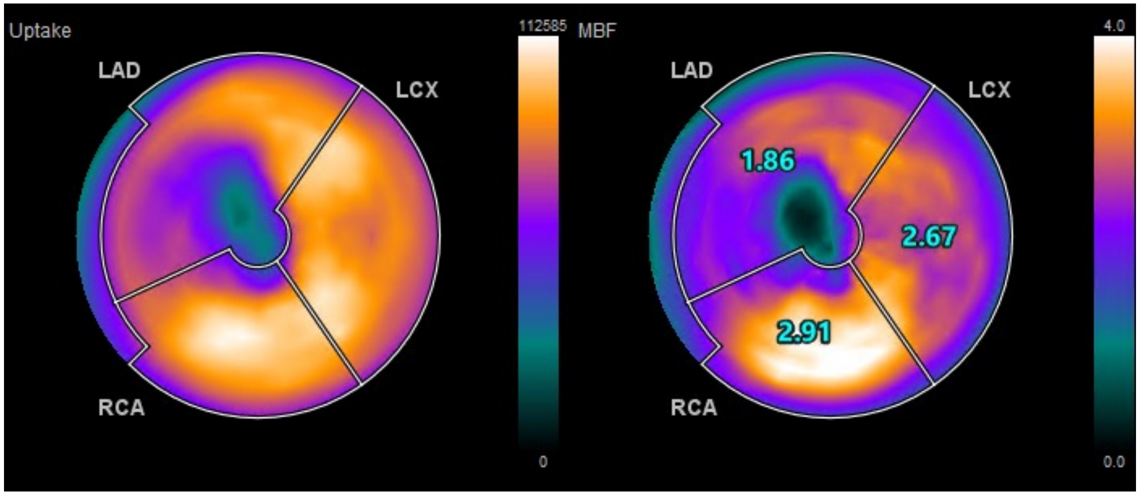
(referred to as the **Uptake**)



MBF vs relative perfusion

- Static relative perfusion images is a mix of uptake and retention
- MBF is only uptake – it shows greater contrast
- Take home : the appearance of relative perfusion and MBF should be similar. Any defects should be matched, albeit with greater contrast on MBF

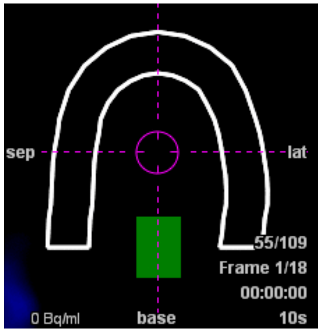
Rel. perf.

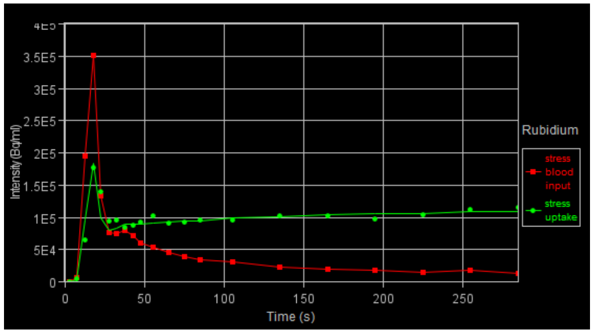


MBF

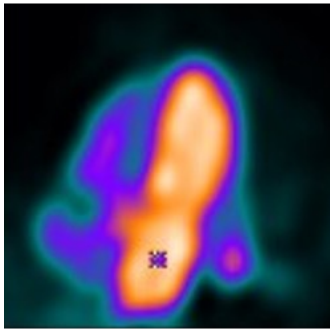
The two approaches

- Single tissue compartmental model
  - Multi-frame dynamic PET reconstruction
  - Regions on **every** frame
  - Creates a model of the tracer uptake

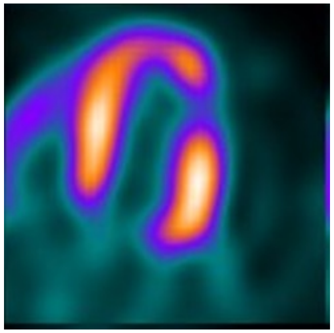




- Simplified retention model
  - Blood and uptake images
  - Assumes all tracer in blood is trapped in myocardium



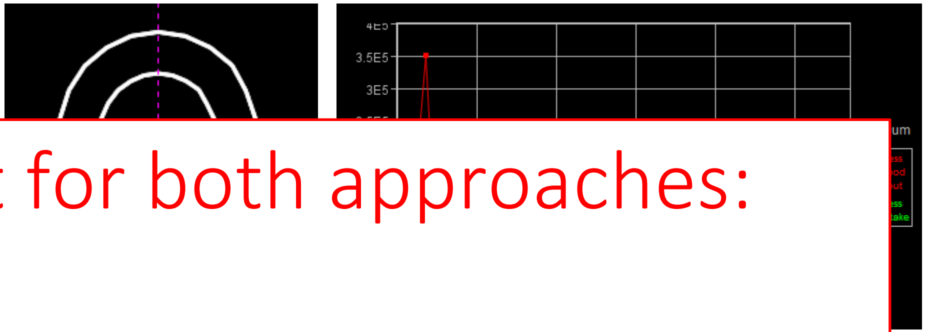
Tracer in blood
(early phase)



Tracer in myocardium
(late phase)

The two approaches

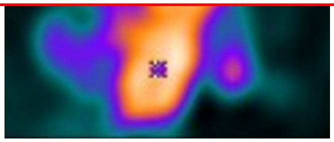
- Single tissue compartmental model
  - Multi-frame dynamic PET



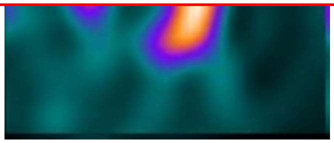
The critical requirement for both approaches:

Complete and accurate measurement
of blood and myocardial tracer

myocardium



Tracer in blood
(early phase)



Tracer in myocardium
(late phase)

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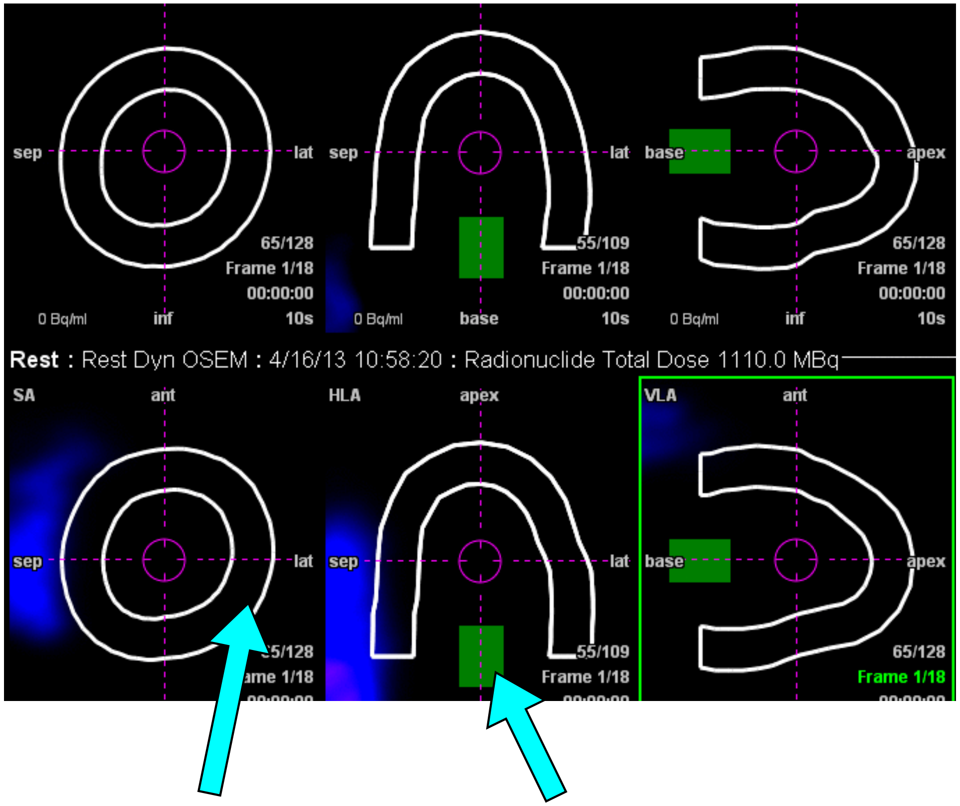
Single tissue compartmental model

Single tissue compartment model

- Create a dynamic reconstruction of varying frame times
- Define two regions: blood and LV
- In **every frame** measure:
  - The blood activity concentration (C_A)
  - The myocardial activity concentration (C_{LV})



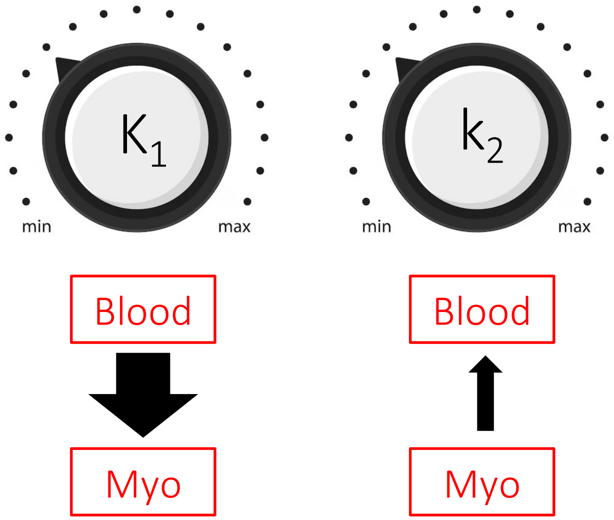
LV region

Blood region

Single tissue compartment model

In every dynamic frame:

- Measure the blood activity concentration (C_A)
  - Used to produce the **blood input**
- Measure the myocardial activity concentration (C_{LV})



Blood
Myo

Blood
Myo

Two model parameters (rate of tracer transfer):

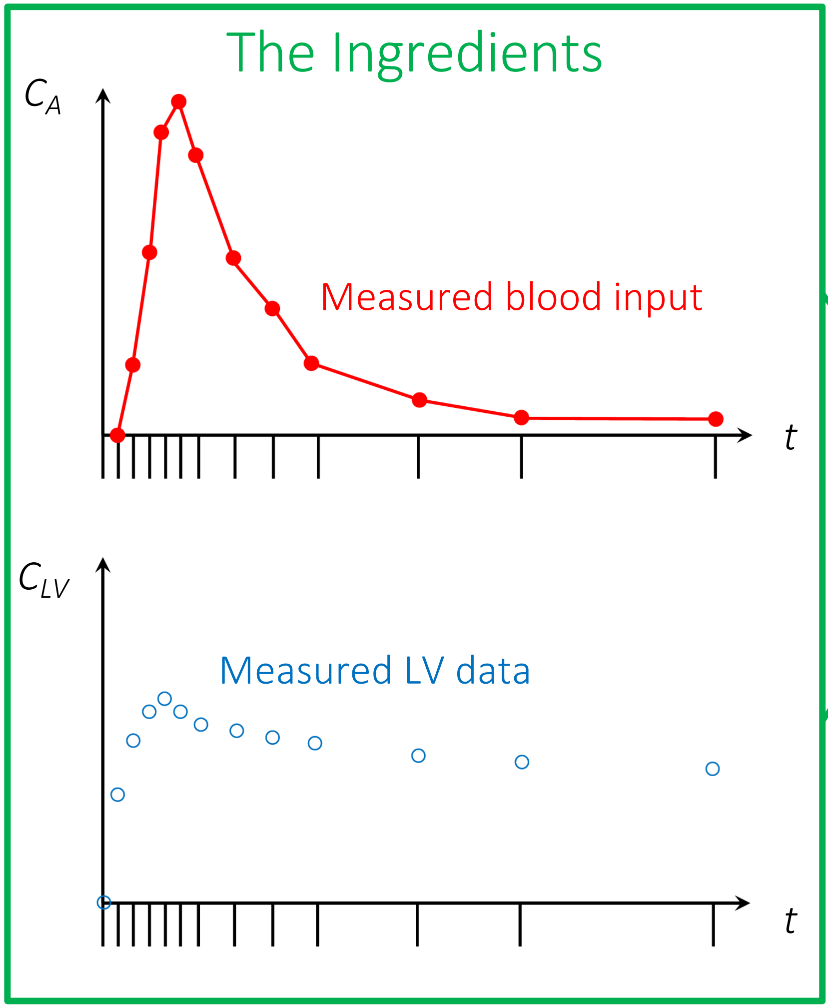
- K_1 : uptake into myocardium (determines MBF)
- k_2 : washout of tracer back into the blood

Each choice of K_1 and k_2 will produce a theoretical model of what the activity concentration in the LV will be in each frame

- Feed in the blood input curve and keep adjusting the parameters until the model LV curve matches the measured data

Single tissue compartment model – the recipe

The Ingredients

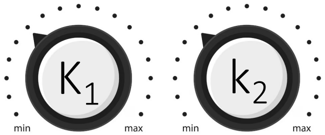


Model

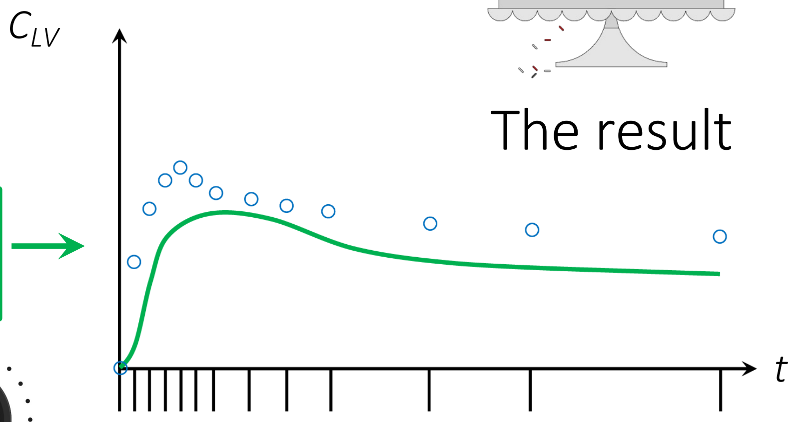
$$C_{LV}(t) = K_1 \int_0^t C_A(t) e^{-k_2(t-\tau)} d\tau$$

Adjust

K_1 and k_2



The oven



The result

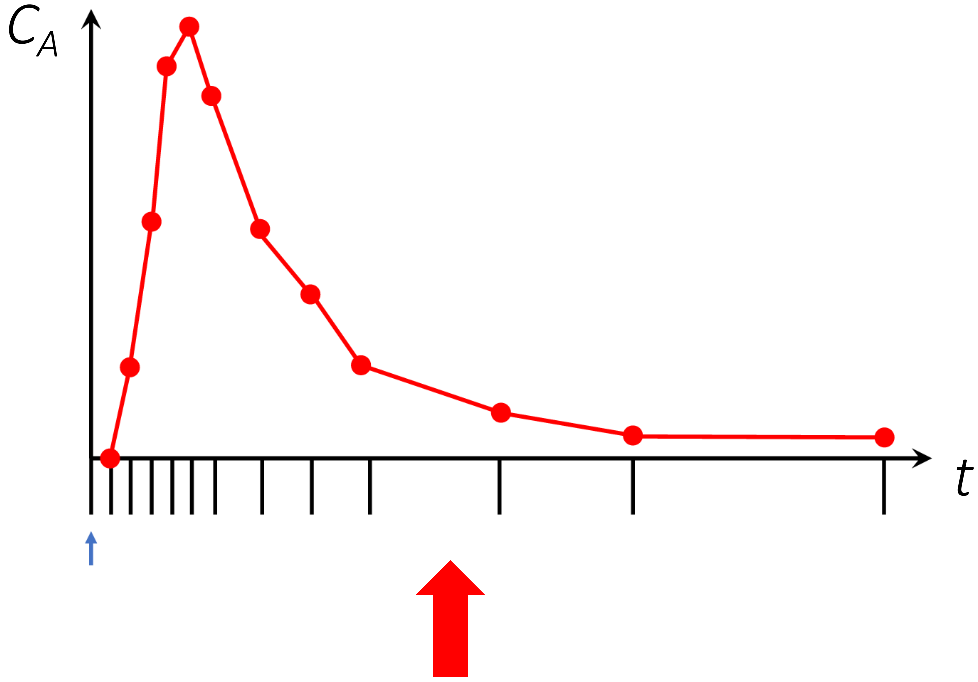
Find the parameters that fit the model to the measured data

The blood input – the golden rules

At each time point the area under the blood input curve is integrated from the beginning of the scan

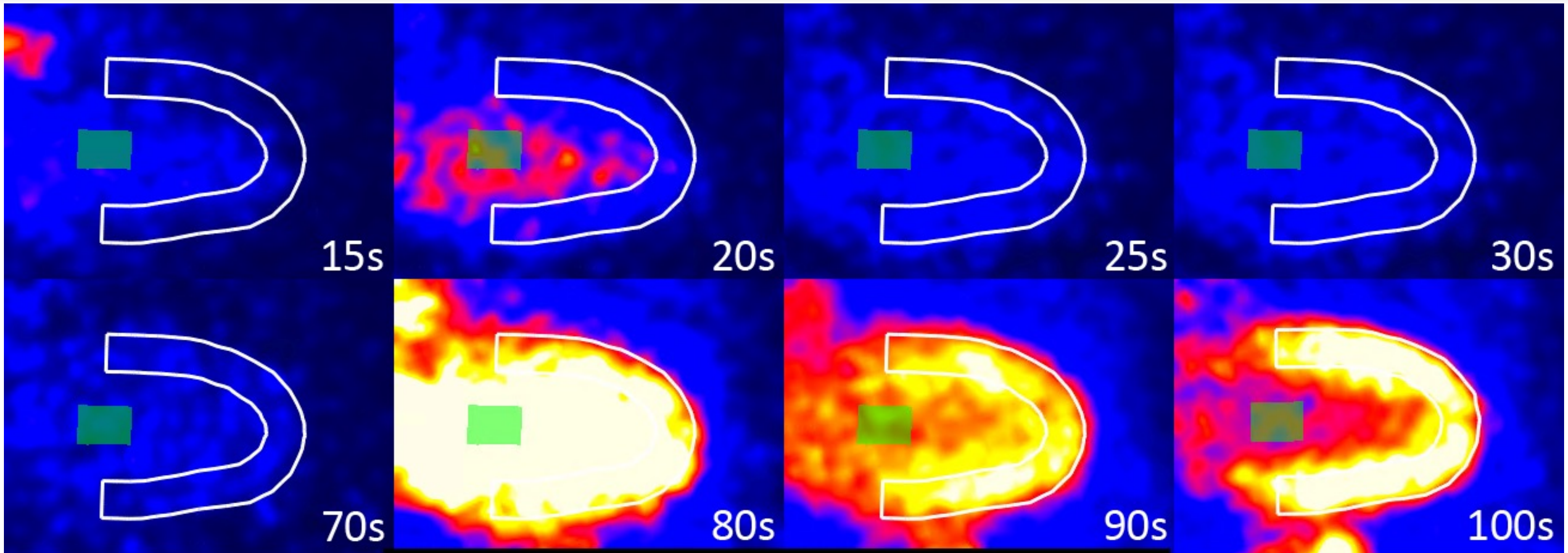
1. The region must remain in the blood for every frame
2. The shape of the blood curve does not matter for single tissue compartmental model
3. It must start from zero

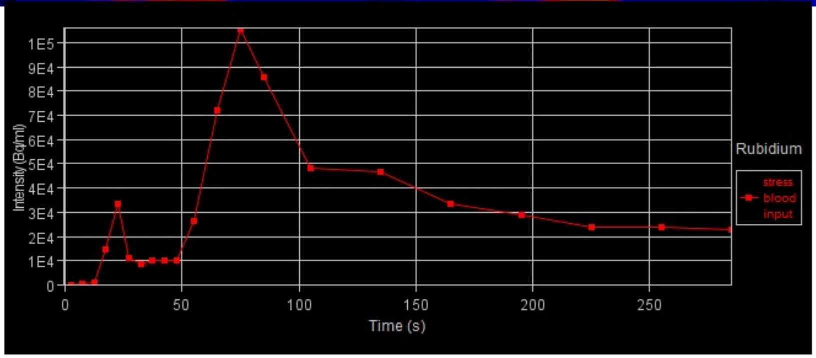
   unless doing residual activity correction – relevant for ammonia and flurpidaz



$$C_{LV}(t) = K_1 \boxed{\int_0^t C_A(t)} e^{-k_2(t-\tau)} d\tau$$

The blood input





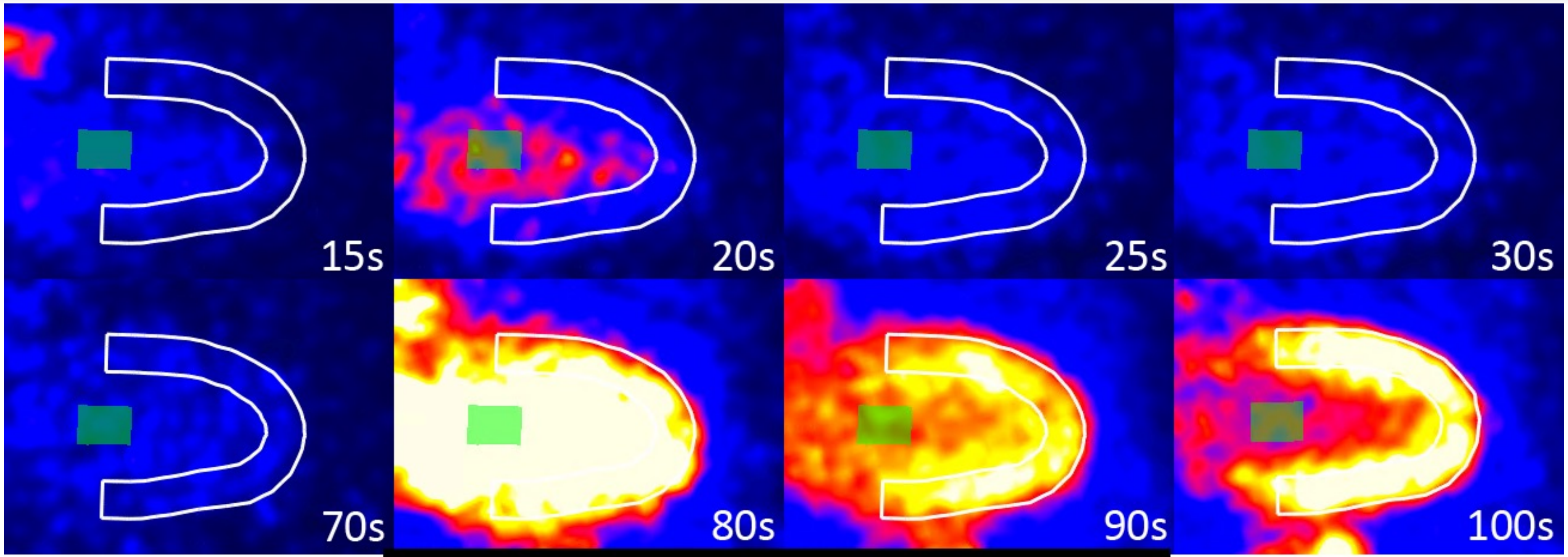
QC checks:

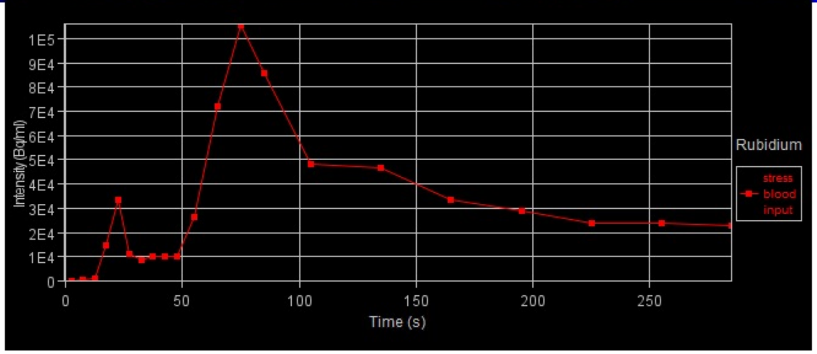
1, ROI in right place ✓

2, Captured beginning ✓

3, No motion ✓

The blood input





QC checks:

1, ROI in right place ✓

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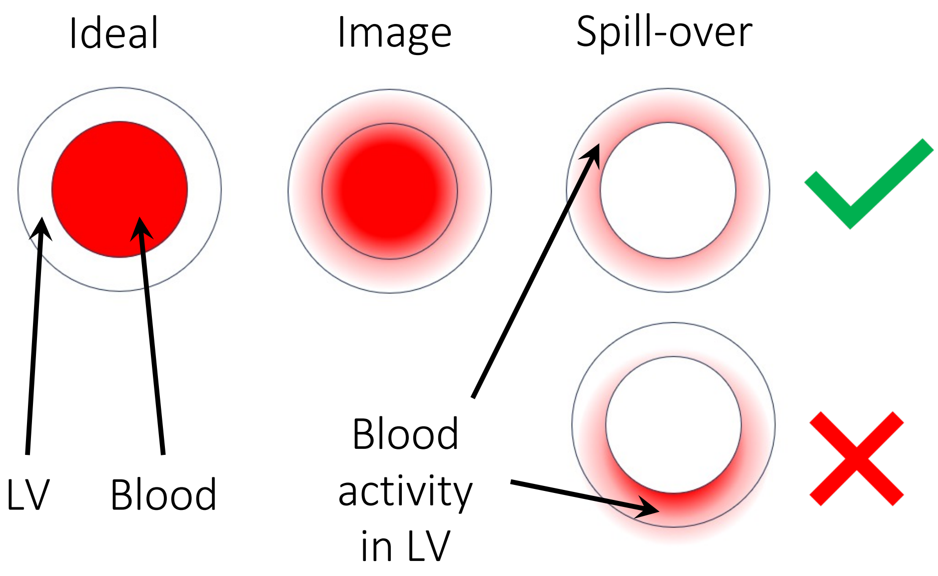
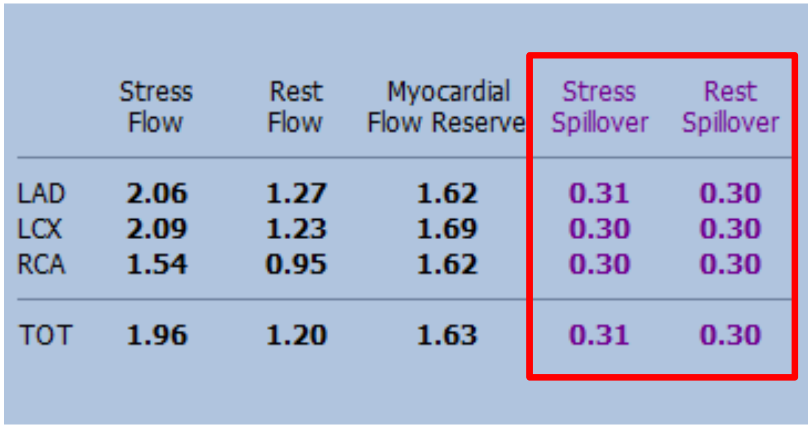
3, No motion ✓

This blood curve is OK!

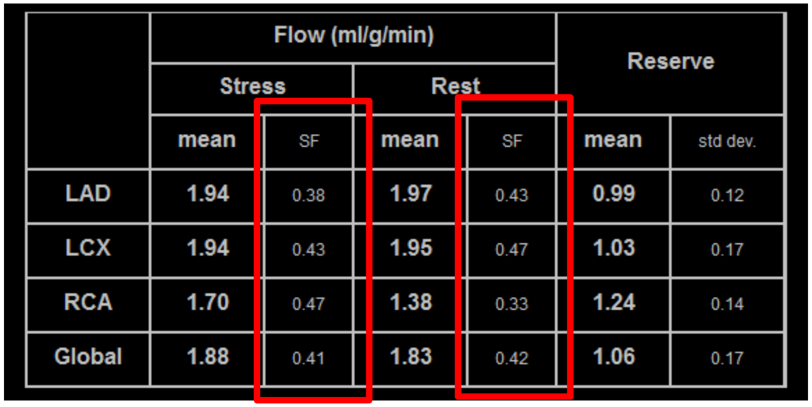
“Spillover” – what is it?

- A lot of software packages report this
- Measure of blood activity that is (incorrectly) present in the LV region
- Most relevant in early phase





	Stress Flow	Rest Flow	Myocardial Flow Reserve	Stress Spillover	Rest Spillover
LAD	2.06	1.27	1.62	0.31	0.30
LCX	2.09	1.23	1.69	0.30	0.30
RCA	1.54	0.95	1.62	0.30	0.30
TOT	1.96	1.20	1.63	0.31	0.30



	Flow (ml/g/min)				Reserve	
	Stress		Rest			
	mean	SF	mean	SF	mean	std dev.
LAD	1.94	0.38	1.97	0.43	0.99	0.12
LCX	1.94	0.43	1.95	0.47	1.03	0.17
RCA	1.70	0.47	1.38	0.33	1.24	0.14
Global	1.88	0.41	1.83	0.42	1.06	0.17

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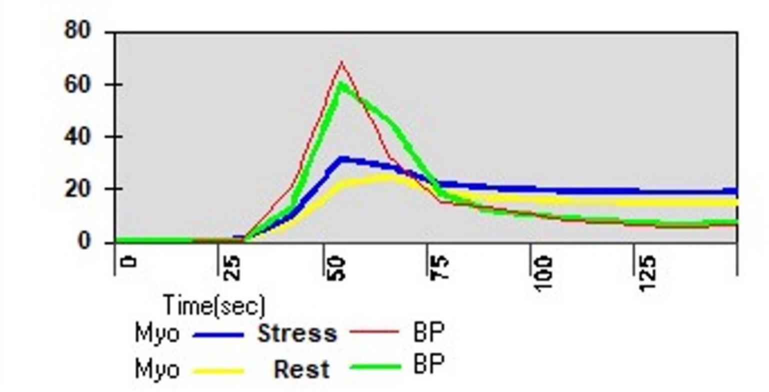
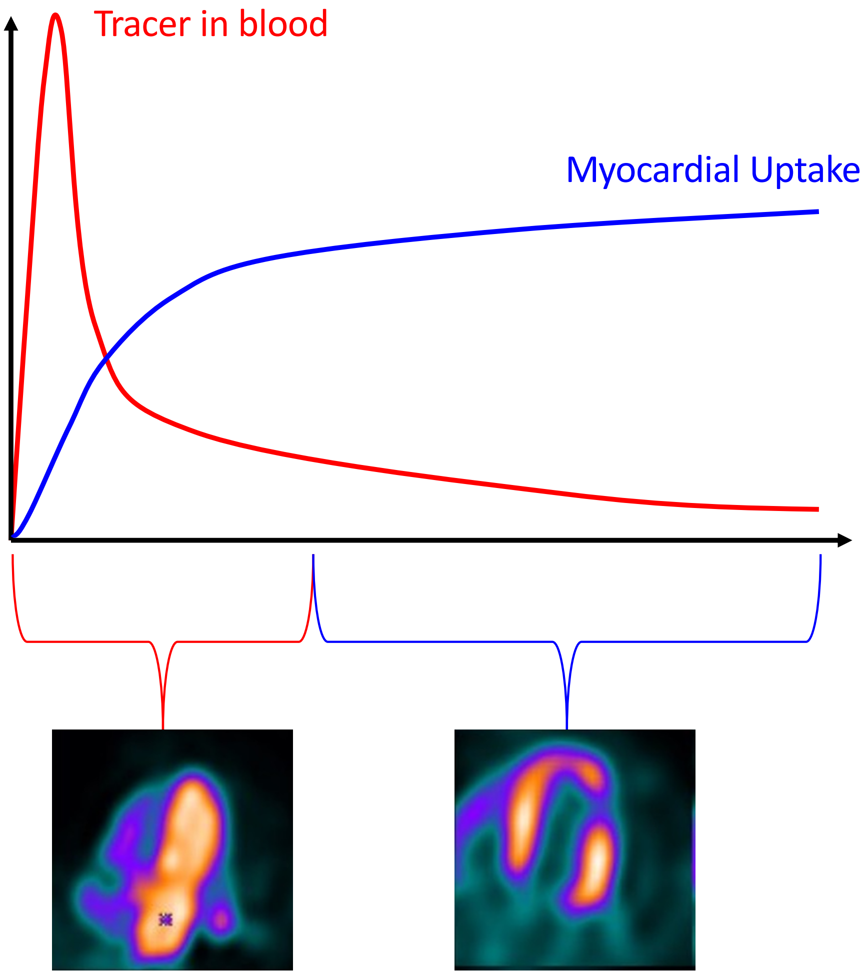
Simplified retention model

Simplified Retention Model

- The SRM is a simplification of the single tissue compartment model
- The blood input and uptake are distilled down into two images
- Some software accepts dynamic reconstruction and sums frames to these two images





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QC checks

QC summary

- Three main things that will compromise MBF

1, Missing the start of the infusion

2, Incorrect region placement / segmentation failures

3, Motion

4, Poor model fit (attributed to all of the above)*

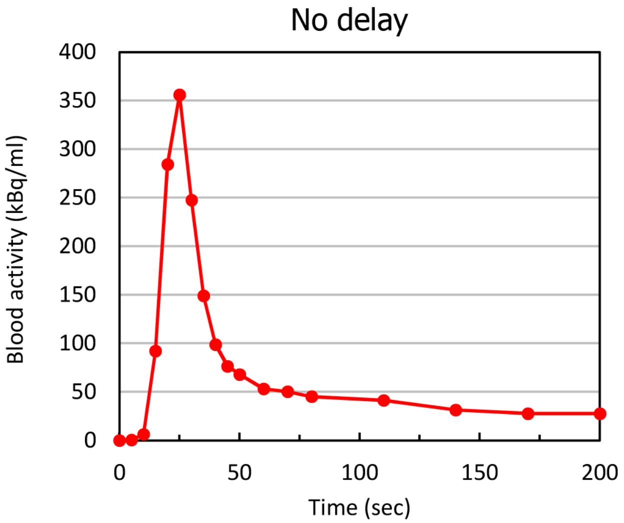
*For single tissue compartmental model

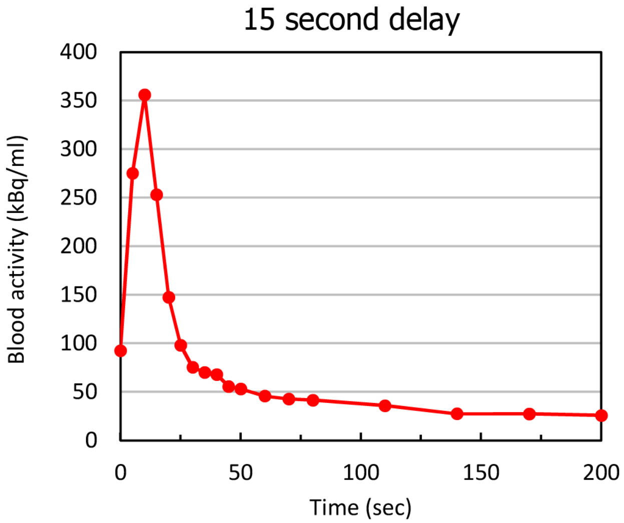
Error in blood input

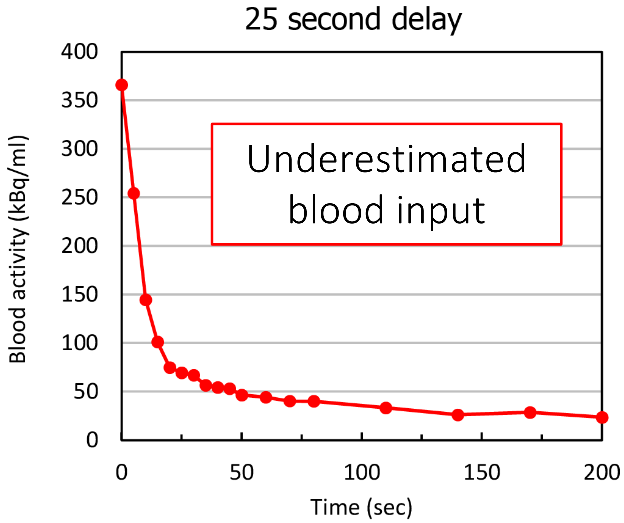
Underestimate blood input

Overestimate MBF

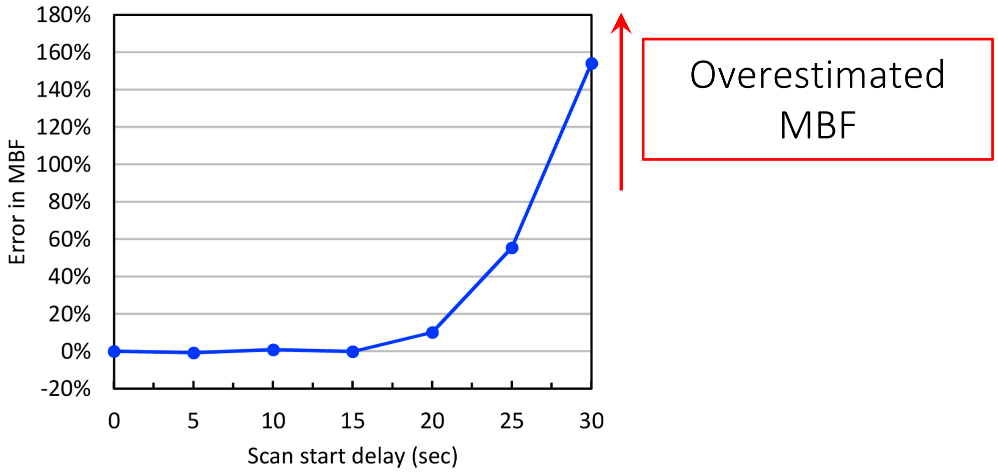
Error in blood input





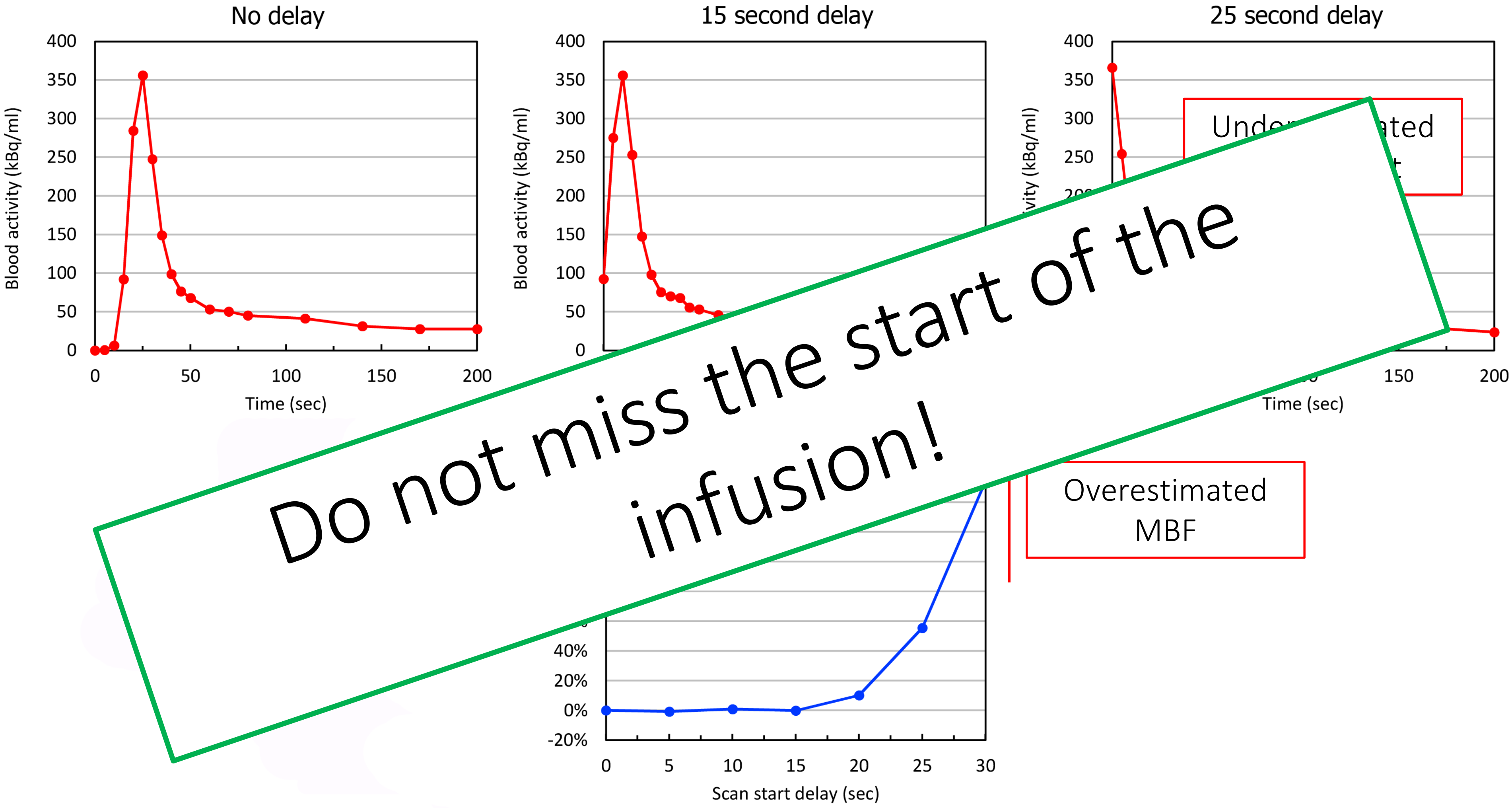


Underestimated blood input



Overestimated MBF

Error in blood input



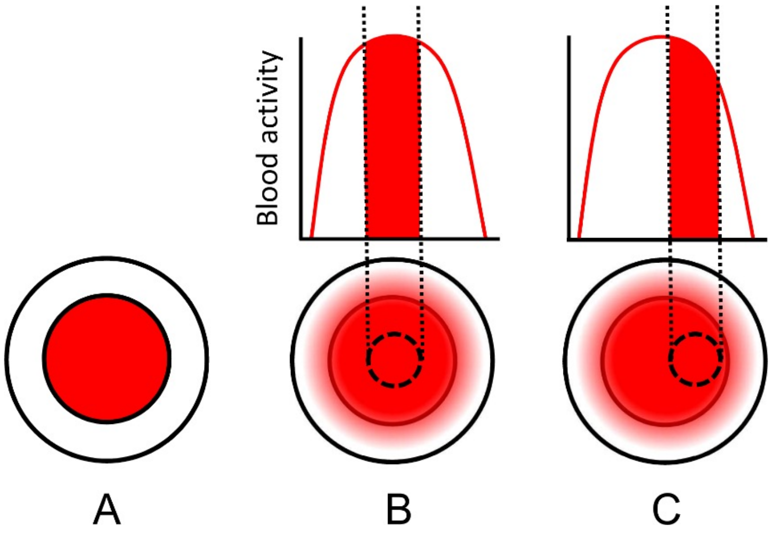
Under ated
t

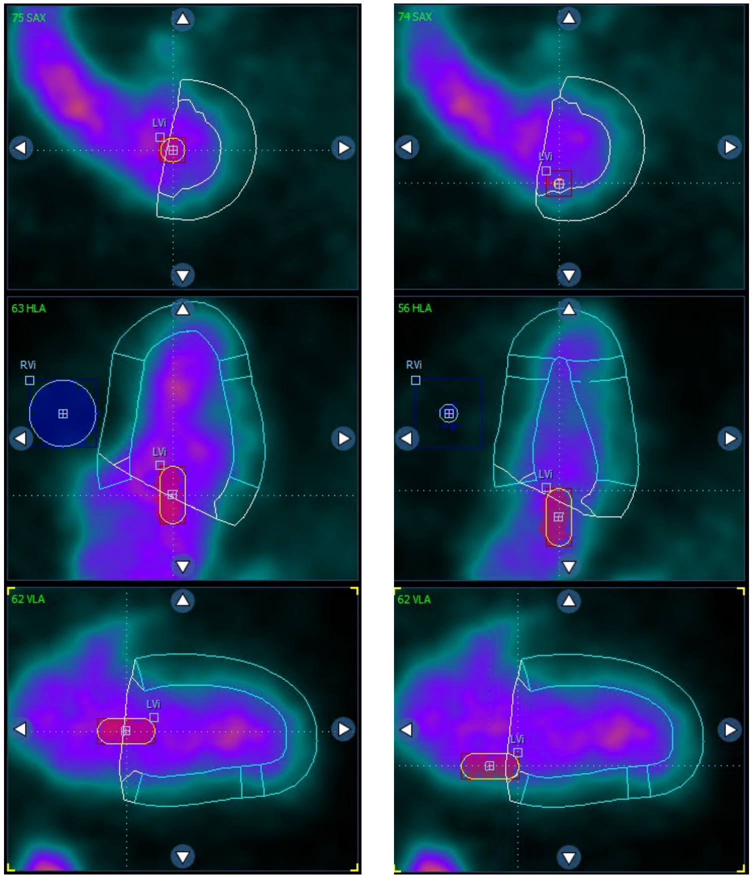
Overestimated
MBF

Do not miss the start of the infusion!

Blood region placement

- The input region should be placed centrally in the cavity
- If it is offset, BIF will be underestimated



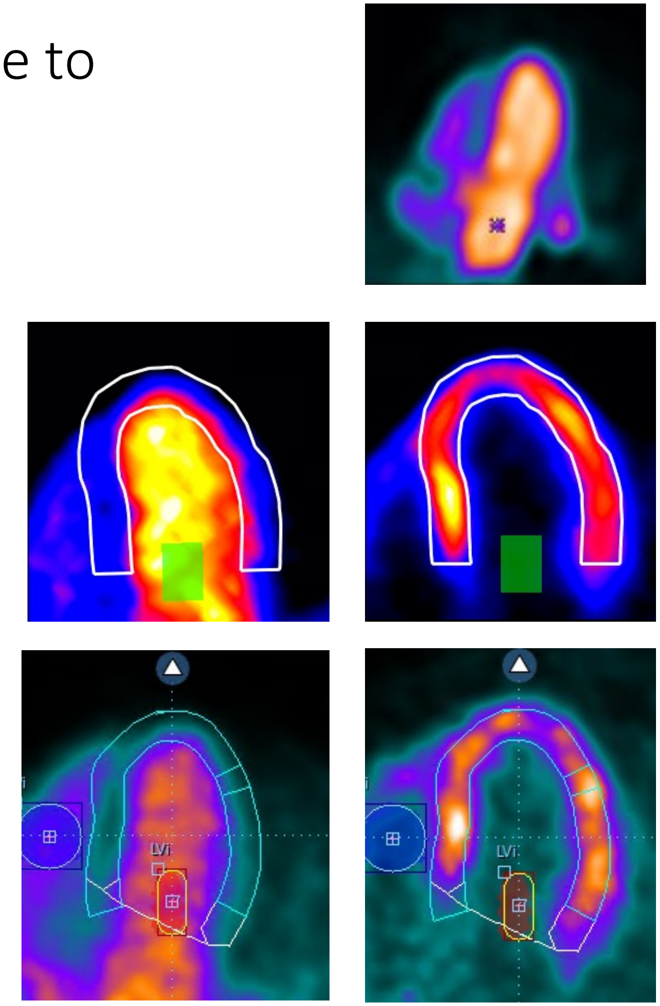


1.34 ✓

1.60 ✗

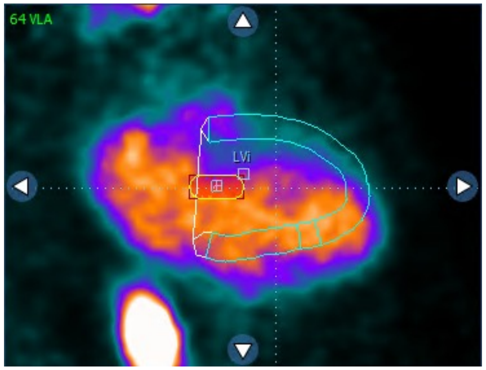
Blood region placement – know your software

- Each software package has requirements on where to place the blood input region
- Positioning may be fully or semi-automatic
- Proceed with care if adjusting
- Position must be consistent for stress and rest
- For dynamic data, look at each frame

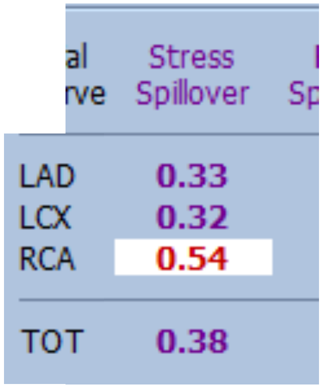


Motion – spillover (dynamic images)

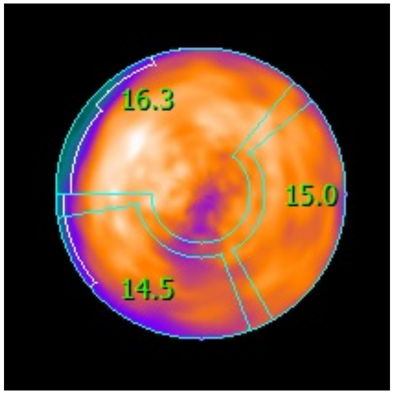
- For dynamic images, early motion can put the blood in the wrong place
- Blood can go in LV region
- This will get MBF wrong!
- Can see mis-match in relative perfusion and MBF
- Motion correction is available on most software



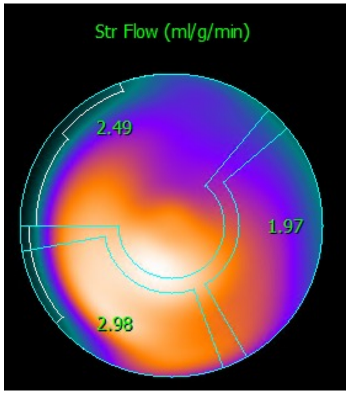
Frame 7 : 30 seconds



al rve	Stress Spillover	Sp
LAD	0.33	
LCX	0.32	
RCA	0.54	
TOT	0.38	



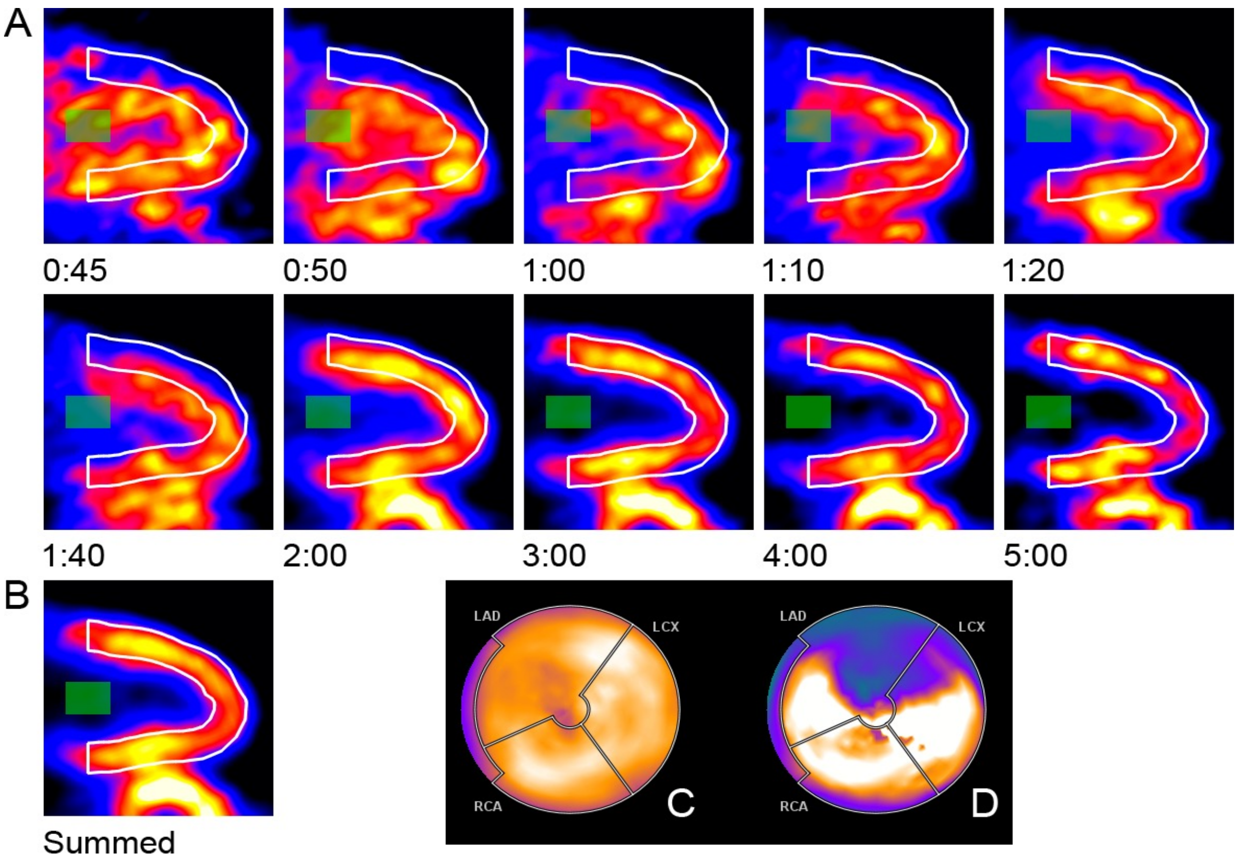
Perfusion



MBF

Motion – uptake errors (dynamic images)

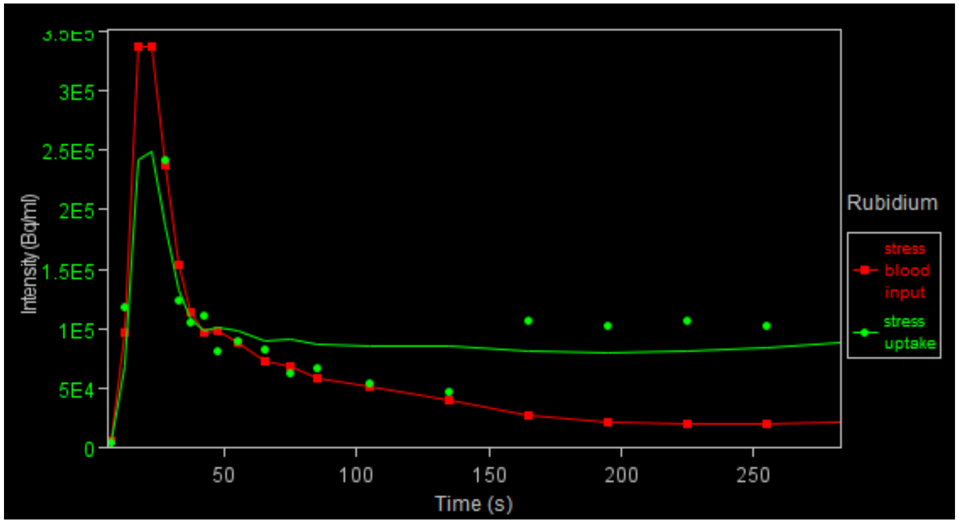
- LV segmentation error will cause underestimation of MBF in the affected area
- This can lead to a mis-match in the relative perfusion and MBF polar maps
- Motion correction is available on most software



Perfusion

MBF

Model fit



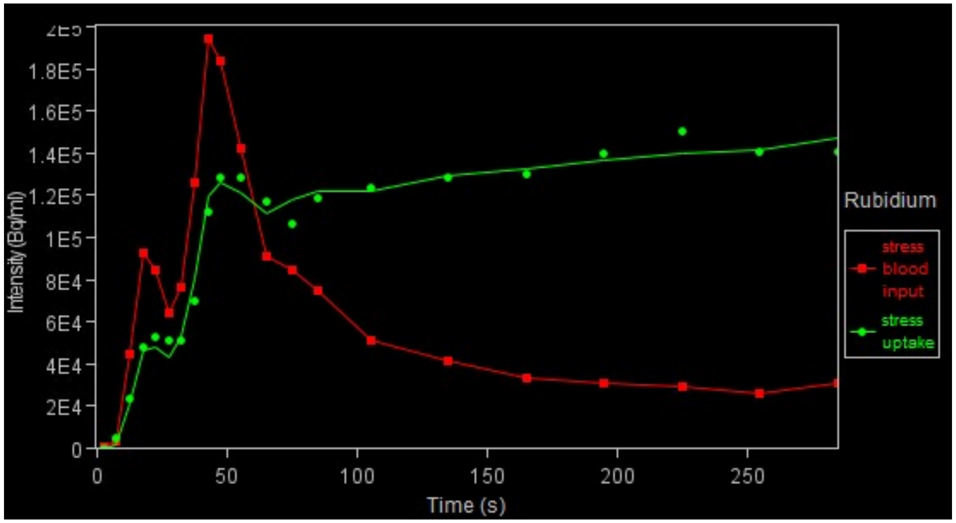
QC checks:

1, LV ROI failures on some frames ✗

2, Captured beginning ✓

3, Motion ✗

4, Poor model fit ✗



QC checks:

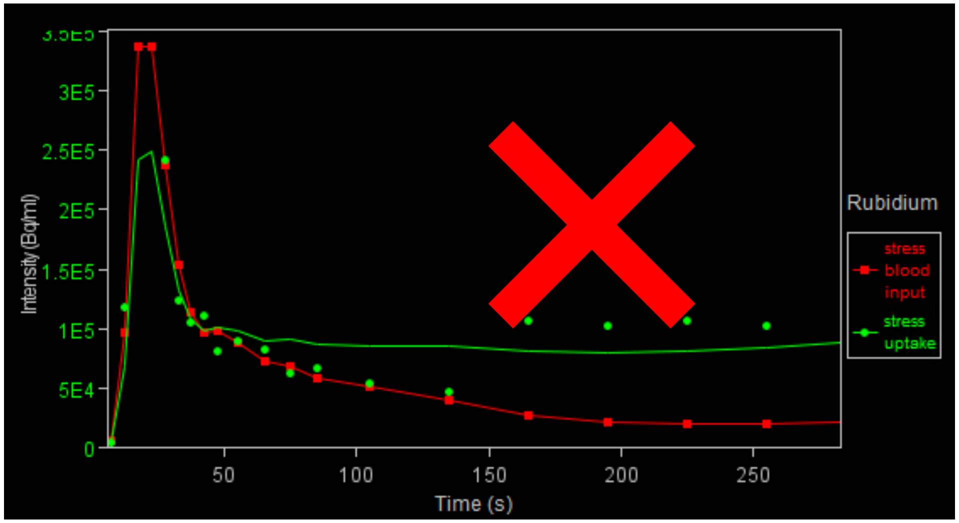
1, ROI in right place ✓

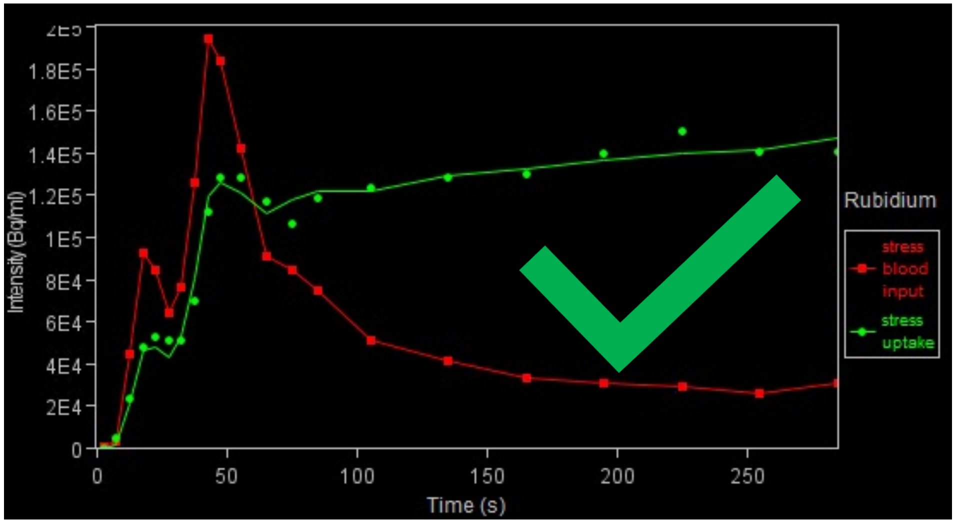
2, Captured beginning ✓

3, No motion ✓

4, Good model fit ✓

Model fit





QC checks:

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4, Poor model fit ✗

QC checks:

1, ROI in right place ✓

2, Captured beginning ✓

3, No motion ✓

4, Good model fit ✓

Summary and take-home points

- MBF is robust
- Two approaches
  - Single tissue compartmental model
  - Simplified Retention Model
- Provided QC steps are followed, numbers are reliable
  - ROIs in right place
  - Captured beginning of scan
  - No motion (or at least corrected)
    - Even spillover
  - Good model fit

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Thanks for listening

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