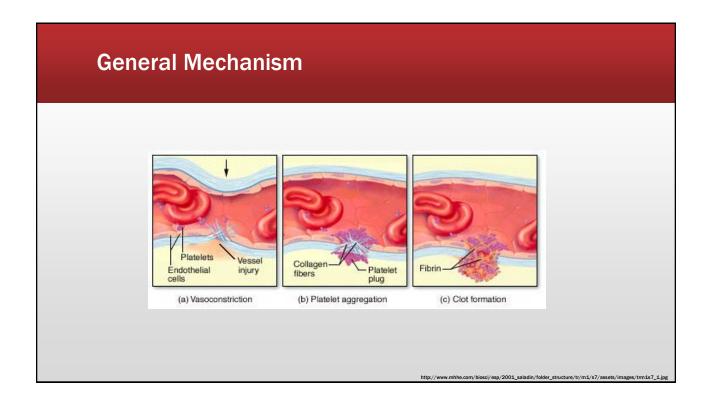
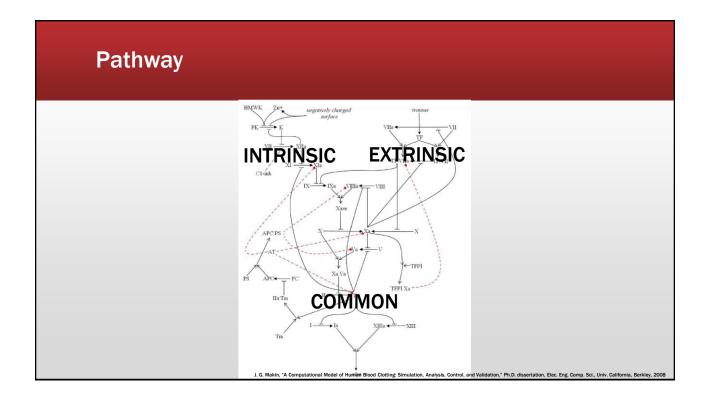


Background WHAT IS BLOOD CLOTTING?





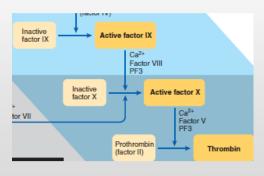
Thrombin (Factor IIa)

- Converts fibrinogen to fibrin, resulting in the fibrin mesh
- Normally in inactive form (Factor II), but production greatly enhanced due to cascade
- Acts in its own positive-feedback mechanism to facilitate the conversion from prothrombin to thrombin
- Thus, a good marker to measure how well the blood coagulates

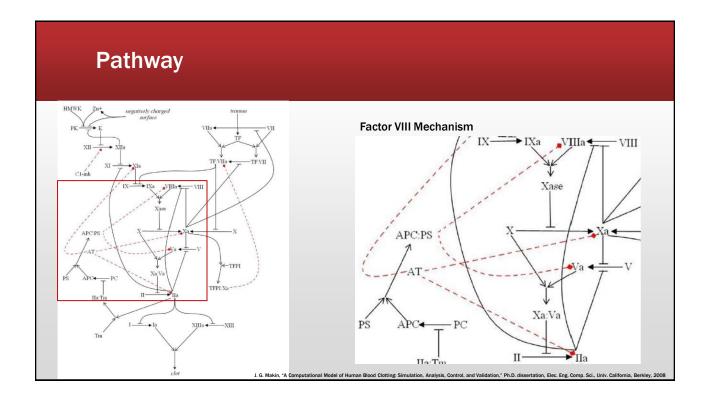
Human Physiology: From Cells to Systems 7E, Sherwood

Disease - Haemophilia A

- Inability to control blood clotting or coagulation due to lack of fibrin formation
 - Caused by Factor VIII deficiency
- 1 in 5,000-10,000 male births
 - X-Linked recessive trait
- Causes increased bleeding
- Thrombin positive feedback mechanism cannot activate more Factor VIIIa to increase production of Factor Xa and thus Thrombin



Human Physiology: From Cells to Systems 7E, Sherwood. Figure 11-14



Current Treatments

- Haemophilia treatment mainly depends on its severity.
- On demand
 - Giving treatment to stop prolonged bleeding when it occurs.
 - More commonly used for patients with mild haemophilia.

purce: Medical News Today, http://www.medicalnewstoday.com/info/hemophilia/treatment-for-hemophilia, accessed 29 Oct 201

Current Treatments

- Haemophilia treatment mainly depends on its severity.
- Preventative treatment (prophylaxis)
 - Medication to prevent bleeding episodes, and subsequent complications, such as joint and/or muscle damage.
 - More commonly used for patients with moderate or severe haemophilia.
 - Clotting factor replacement therapy (Factor VIII infusion)
 - Inject the factors into the bloodstream through a vein.
 - However, some people develop antibodies against the transfused factor VIII
 - Approximately 30% of people with severe haemophilia A

Source: Medical News Today, http://www.medicalnewstoday.com/info/hemophilia/treatment-for-hemophilia, accessed 29 Oct 2013

Project Objectives

FOR MODEL VALIDATION

Objectives

- To critique or validate a current mathematical model for blood clotting
 - Created a mathematical model from existing literature
- Examine a disease mechanism from the model
 - Haemophilia A

Methodology

- Model Validation
 - Looked at thrombin concentration
 - Activated different pathways
 - Intrinsic Pathway
 - Extrinsic Pathway
 - Changed the intensity of each pathway
- Examine a disease mechanism from the model
 - Added a "haemophilia constant" factor
 - Looked at how that constant changed the thrombin concentration as the different pathways are activated

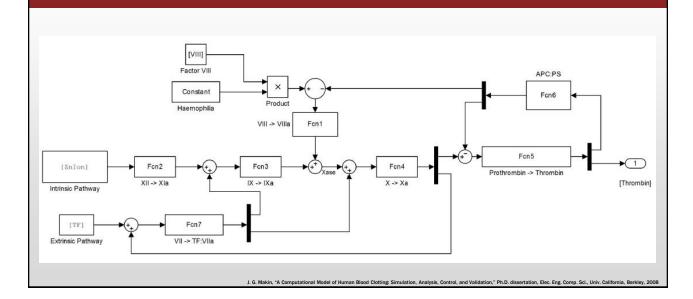
Rationale

- While we understand how the pathway works, there is currently no model for this
- Will help understand the different factors involved in the cascade
- Will help us find a way to target haemophilia A and hopefully find more effective methods to cure it

MODEL

WHAT WE BUILT

Simplification and Specific Modification



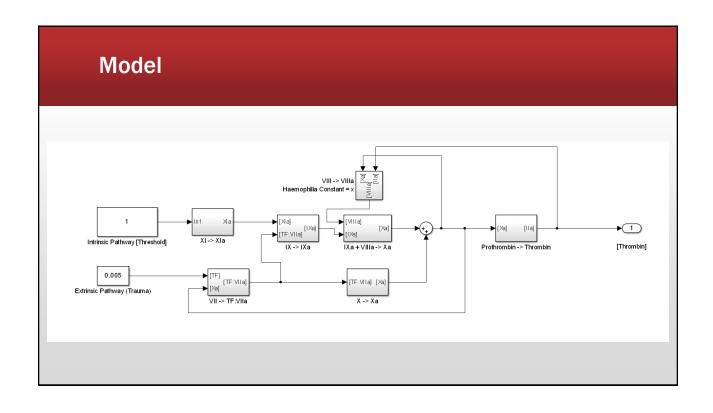
Modelling Equations

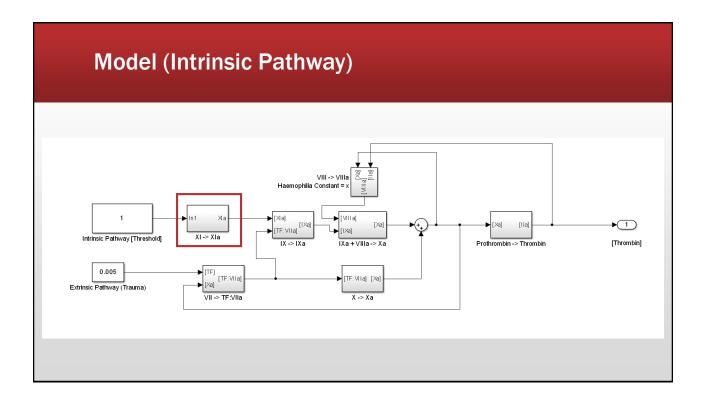
IN1----> OUT (catalyzed by IN2)

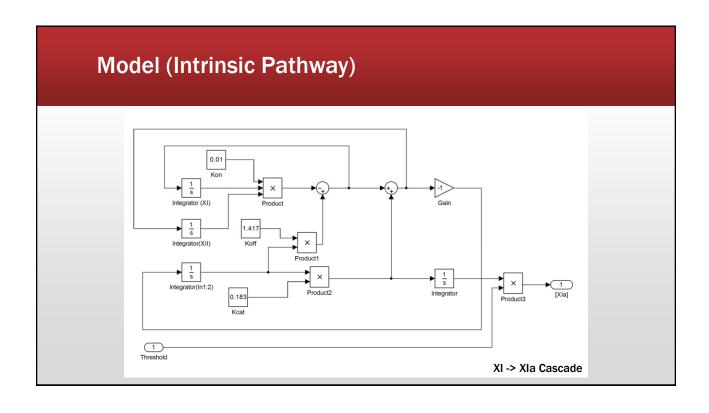
$$\begin{split} \frac{d[IN_1]}{dt} &= k_{off}[IN_1:IN_2] - k_{on}[IN_1][IN_2] \\ \frac{d[IN_2]}{dt} &= k_{off}[IN_1:IN_2] - k_{on}[IN_1][IN_2] + k_{cat}[IN_1:IN_2] \\ \frac{d[IN_1:IN_2]}{dt} &= k_{on}[IN_1][IN_2] - k_{off}[IN_1:IN_2] - k_{cat}[IN_1:IN_2] \\ \frac{d[OUT]}{dt} &= k_{cat}[IN_1:IN_2] \end{split}$$

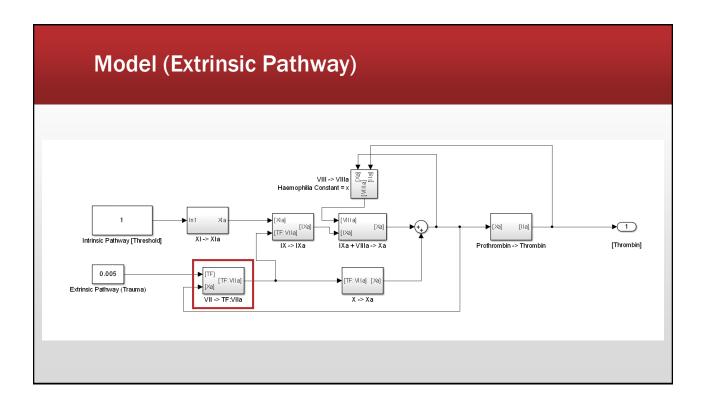
• IN1 + IN2 -----> OUT (no catalyst)

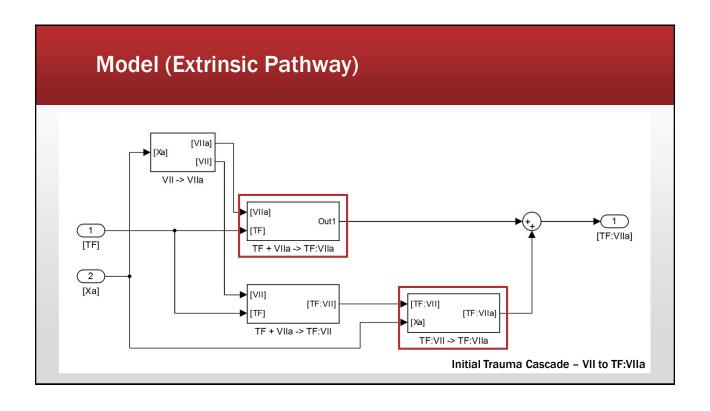
$$\begin{split} \frac{d[IN_1]}{dt} &= k_{off}[OUT] - k_{on}[IN_1][IN_2] \\ \frac{d[IN_2]}{dt} &= k_{off}[OUT] - k_{on}[IN_1][IN_2] \\ \frac{d[OUT]}{dt} &= k_{on}[IN1][IN2] - k_{off}[OUT] \end{split}$$

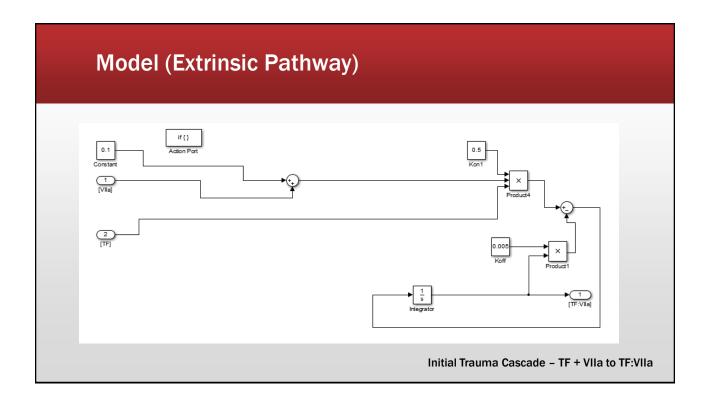


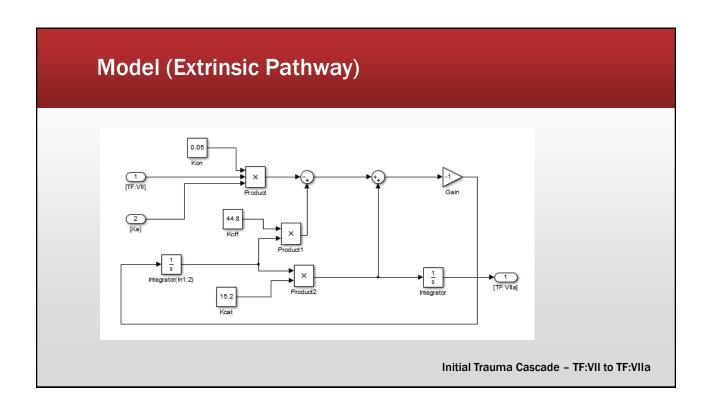


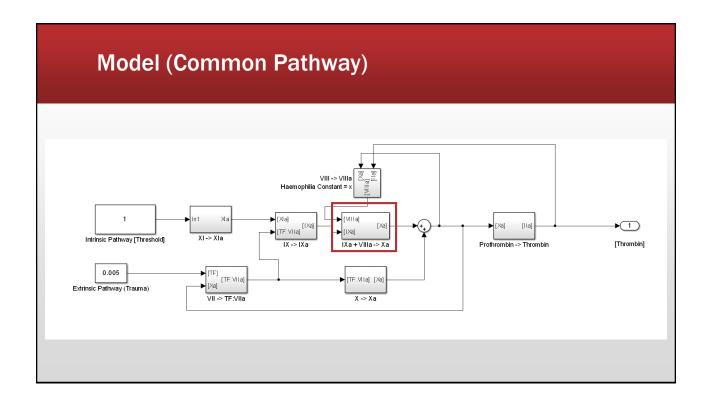




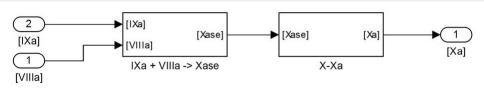








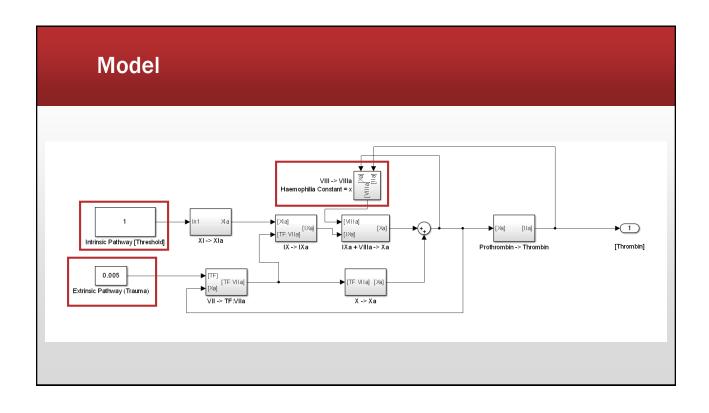
Model (Common Pathway)



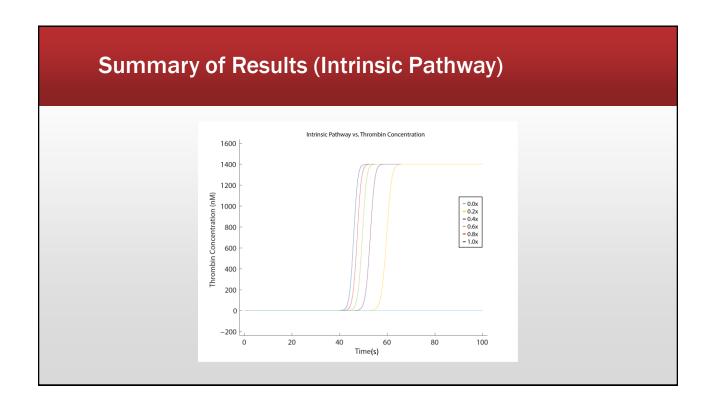
Bridge from Extrinsic/Intrinsic Pathway to Common Pathway

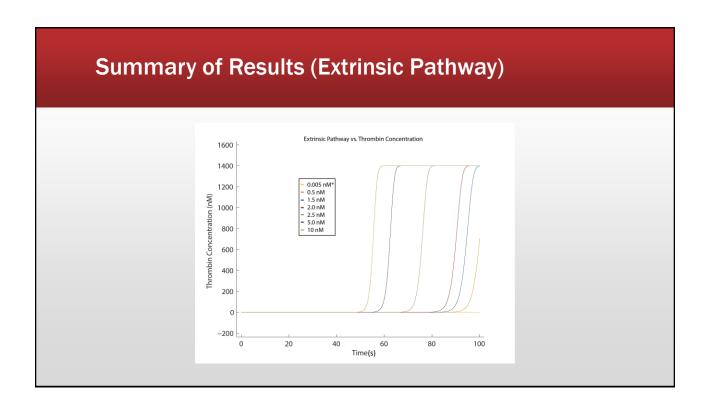
Variables Analyzed

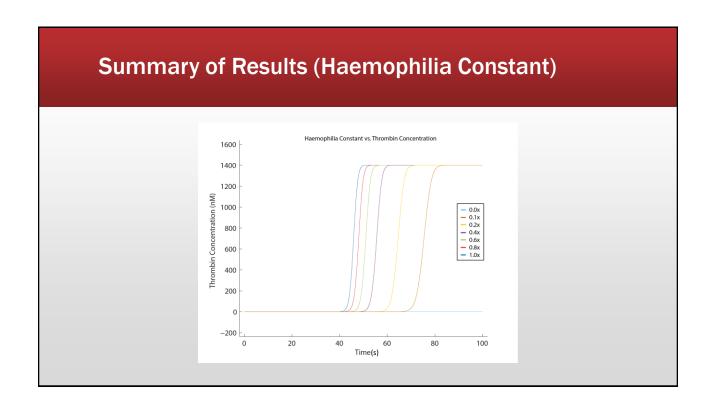
- Intrinsic Pathway Threshold
 - From 0x to 1x factor XIa
- Extrinsic Pathway [TF] in nM
 - Ranged from 0.005 ("off") to 15nM
- Haemophilia Constant
 - Ox to 1x factor VIII
- Looked at how long it took Prothrombin to convert to Thrombin
 - Hence why we see a plateau at 1400nM (initial concentration of prothrombin)

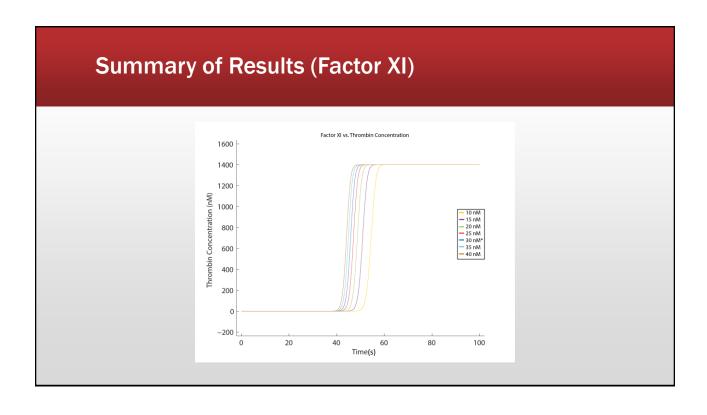












Model Approximation

- The differential equations used assume that all the cascade pathways are similar and can be modelled using the same series of equations.
- Not all the cascade pathways were modelled.
- The constants used are assumed to correctly model that in the human body.

Model Limitations

- Very simplified skips a lot of the more intricate mechanisms
- The model assumes all the cascade reactions follow the same set of equations.
- The model was simplified to not include lipid binding sites (LBS) which have different affinities for different factors which may affect the cascade reaction.

Possible Improvements

- Modelling the intrinsic pathway completely.
- Add the final stages of coagulation
 - Fibrinogen -> Fibrin
 - APC feedback mechanism
- Modelling the cascade using the LBS intermediates.

QUESTIONS?

