

Prediction of maternal-fetal exposures of CYP450-metabolized drugs using physiologic pharmacokinetic modeling implemented in R and *mrgsolve*

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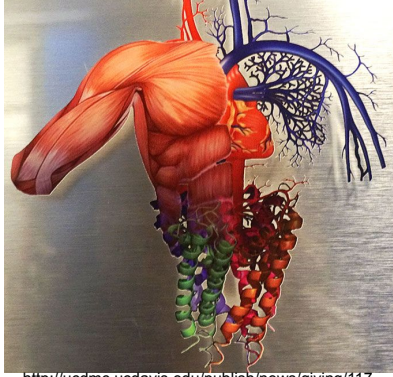
Clinical Pharmacology in Pregnancy

- Women use an average of 2-5 medications throughout pregnancy
- Several unaddressed questions
 - Drug development
 - Clinical therapeutics
- Orphan Population
 - Limited data available

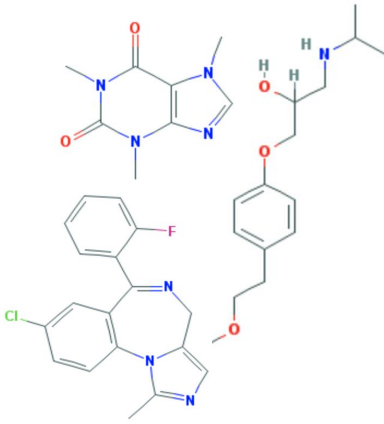


<https://www.medicalnewstoday.com/articles/317397.php>

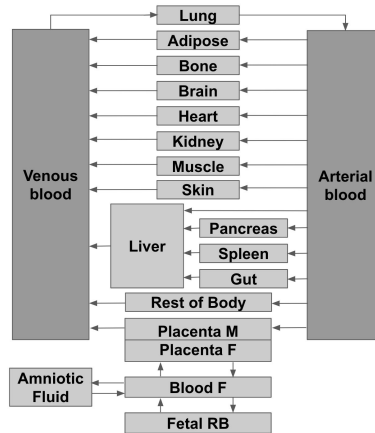
Possible Solution



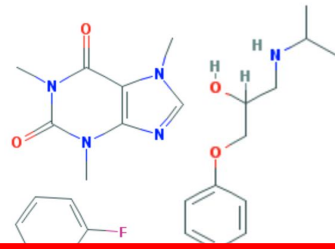
<http://ucdmc.ucdavis.edu/publish/news/giving/117>
72



https://www.pngkey.com/download/u2e6t4w7o0q8g8u2_ca/toon-pregnant-woman-pregnant-clip-art/



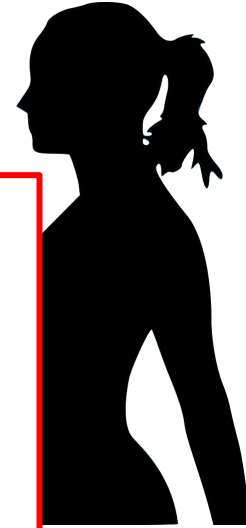
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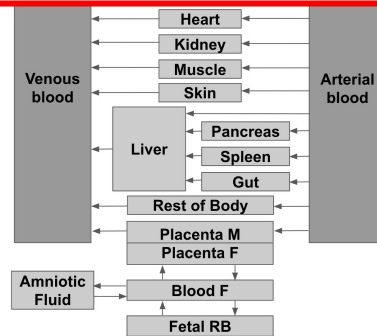
<http://ucdmc.ucdavis.edu/publish/news/giving/11772>

This Approach Allows Us To:

- Integrate knowledge across multiple sources for decision-making in clinical therapeutics and drug development
- Explore answers to questions that are not directly addressed in clinical studies



https://www.gettyimages.com/download/u2e6t4w7o0q8g8u2_ca/woman-pregnant-clip-art/

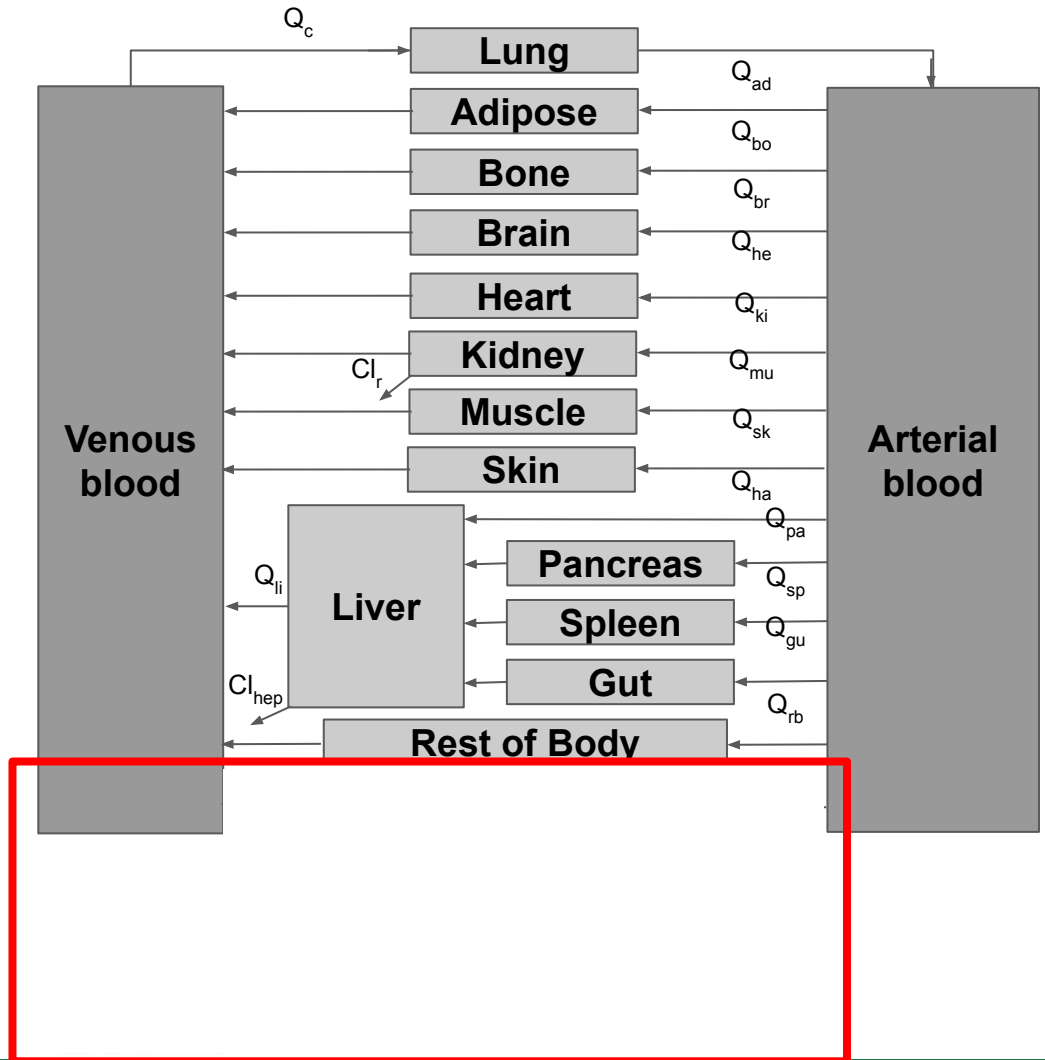


Workflow

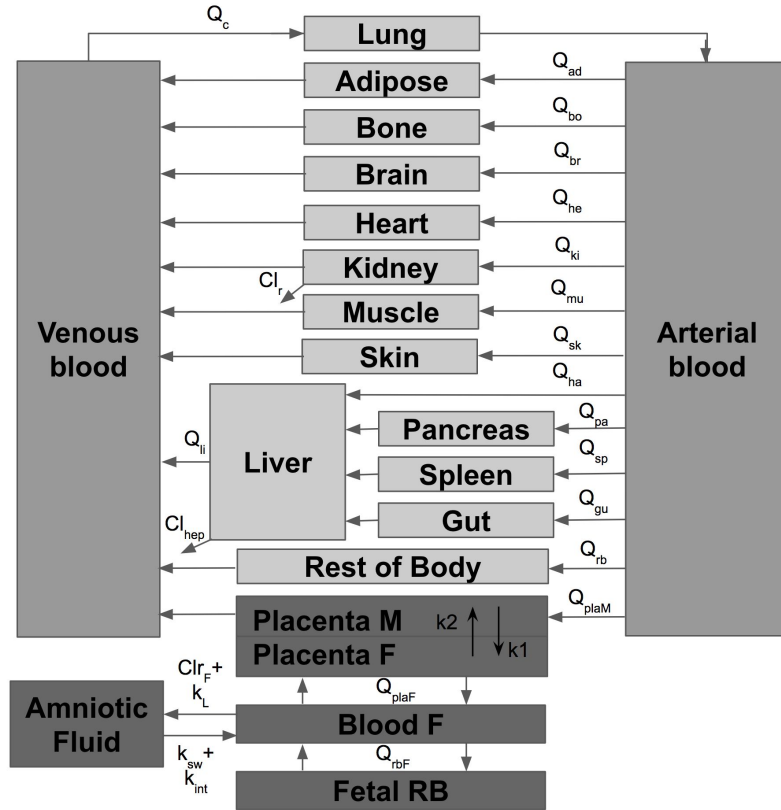
Model Structure

Female Physiology:

- 15 Compartments
- 17 Differential Equations



System of Ordinary Differential Equations



$$\frac{dA_T}{dt} = Q_T \cdot \left(C_{art} - \frac{C_T}{\frac{Kp_T}{B:P}} \right)$$

Where Q_T represents tissue blood flow in l/h, C_T is tissue concentration in mg, Kp_T is the partition coefficient of the tissue, and $B:P$ is the blood to plasma partition coefficient.

$$Qc = 365.4 \cdot e^{-e^{-0.352 \cdot \log(FA) + 1.36}} + 354$$

$$CYP1A2 = 1 + 0.0227 \cdot GA - 0.00035 \cdot GA^2$$

Implementation in R



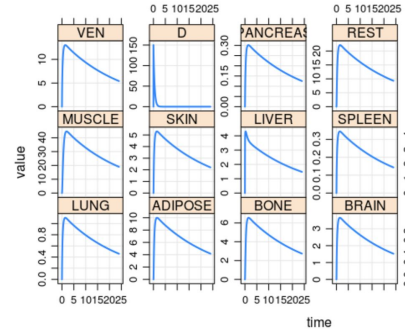
PBPK Model Code

MFPBPKmodel.cpp

```
//Differential Equations
dxdt_ADIPOSE = Qad*(Carterial - Cadipose/(Kpad/BPP));
dxdt_BRAIN = Qbr*(Carterial - Cbrain/(Kpbr/BPP));
dxdt_HEART = Qhe*(Carterial - Cheart/(Kphe/BPP));
dxdt_KIDNEY = Qki*(Carterial - Ckidney/(Kpki/BPP))- Ckidneyfree * CL_r;
dxdt_GUT = Qgu*(Carterial - Cgut/(Kpgu/BPP)) + Ka*D*fg*fa;
```



R
Rcpp
C++
DLSODA (ODEPACK)



Simulate Using *mrgsolve*



```
mod <- mread("../model/MFPBPKmodel.cpp")
```

```
Pars_caf <- chooseDrug(drug = "caffeine", method = "PT", timeDep = TRUE)
```

```
mod %>%
```

```
  param(c(Pars_caf, GA = 36)) %>%
```

```
  ev(amt = 150, cmt = "D", ii = 12) %>%
```

```
  mrgsim(end = 24, delta = 0.001) %>%
```

```
  plot()
```

1. Load a model
2. Choose parameters
3. Select intervention
4. Simulate
5. Post-process (plot, summarize, ...)

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Shiny App



Choose Drug
Metoprolol

Choose Model
Pregnant

Graph Fetal Plasma Concentration

Dose Type
IV

Dose Amount (mg)
10

Interval Between Doses (h) Additional Doses
0 0

Infusion Rate (l/h)
0

Y-axis Upper Bound 1 **Simulation End** 12

Partition Coefficient Method
Rodgers and Rowland

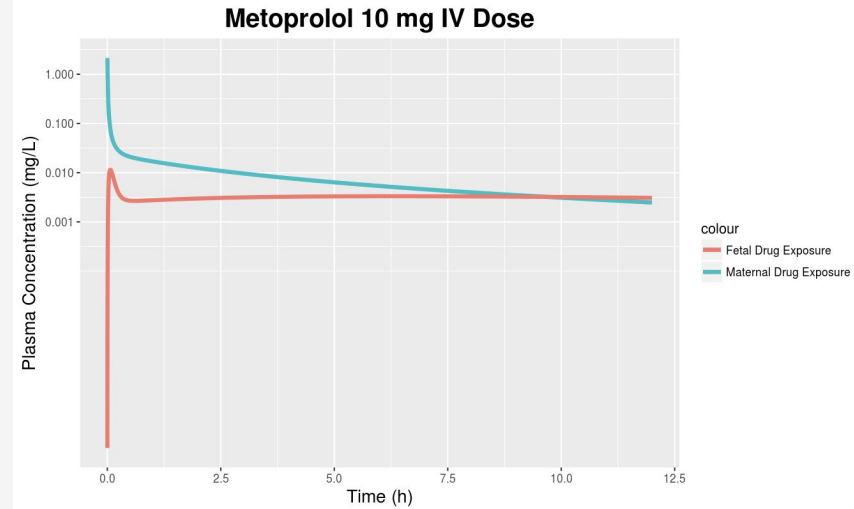
Optimized Parameters?

Gestational Age (weeks)
0 37 40

Initial B:P
0 1.127 2

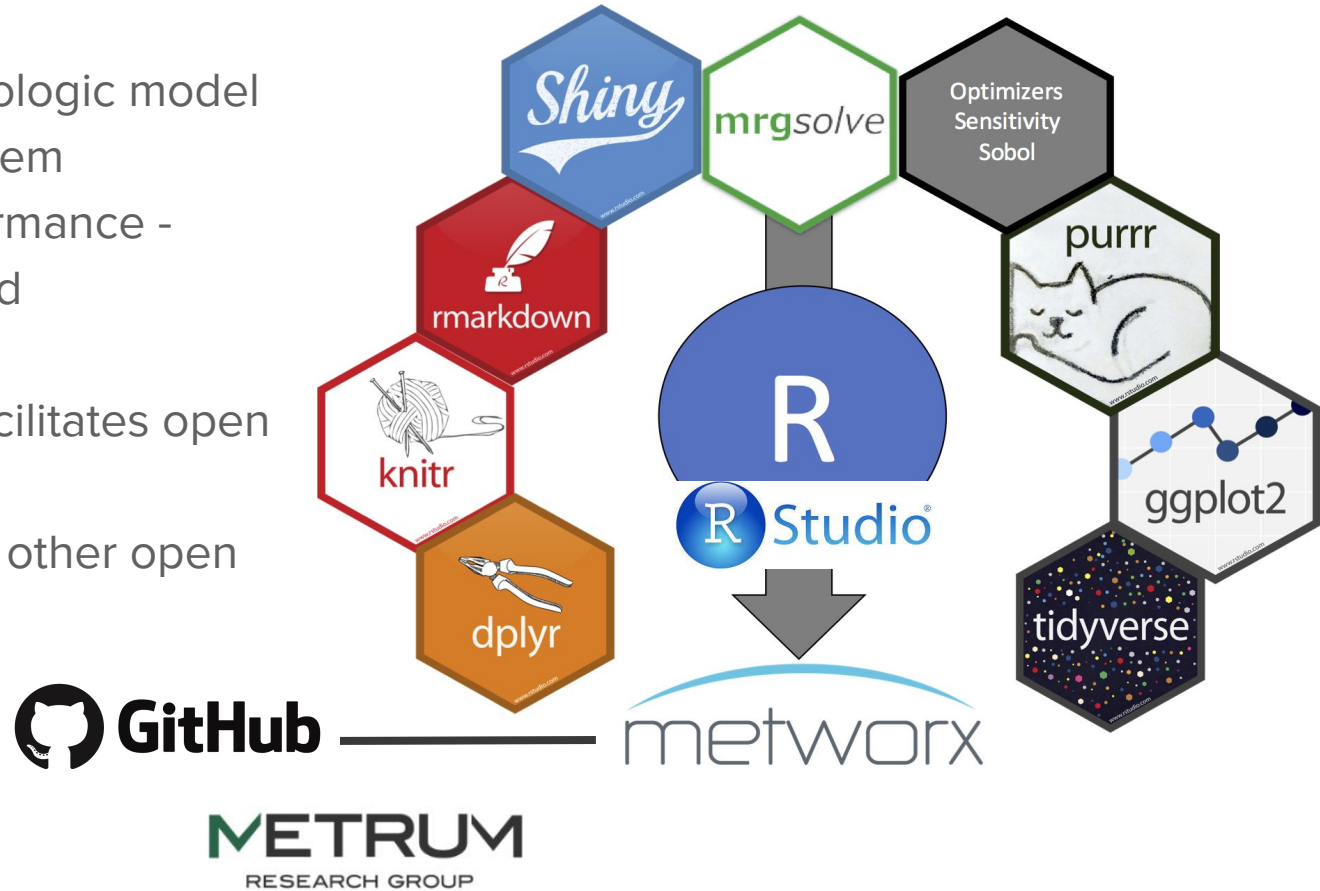
Initial Fraction of Unbound Drug in Plasma
0 0.879 2

Initial Intrinsic Hepatic Clearance (l/h)
195 7,000



Why R instead of Commercial PBPK Software?

- Customizable physiologic model
- Access to R ecosystem
- Optimized for performance - cloud computing and parallelization
- Full transparency facilitates open science
- Interoperability with other open science projects



Acknowledgements

- Ahmed Elmokadem, PhD
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