

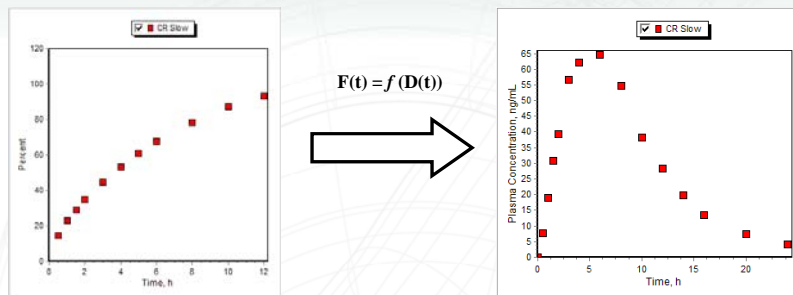
GastroPlus: Mechanistic Deconvolution and the Future Role of Physiological Modeling in IVIVC

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PQRI Workshop, Sept. 2012

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IVIVC



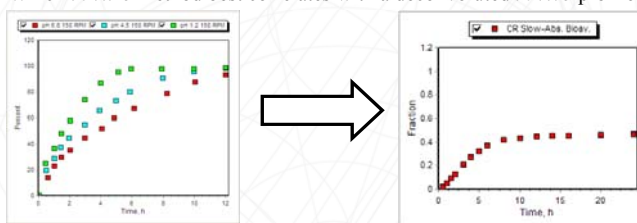
- Can we find a mathematical input function that allows us to use the *in vitro* release data (on the left) to predict the *in vivo* plasma concentration-time data (on the right)?
- If we generate such a function, can we use that function to predict the plasma concentration-time for different formulations with different *in vitro* release-time profiles?

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What is the purpose of an IVIVC?

- IVIVC can be used for many purposes:
 - To reduce regulatory burden (IVIVC in lieu of additional *in vivo* experiments)
 - To reduce cost burden associated with bioequivalence trials
 - For dissolution method development:

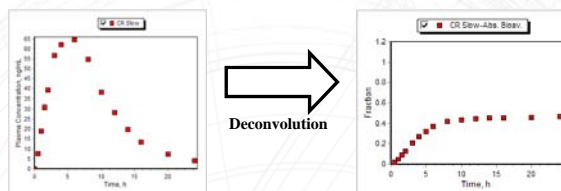
- Which *in vitro* method best correlates with a deconvoluted *in vivo* profile?



- For formulation design:
 - How do I develop my formulation to produce an *in vitro* dissolution rate that will achieve bioequivalence?

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Step 1: Deconvolution in GastroPlus with traditional methods



Deconvolution

- Determine the *in vivo* bioavailability (**F%** - NOT dissolution or absorption) from plasma concentration data
- Traditional options:
 - Model-dependent:
 - Based on mass balance among PK compartments
 - Wagner-Nelson, Loo-Riegelman
 - Model-independent:
 - Based on theory of linear systems analysis
 - Numerical deconvolution

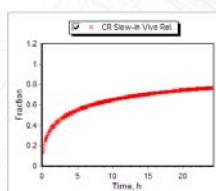
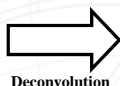
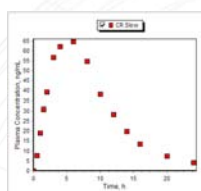
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Drawbacks to using the traditional methods for deconvolution

- Output?
 - Amount of drug reaching central compartment vs. time (systemic availability or F%)
 - Does not tell us anything about how it got there:
 - Was it all absorbed and some lost to first pass extraction?
 - Was only some of it absorbed with little or no first pass extraction?
 - Was the *in vivo* release/dissolution anything like the *in vitro* experiment?
- Assumptions:
 - Drug obeys one-, two, or three-compartment open model
(*limitation – does not consider drug's true distribution*)
 - First-order absorption
(*limitation – not realistic*)
 - No saturable (nonlinear) absorption or clearance
(*limitation – what if drug is substrate for enzymes/transporters?*)
 - Terminal oral plasma concentration-time points independent of absorption
(*limitation – what about colonic absorption?*)

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Step 1: Deconvolution in GastroPlus with Mechanistic Absorption method



in vivo dissolution vs. time along the gut– NOT F!

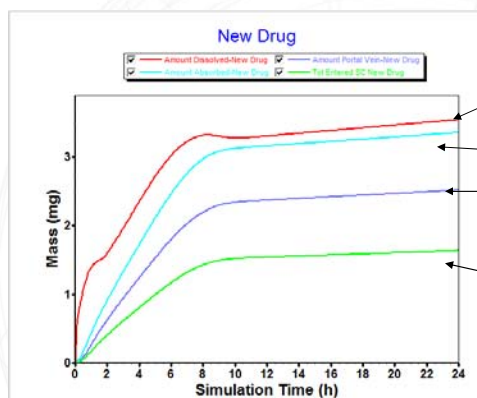
- Inputs (in addition to the data required for the traditional methods):
 - Physiological parameters
 - Drug properties (solubility, Peff, logP, pKa, etc.)
- Outputs:

A model that combines all available *in silico*, *in vitro* and *in vivo* information and provides:

 - *in vivo* dissolution, absorption and bioavailability vs. time profiles
 - Description of site-dependent absorption
 - Description of tissue contributions to first pass extraction

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Formulation vs. Bioavailability

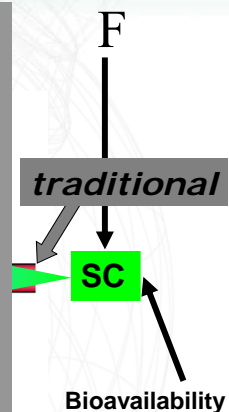


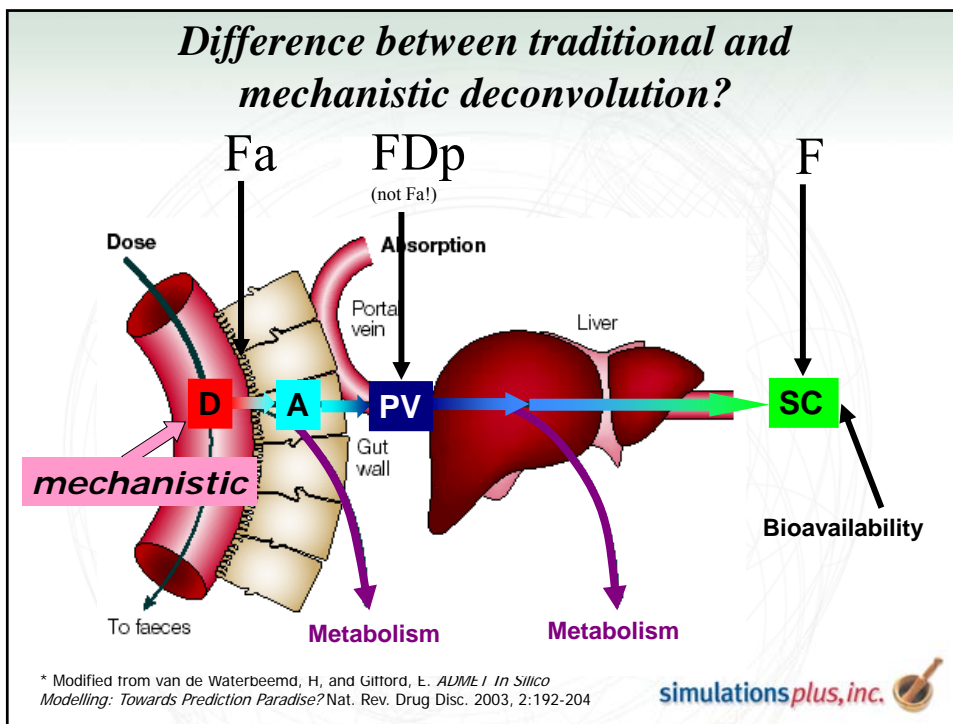
- Total amount dissolved
 - Deconvoluted profile from the GastroPlus mechanistic approach
- Total amount absorbed
- Total amount into portal vein
- Total amount into systemic circulation (bioavailability)
 - Deconvoluted profile from traditional methods



Difference between traditional and mechanistic deconvolution?

Absorption and first pass extraction?





Mechanistic Absorption Deconvolution: “Deconvolute Then Correlate”

Fit the *in vivo* release profile (using single or double Weibull function or Z-Factor) for each formulation used in IVIVC

➔

Find one correlation function to best fit *in vivo* vs. *in vitro* release profiles across all formulations used in the IVIVC

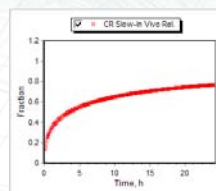
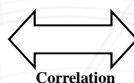
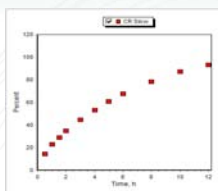
Find the *in vivo* dissolution vs. time profile that best fits the plasma concentration-time data once absorption and PK are well-established from IR (and IV, if available) doses.

Deconvoluted *in vivo* dissolution vs. time profile obtained using the Weibull function (single or double)

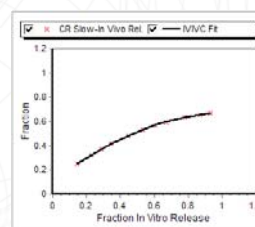
Weibull Parameters	
Phase 1	Phase 2
f_1 function	f_2
k (Phase scaled by k_2)	k_2
n (shape)	n_2

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Step 2: Correlation



- Find the correlation between the deconvoluted *in vivo* release and *in vitro* dissolution profiles:
 - Linear
 - Power function
 - 2nd order polynomial
 - 3rd order polynomial

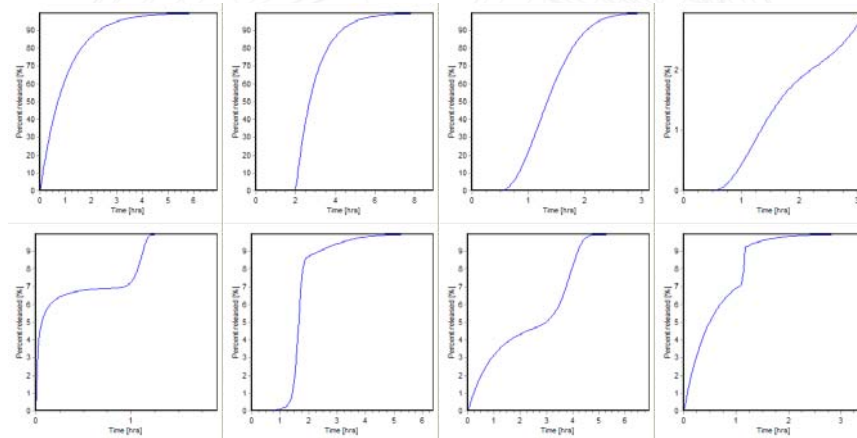


*Now, THAT'S information a formulator can really use!

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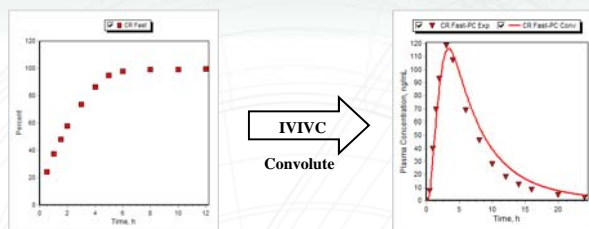
Flexibility of the Weibull Function?

- The first step is optimization of *in vivo* release profile in a form of a Weibull function.
- GastroPlus offers single- and double-Weibull function for optimization of *in vivo* release profile, which cover wide variety of release profile shapes



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Step 3: Convolution



- Predict the plasma concentration-time profile using the IVIVC and *in vitro* dissolution curve:
 - Internal validation: use the formulations involved in the development of the IVIVC
 - External validation: use the formulations NOT involved in the development of the IVIVC
- Acceptance criteria:
 - Internal validation:
 - $\leq 15\%$ absolute prediction error (PE) for C_{max} and AUC of each formulation
 - $\leq 10\%$ mean absolute prediction error (PE) for C_{max} and AUC
 - External validation:
 - $\leq 10\%$ absolute prediction error (PE) for C_{max} and AUC

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Modeling Controlled Release Formulations in GastroPlus

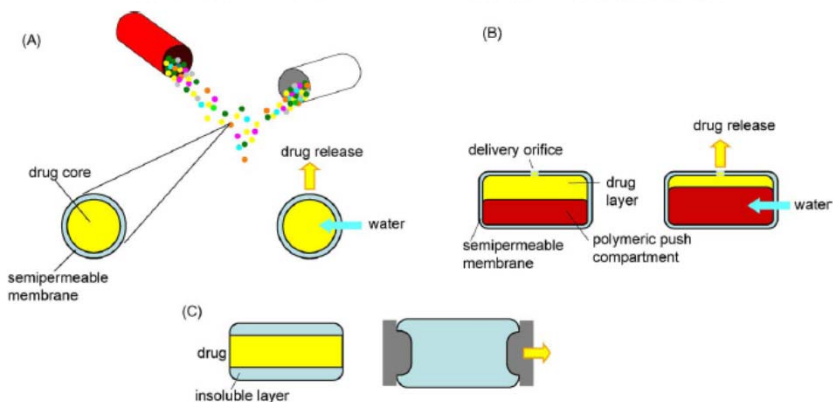


Fig. 1. Schematic representations of different MR technologies: (A) multi-unit membrane-coated pellets, (B) Oros[®], (C) GeoMatrix[®].

Figure from Michel et al, European Urology Supplements 4 (2005) 15-24

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Let's build the IVIVC...

Deconvolution Methods:

- Mechanistic Absorption Model (GastroPlus)
- Numerical Deconvolution
- Loo-Riegelman (3-compartment model)
- Loo-Riegelman (2-compartment model)
- Wagner-Nelson (1-compartment model)

IVIVC Procedure

- Deconvolute Then Correlate
- Correlate

Weibull Function:
Select Weibull Function

Buttons: Deconvolute, Form Correlation, Stop, Save IVIVC

Y-axis scaling: Logarithmic Scale Linear Scale Hide Legend

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Status Window:
Power Function:
 $y = 0.923 * (x)^{0.970}$
where x = Fraction in vitro release and y = Fraction absolute bioavailability

Correlation Function:

- Select All
- Linear
- Power Function
- Second Order Polynomial
- Third Order Polynomial

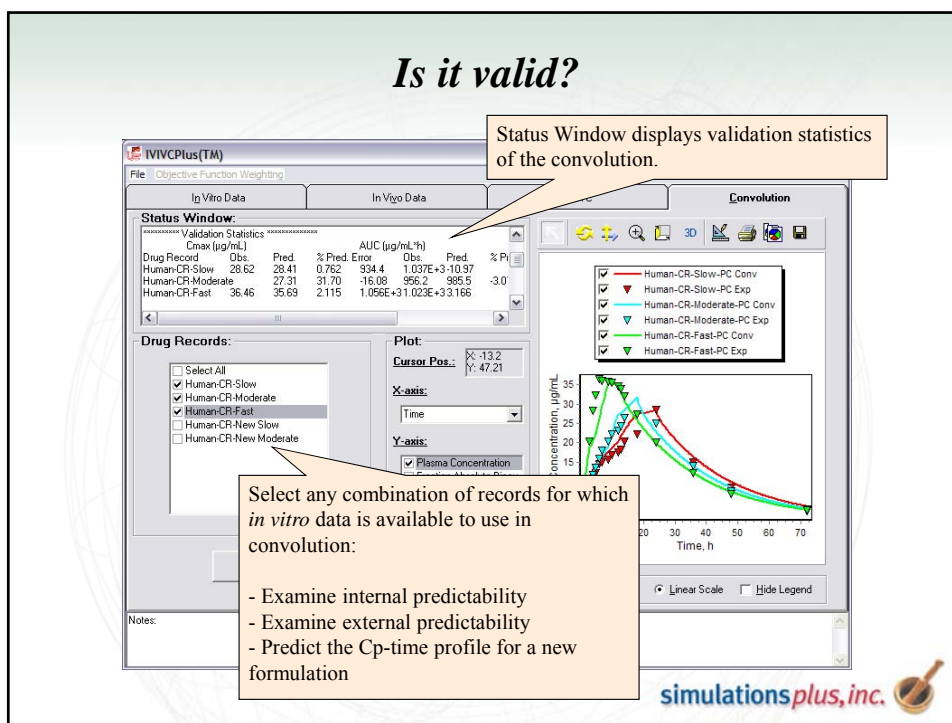
Buttons: Deconvolute, Form Correlation, Stop, Save IVIVC

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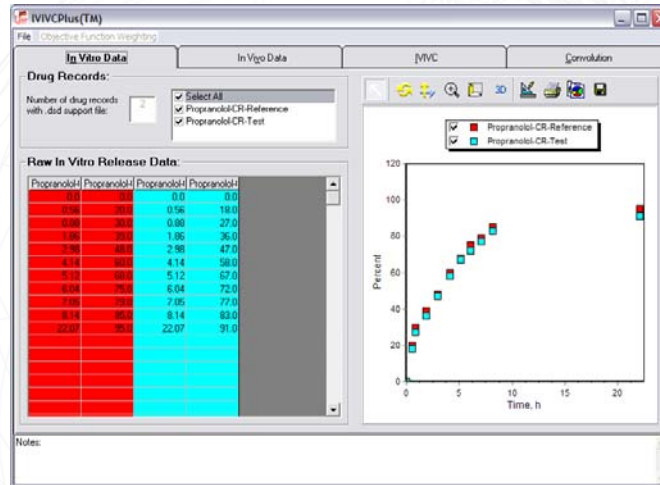
Is it valid?



Using Test and Reference Product Data to Identify the Target *in vitro* Dissolution Profile

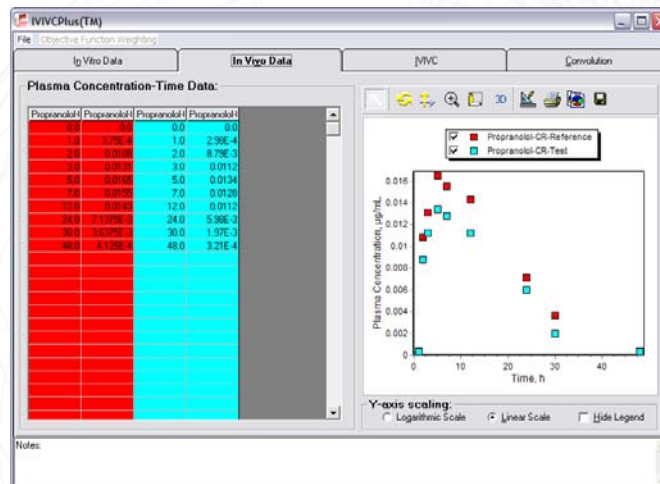
- Predict the performance of a new Test product before the first clinical study assuming the *in vitro* release = *in vivo* release:
 - IVIVC: $y = x$
 - *Run the study and fail bioequivalence! Now what? We need to know the true *in vivo* release rate using mechanistic deconvolution.*
 - Step 1: Deconvolute the Reference product's *in vivo* release to identify the target profile
 - Step 2: Design new formulation which can match the target *in vivo* release profile
- Is there something I can do to predict how well the new formulation (Test2) will match the target *in vivo* profile before running the next clinical study?
- Use IVIVC built on our current test formulation

What are we trying to do before our first bioequivalence trial?



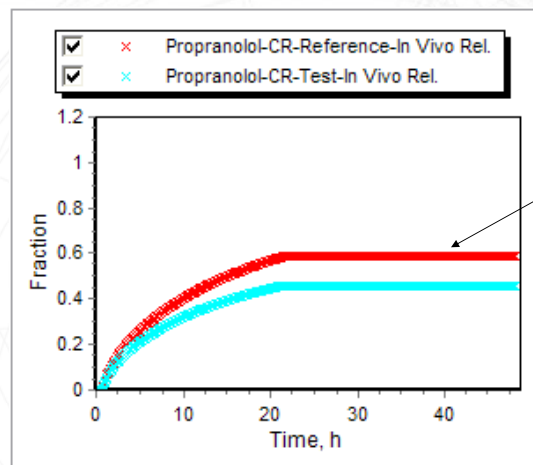
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Umm... what happens if we fail?



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Use IVIVC built on our current test formulation



Deconvoluted *in vivo* release:

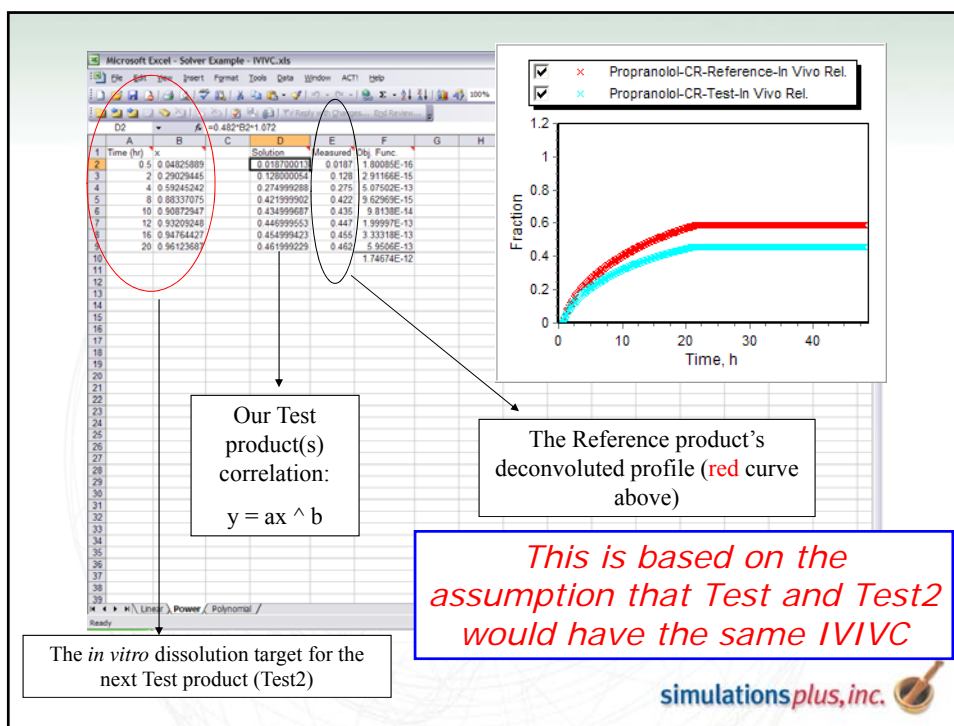
The Reference profile (in red) is what we need to match with our next (Test2) product

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OK... we have an IVIVC. Now what?

- We have our Test product IVIVC
(even though it's only a single formulation):
$$y = ax^b$$
- Now that we have an idea how our Test product behaves *in vivo*, we can identify the target *in vitro* dissolution for our 2nd Test product:
 - y = the deconvoluted *in vivo* release of the Reference
 - Let's solve for "x"

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Design the formulation and dissolution method

DDDPlus™
Dose Disintegration
And Dissolution
Software

Test Modifications:

- RPM
- Volume
- pH
- Polymer matrix
- Particle Size Distribution
- Excipients
- Multi-stage dissolution

Formulation Composition

Ingredient Name	Ingredient Type	Amount (mg)	Unit (g/ml)	Diss. Coeff. (1/h)	Size (µm)
Propranolol	Active	140	200.4	0.829	15
H-PAC K40	Polymer	15	9000	0.0005	15

Experimental Setup

Apparatus Type: USP Paddle

Instrument Speed (RPM): 75

Medium Volume (mL): 900

Medium Viscosity (g/cm³·s): 0.007

Medium pH: 6.5

Fluid Velocity (cm/s): 7.504

Medium Type: FaSSSFS

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Summary

- Applied correctly, IVIVCs can save substantial resources when registering products changes (i.e., biowaivers) or to assist with formulation design activities
- Traditional IVIVC methods determine the *in vivo* input rate to the systemic circulation (i.e., F% vs. time – not absorption and not dissolution!)
- The GastroPlus Mechanistic Absorption method allows you to separate *in vivo* dissolution of your formulation from absorption & first pass extraction:
 - Best estimate of the true *in vivo* dissolution/release of your product
- And finally, DDDPlus™ lets you design hypothetical formulations and experimental conditions to help aid in dosage form design and *in vitro* dissolution experiment design

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Controlled Release Technologies

- **Gastric release:**
 - Unreleased drug remains in stomach
- **Integral tablet:**
 - Unreleased drug remains in tablet – moves from one compartment to the next (e.g., erosion tablet, pulsed, multi-layer systems)
- **Dispersed:**
 - Unreleased drug disperses among compartments (e.g., beads)

U = unreleased D = drug in solution

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Controlled Release Technologies

- **Enteric Coated Tablet**
 - the whole tablet stays in stomach for the period of stomach transit time
 - after leaving stomach the dissolution continues as for IR formulation
- **Enteric Coated Capsule**
 - the small enteric coated pellets can get distributed throughout the GI tract
 - the pellets start leaving stomach immediately at the rate calculated as “1/transit time”
 - Only the pellets that already left stomach will start dissolving (dissolution as for IR formulation)

U = unreleased D = drug in solution

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