

*Approaches to Overcoming Variance Due to
Heterogeneity -
Case study in a Rare Disease*

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cTAP

The collaborative **T**rajectory Analysis Program

1. Why?
2. Hypothesis and Preliminary Results
3. From Consortium to Platform?

The Problem (2010-2015)

<u>TRIAL</u>	<u>PHASE</u>	<u>PATIENTS**</u>	<u>Met Primary endpoint</u>
DEMAND II	Ph 2	53	yes
DEMAND V	Ph 2	51	no
DEMAND III	Ph 3*	186	no
PTC 007	Ph 2*	174	no
DMD-ACT	Ph 3*	228	no
Tadalafil	Ph 3*	331	2016
Pfizer	Ph 2	105	2017

* Pivotal trial

**Total # patients = 1719 patients; ~ 400 randomized to placebo

Failed Trial – or Failed Drug?

- Is the drug ineffective?
- Or effective only in a subset of patients?
- Was the study underpowered?

Clue #1 – High unexplained variance

DMD patients lose approximately **40-60 meters** in 6MWD per year

Summary from Prosensa Investor presentation, 2014

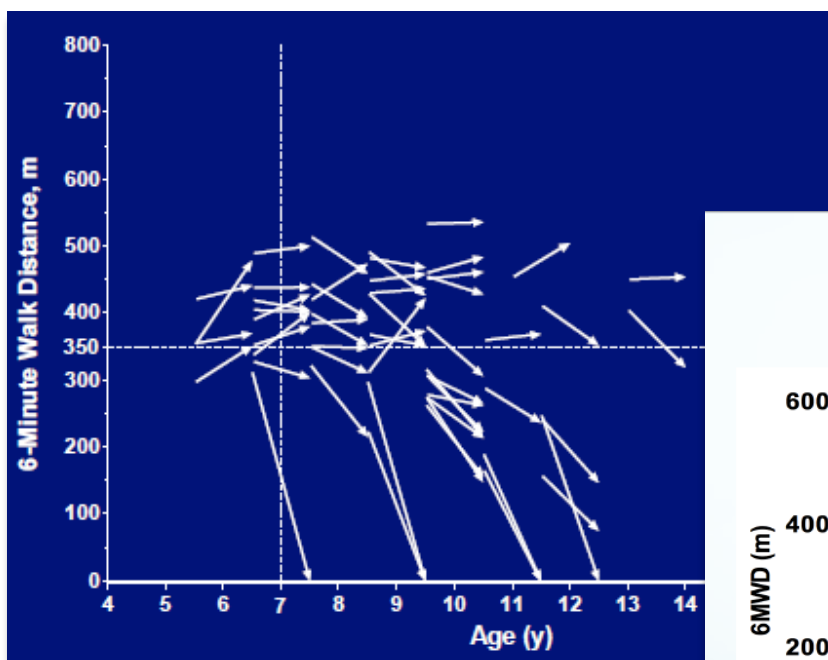
Study	Design	Δ 6MWT (m)	SD (m)	Study (weeks)	n
McDonald 2010*	Natural History	-57	104	52	18
Ataluren 2010*	Placebo arm	-42	90	48	57
Mazzone 2011**	Natural History	-42	74	52	71
Goemans 2012*	Natural History	-38	96	52	19
McDonald 2013**	Natural History	-59	82	48	33
Drisapersen 2014	Placebo Arm	-53	78	48	61

Hindsight: poor Signal to noise, underpowered

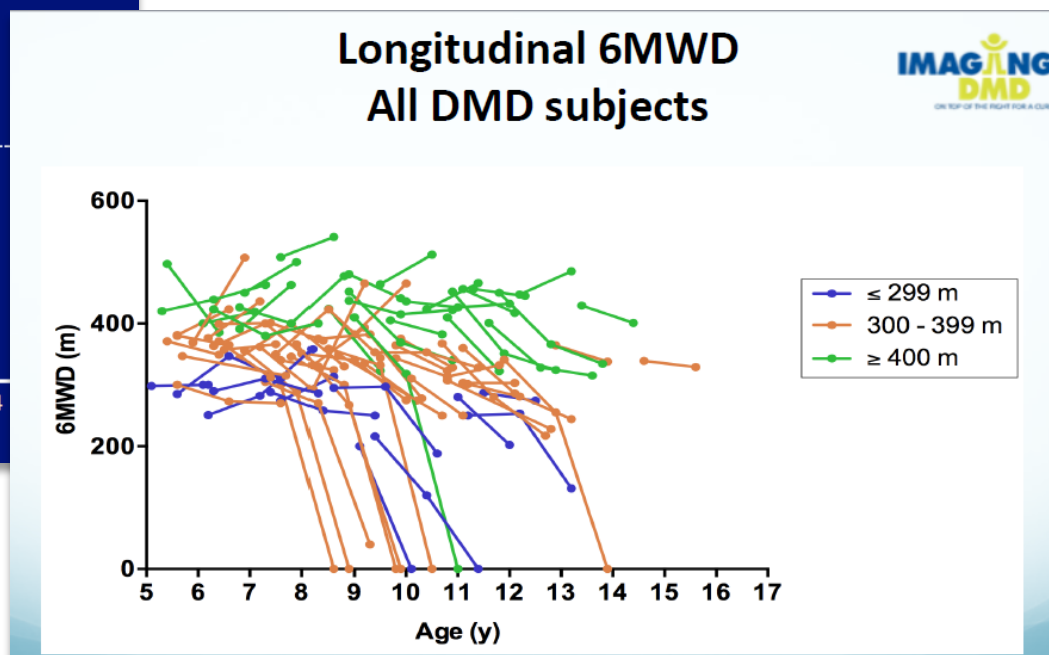
PUBLISHED AFTER TRIALS DESIGNED

Phenotypic Heterogeneity – a major source of variance

Ataluren PIIb placebo arm



Imaging DMD data



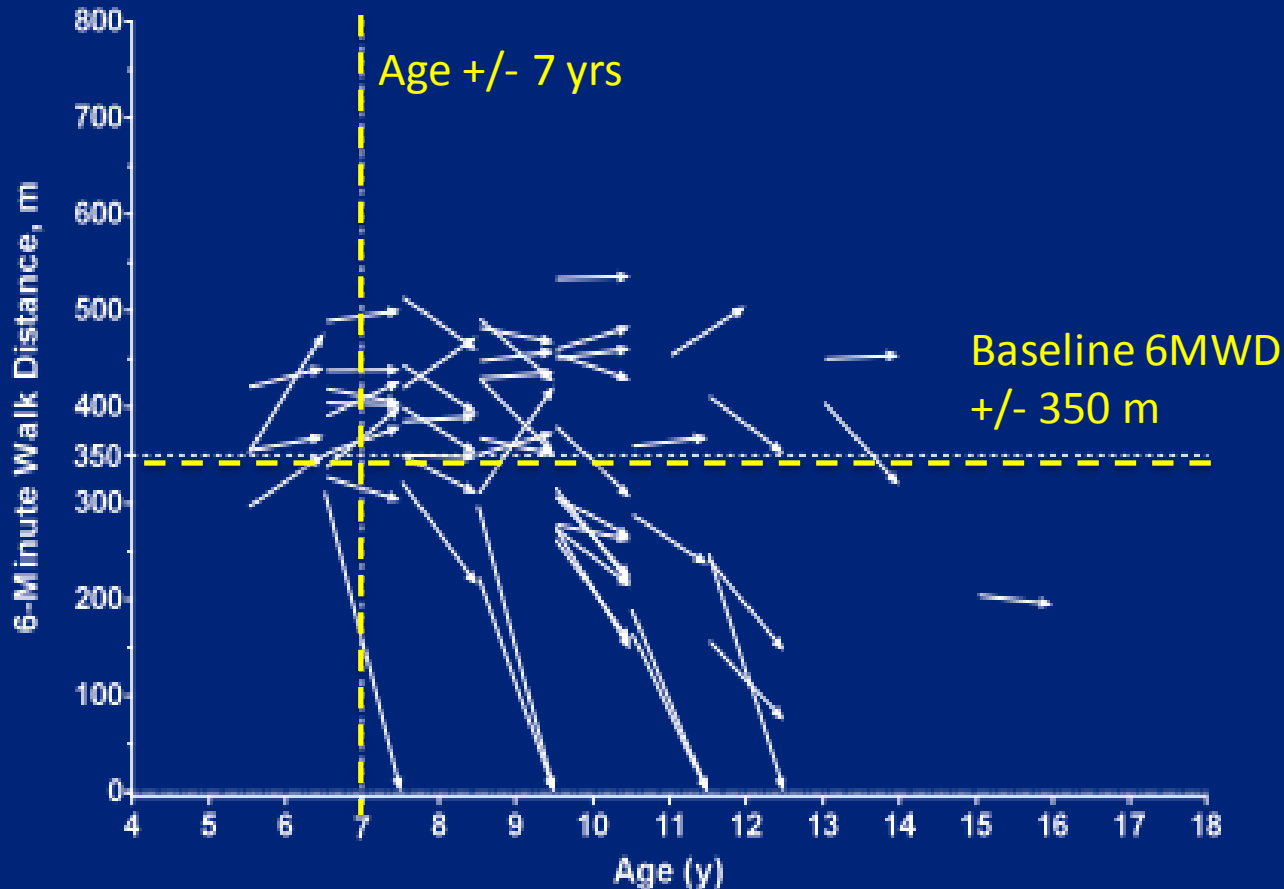
Approaches to overcoming heterogeneity-driven variance in clinical trials

- Account for known prognostic markers
- Improve consistency in measuring outcomes
- Change outcome measure
- Develop biomarkers
- Run a bigger trial

Rarely an option in rare disease!

Proposed Prognostic Factors

Ataluren placebo – n= 57



*Reduction in
variance SD:
90m => 82m*

*Some, but
limited benefit*

In 1Q 2014....

- > 5 years clinical development
- > 1000 open port biopsies
- # Drug approvals – zero
- Reduction in heterogeneity-based variance ~ 10-15%

*What can we learn from other diseases?
Other disciplines?*

Idea: Focus on the entire longitudinal trajectory

PREMISE

- Each patient has own distinctive longitudinal trajectory of disease progression
- Clinical trials - a window into each patient trajectory
- Natural history - a composite of trajectories

TESTABLE “HYPOTHESIS”

- Cluster heterogeneous longitudinal trajectories of disease progression => reduce variance

Proposed Collaboration Overview

PRE-COMPETITIVE COLLABORATION

SPONSOR-SPECIFIC

DISCOVER

VALIDATE

TRANSLATE

DEPLOY

Find and understand
trajectory clusters in
Natural History*



Reproducible?

Does placebo differ?

Detects Efficacy?



Prognostic

Trial design and
analysis



Drug Efficacy

ENGAGE REGULATORS

COMMUNICATE

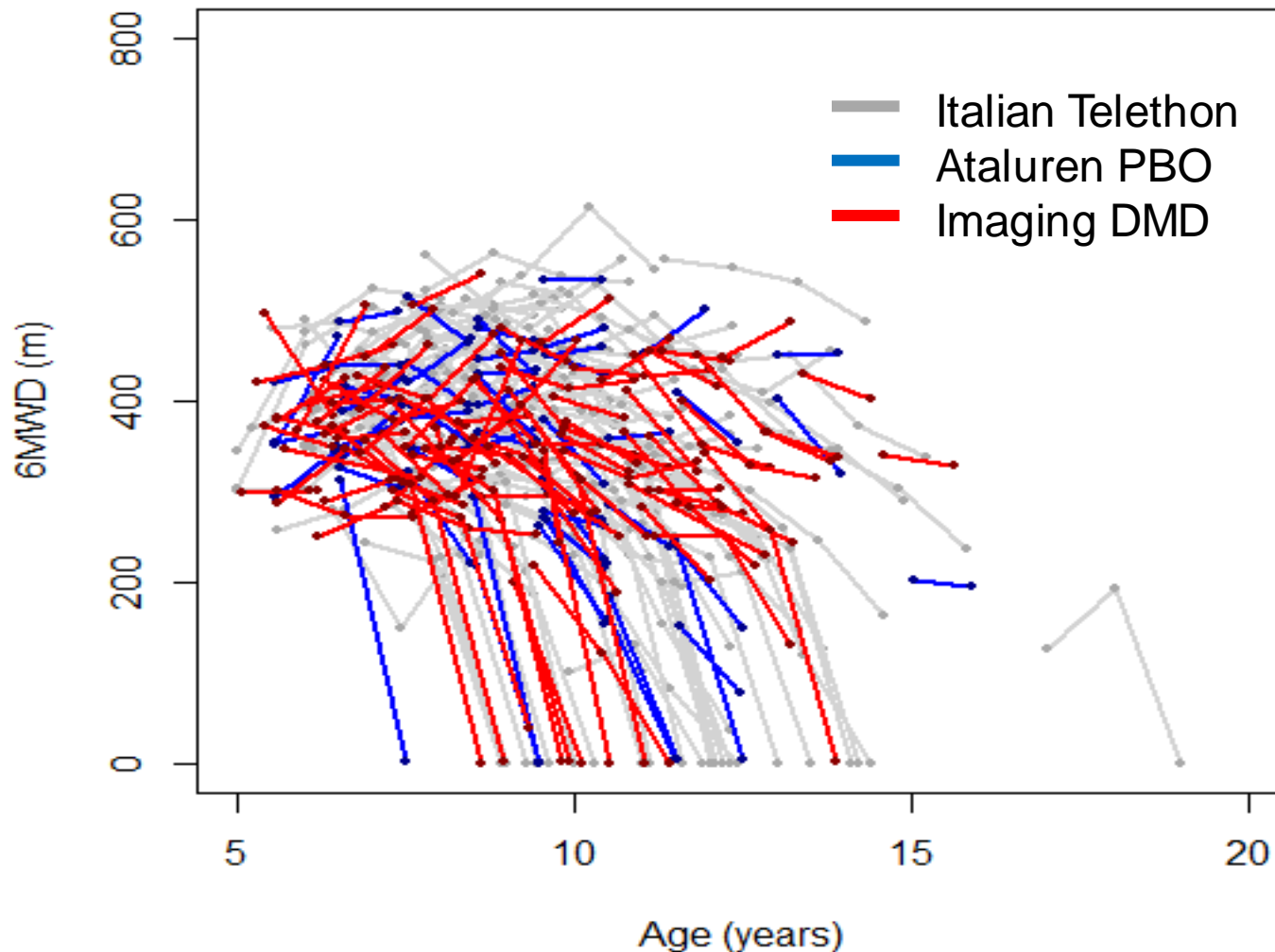
**Latent Class Trajectory Analysis*

Latent Class Trajectory Analysis

- Methodology developed in social sciences and healthcare economics
- Developed to handle variance due to heterogeneity in longitudinal clusters
- Of Growing interest (Pub Med)

See references

Rough Proof of Concept: data digitally traced from published figures



Latent Class Trajectory analysis

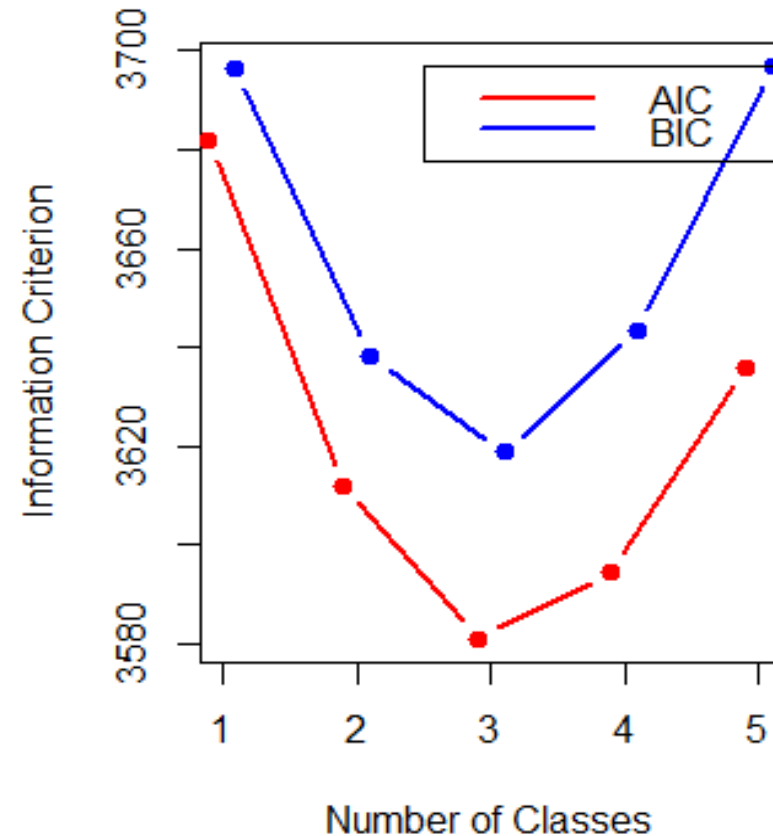
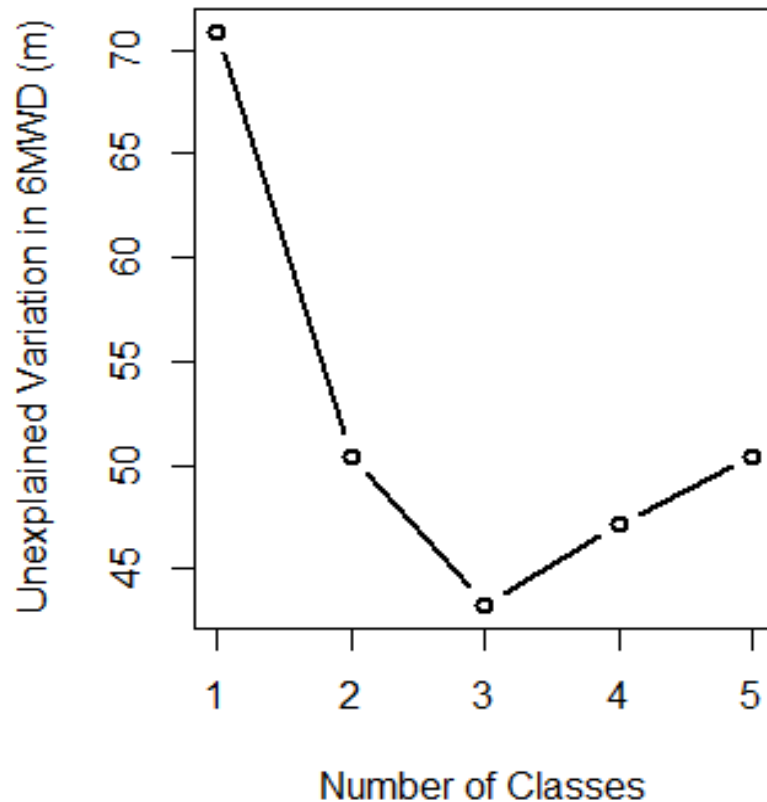
Cluster age-based 6MWD trajectories?

Models for 6MWD trajectories to be compared:

- A. $age + age^2$***
- B. $age + age^2$ with 2 classes***
- C. $age + age^2$ with 3 classes***
- D. $age + age^2$ with 4 classes***
- E. $age + age^2$ with 5 classes***

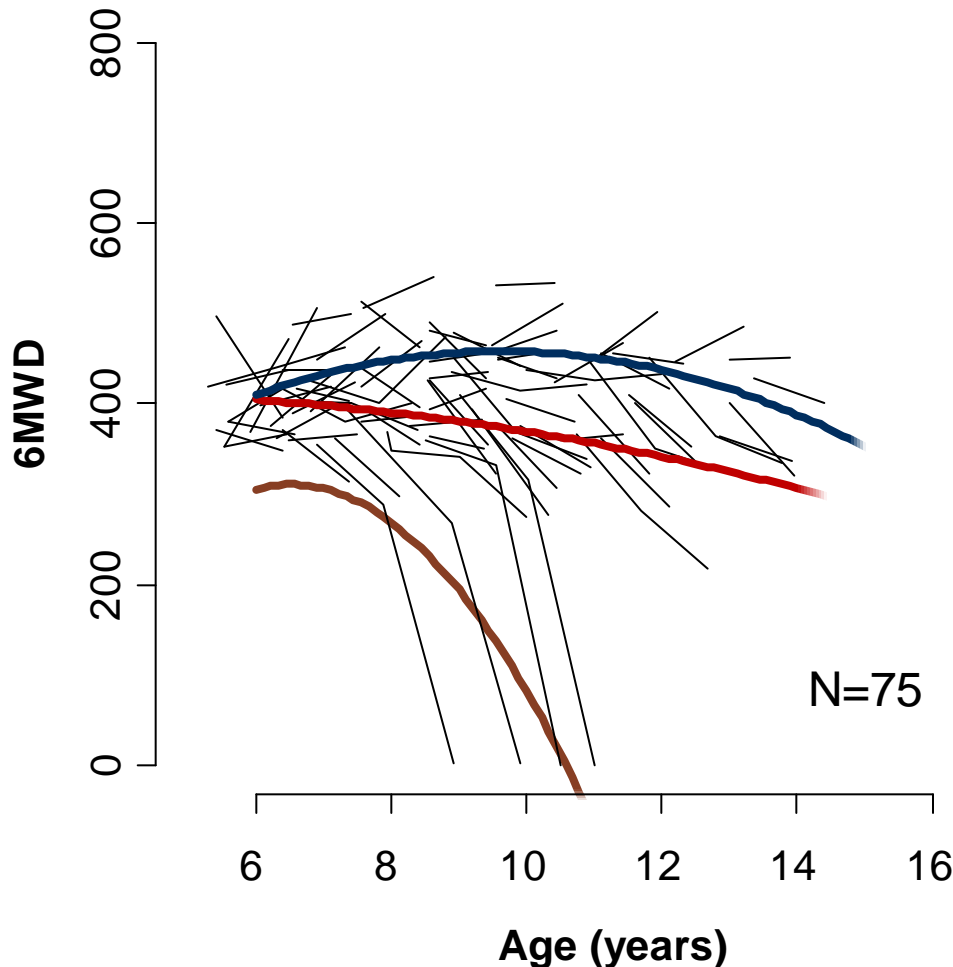
Which model best explains the data?

How many clusters?



- 3 classes fit better than 1 or 2
- SD for unexplained variation reduced **71m → 43 m**

Incorporating more data for boys with baseline 6MWD > 350 m



Additional data extracted
from Lee Sweeney et al.

Total N = 75

Three clusters vs. two
vs. one:

- Improved statistical measures of model fit; three clusters was best
- Three clusters reduced unexplained variance in 6MWD **71m => 43m**

Take-aways

- There are strong signs of trajectory clustering
- Marked reduction in unaccounted for variance ($> 50\%$)
- Next: Validation in independent, larger samples

cTAP Access to Patient Data

Progress in Year 1

- Data Sources
 - 2 multi-center clinical registries
 - 2 large neuromuscular clinical practices
 - US and EU
- >1260 patients
- > 90% with dystrophin genotype
- >5000 patient-years
- >>35,000 data points

But wait – so much patient data beyond 6MWD

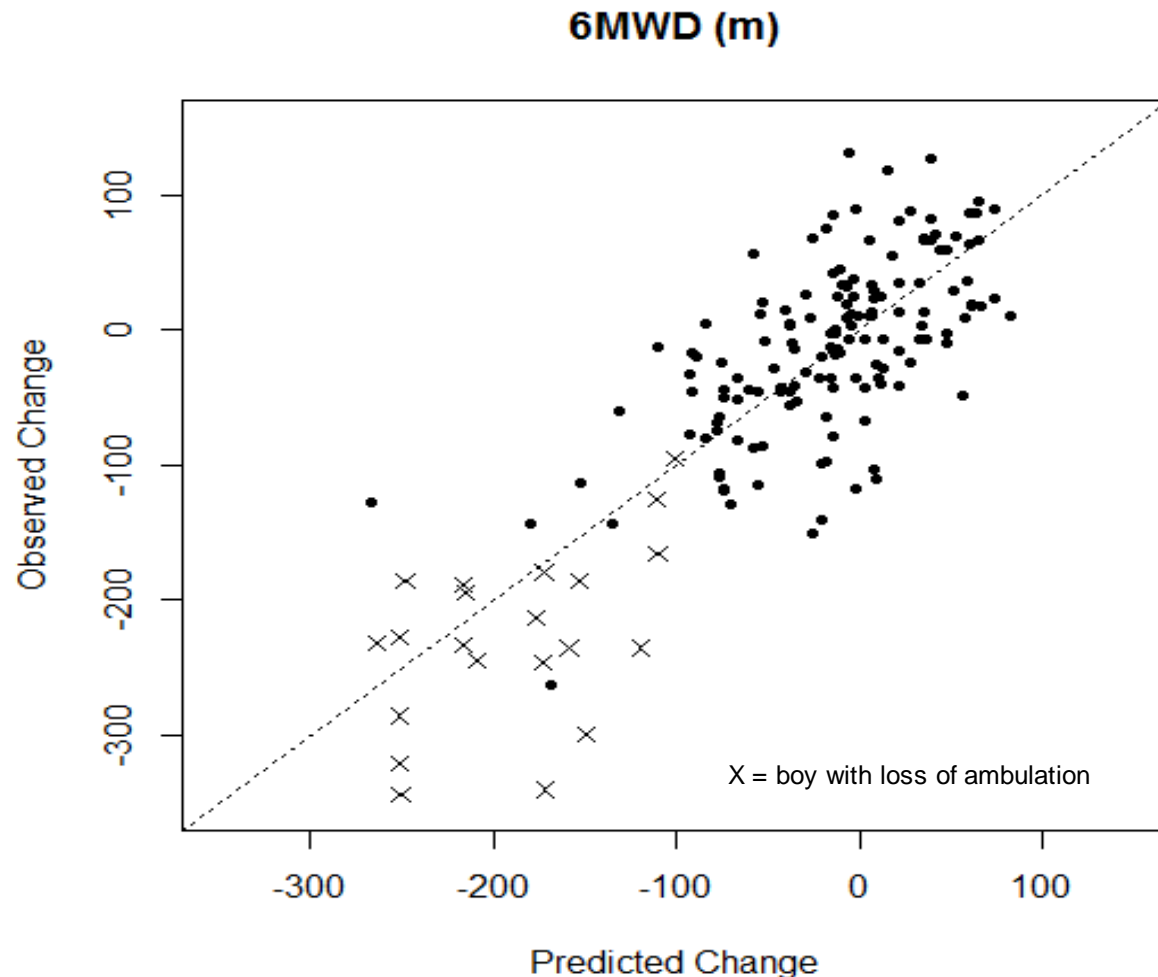
- Ambulatory function
 - NorthStar Ambulatory Assessment (NSAA)
 - 21 parameter assessment
- Timed Functional tests
 - Rise from supine
 - 10 mwr
 - 4 SC
- Non-ambulatory function
 - pulmonary
 - cardiac
 - Bone density

- Patient Reported Outcomes
- History of steroid use
 - Drug, regimen
 - Age at GC start, duration
- Dystrophin genotype
- Age, Height, weight, BMI

Will additional parameters improve prognosis?

Prognostic model Preliminary Results

Observed vs. predicted annualized change in 6MWD



*Don't assume
traditional methods
have been
exhausted!*

Multiple pivotal trials failed to meet primary endpoint

Impact of reduced variance on power

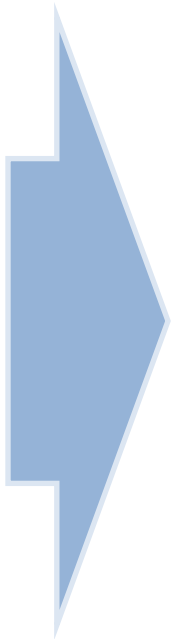
Treatment effect (m)	Unexplained variation (m)						
	40	50	60	70	80	90	100
20	96%	84%	69%	56%	45%	37%	31%
25	100%	96%	87%	75%	64%	54%	45%
30	100%	99%	96%	89%	79%	69%	60%



Approximate power in a trial of n=110 treated vs. n=110 controls

Reduced variance: Translation to Drug Development

Describe, Predict, Simulate



- Inform trial design and analysis
- Enable natural history controls
- Inform biomarker evaluation
- Establish value of endpoints for regulators and payers

Regulatory Science Workshop - Implications

Tension:

Impact/Value of markedly greater power

VS

Regulatory Risk (Guinea-pig(s))



- Any “Non-traditional” statistical approach
- Safe(ish) Zones => Regulated applications
- Leverage beyond Duchenne

cTAP: a collaborative, analytical Platform

Pre-Competitive	OBJECTIVE, INDEPENDENT
De-identified patient data	SHARE DATA EQUALLY
Analyses, at scale	IMPACT- NOW
Financial Resources	FLEXIBLE
All stakeholders	A FIRST IN DMD

*More effective drug development => enable
drugs to patients sooner*

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