## **Biology as a Search Problem**

Milo Lin Green Center for Systems Biology Department of Biophysics Center for Alzheimer's & Neurodegenerative Diseases



Levent Sari Ph.D.



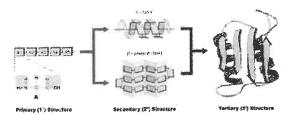
Mario Di Salvo Ph.D.



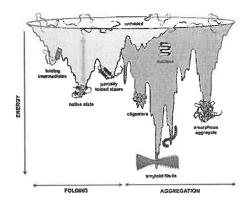
Paul Blazek MSTP



Preamble: Protein Folding

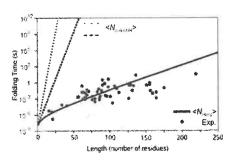


#### Many states in protein conformation space



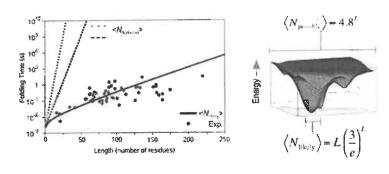
...but life chooses only a few

## How Do Proteins Fold So Quickly?



Lin & Zewail, PNAS 2012

Lin & Zewail, PNAS 2012



...there is a length limit

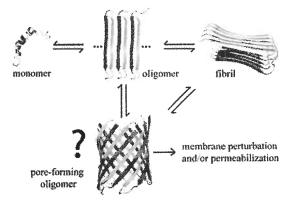
confolded

saiding intermediates
portally societ states
autoparates
amplicat Rains

FOLDING AGGREGATION

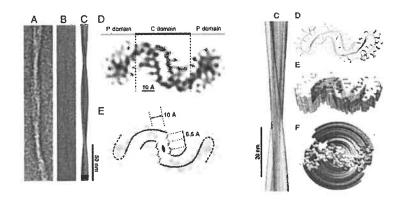
...but life chooses only a few

# Unraveling how protein aggregation leads to Alzheimer's Disease



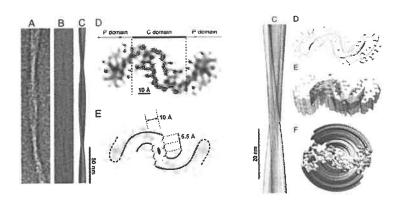
...and what kind of aggregate causes disease?

#### The amyloid is the easiest to see



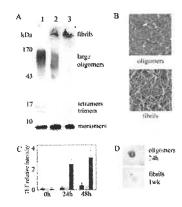
Schmidt et al, PNAS 2015

#### Much effort has focused on the amyloid



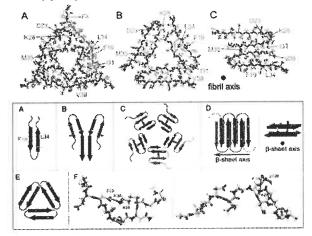
...yet drugs targeting the amyloid have all failed

#### In fact, the oligomers seem to be the toxic agents



perhaps we should find and target oligomer structure

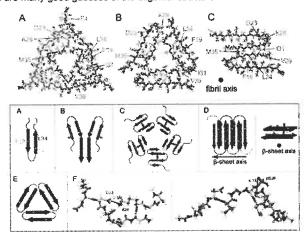
## There are many good guesses of the oligomer structure



Petkova, Leapman, Guo, Yau, Mattson, Tycko, Science 2005 Luhrs et al, PNAS 2005

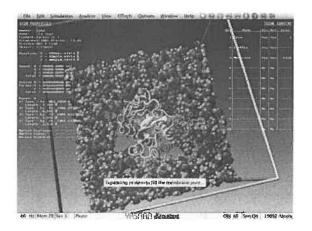
Ahmed et al, Nature Struc Mol Biol 2010 Spencer, Li, Nowick, J Am Chem Soc 2014

## There are many good guesses of the oligomer structure

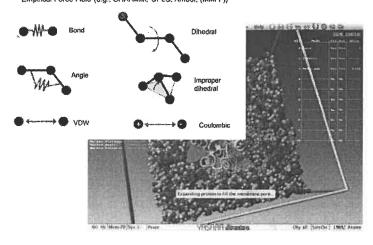


...but we do not yet know the structure(s)

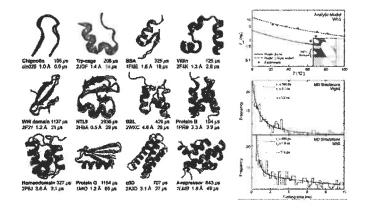
#### Simulating protein folding using Newtonian mechanics



#### Potential Energy Empirical Force Field (e.g., CHARMM, OPLS, Amber, (MMFF))



## Simulating protein folding using Newtonian mechanics



Lindorff-Larsen et al, Science 2011

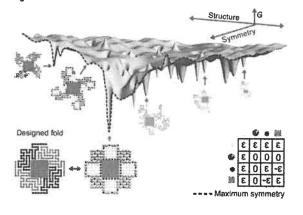
Lin et. al, PNAS 2011, 2012, 2014

This is hard to compute for two main reasons:

- I. Conformational space is huge
  - conformation space scales as e  $(L^*N)$  where L= protein length and N= # of proteins
- II. Kinetic trapping

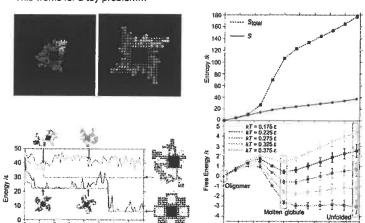
energy barriers of a few tens of kT are common for proteins

#### Tackling challenge I

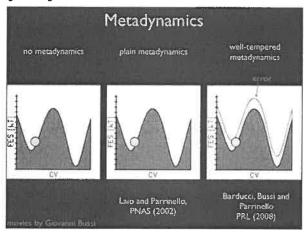


...there is folding symmetry that we can exploit

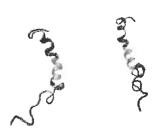
#### This works for a toy problem...



Tackling challenge II



Abeta42 dimers

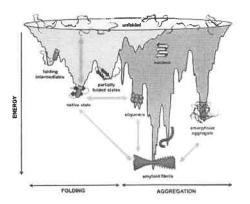


NO SYMMETRY CONSTRAINT

Ment .

WITH SYMMETRY CONSTRAINT

#### A real free energy landscape for protein folding and aggregation



#### Thanks!







Friends of the Alzheimer's Disease Center

Cecil H. and Ida Green Endowment UTSW Endowed Scholars Program