Multiple Myeloma

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Multiple myeloma

- Cancer of **malignant plasma cells in the bone marrow** which produce abnormal proteins
- ISS staging
  - Indication of severity of disease
  - Primarily determined by levels of **albumin** and **abnormal monoclonal immunoglobulin** in blood
- Moderate prognosis
  - Median survival: 3 years
  - Ranges up to a life expectancy of 10 years

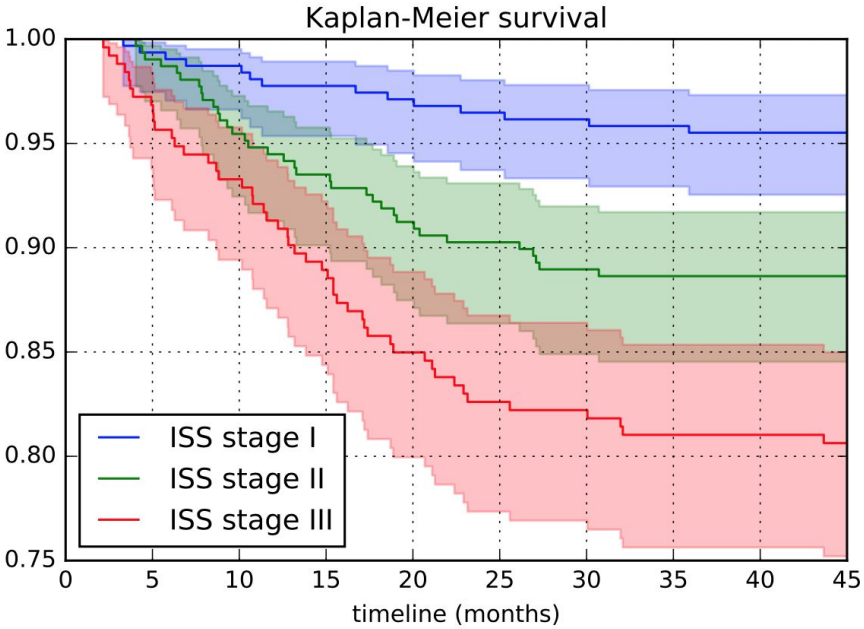
Datasets

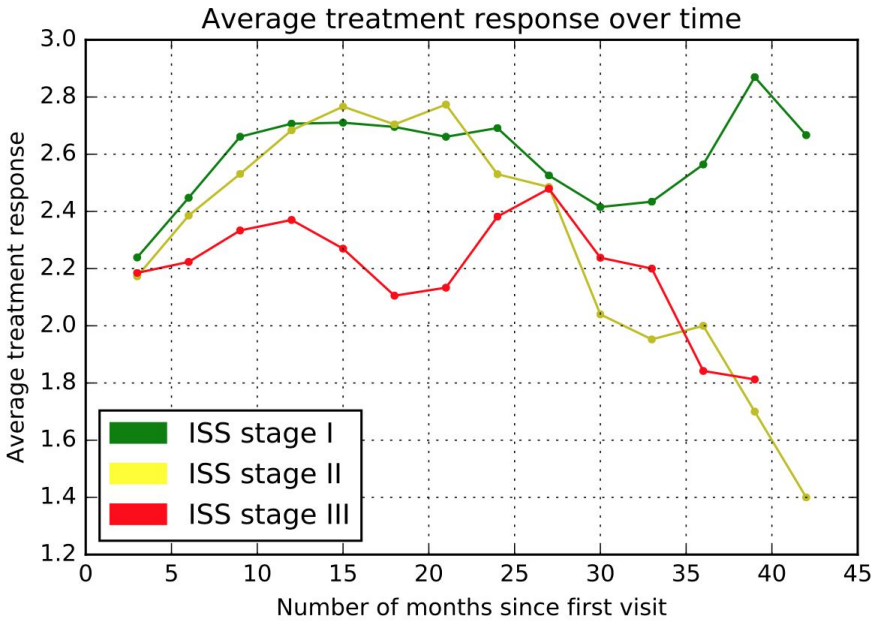
- CoMMpass dataset: ~1000 patients
- Clinical Data
  - Demographic: race, ethnicity, height, weight, age
  - Medical history: number of pre-existing conditions
  - Nominal characteristics: transplant, non-responder
  - Per visit: treatments assigned and therapy class, had transplant, treatment response
  - Lab test results
- Genomic data
  - **FISH** (fluorescence in situ hybridization): measure levels of **genetic material** in cells to assess expression of **cancerous abnormalities**

Investigated problems

- Identifying patient subgroups
  - Treatment **non-responders** (died within 2 years) vs. responders
  - Abnormal genetic differences
- Investigating **genes** targeted by **treatments**
- Predicting **treatment response**

Survival and treatment response





Non-responder Subgroups

ISS Stage	Number of Non-responders	Total Size of Subgroup
1	11	312
2	30	308
3	44	253

Patient	Bob
Age	70
Height/Weight	64.96 in / 154.32 lb
Pre-existing Conditions	2
Race	White

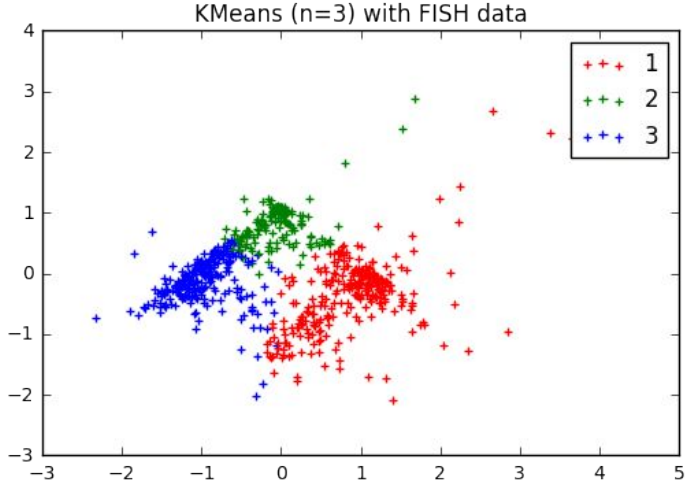
Visit Day	78	161	189	302	427	505
Treatments Started	Bor, Len, Dex (Autologous)			Bor, Len, Dex		Bor, Len, Dex
Treatements Ended		Bor, Len, Dex		Bor, Len, Dex		
Response	Partial Response	Very Good Partial Response	Very Good Partial Response	Very Good Partial Response	Progressive Disease	Progressive Disease

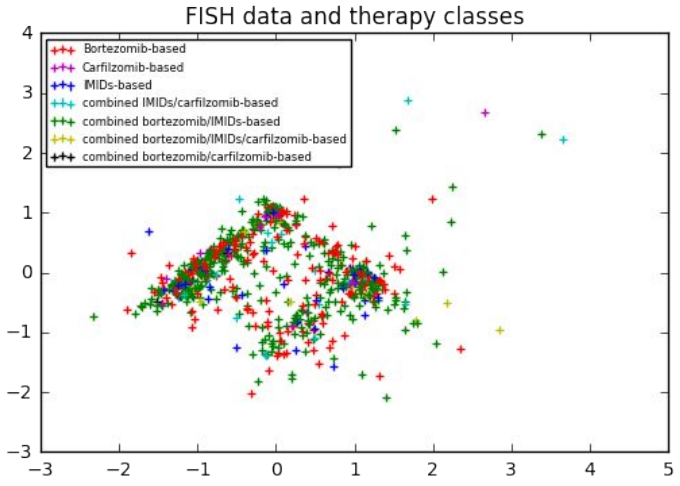
ATE of transplant on nonresponse

- Non-response: died within 2 years
- **~45%** of patients received a transplant (stem cell or autologous)
- Used logistic regression to calculate propensity scores
  - AUC = 0.87
- ATE = **-0.501**
  - Patients who get transplants have better outcomes on average

Linking treatments with genetic targets

- Most changed genetic abnormalities for each therapy class
  - **Carfilzomib-based:** CDKN2C, RB1, TRAF3
  - **Combined bortezomib/IMIDs-based:** 13q14, 13q34, 17p13, BIRCs, CDKN2C, CYLD, RB1, TP53, TRAF2, TRAF3, UTX





Predicting treatment response

- Features included demographic information, previous treatment and response, current treatment and therapy class, FISH data, etc.