## AI-based identification of Tumor Neoantigens from NGS data

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Korea-Japan-China Bioinformatics Symposium 2018

## BM<sup>2</sup>: Biological and Medical Big data Mining group





AI & Machine Learning Methodology and Platform

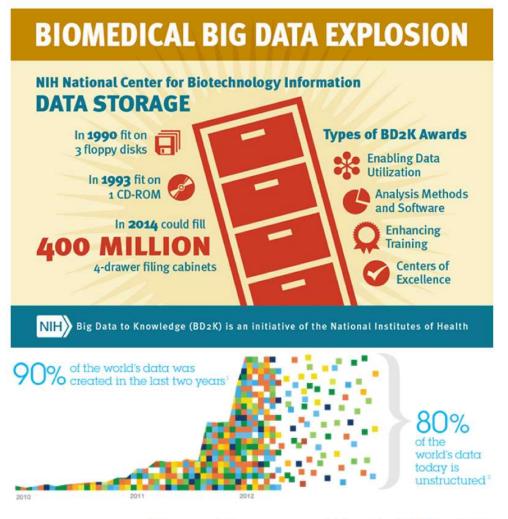


**Drug informatics** 

**Genome editing analysis** 

Tumor immuno-therapy data analysis

- ⋆ biomedical big data explosion
  - "..exceeds researchers' ability to capitalize.." (NIH)



source: National Institutes of Health (NIH), IBM

- \* needs for precise analysis
  - ► BD2K initiative (\$656 mil)
  - ► PM initiative (\$215 mil)



## Al/machine learning boom in biomedicine





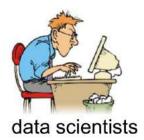




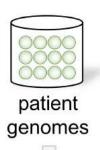


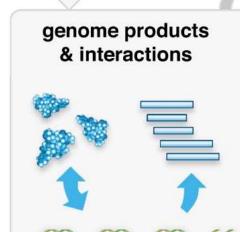


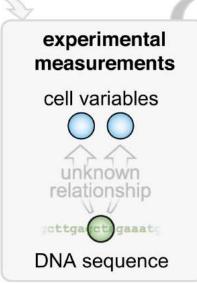


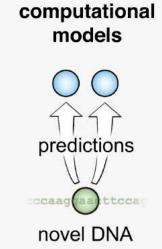


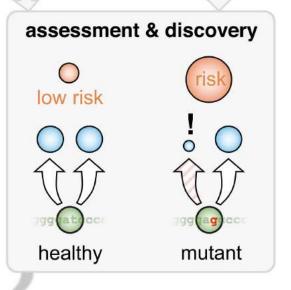




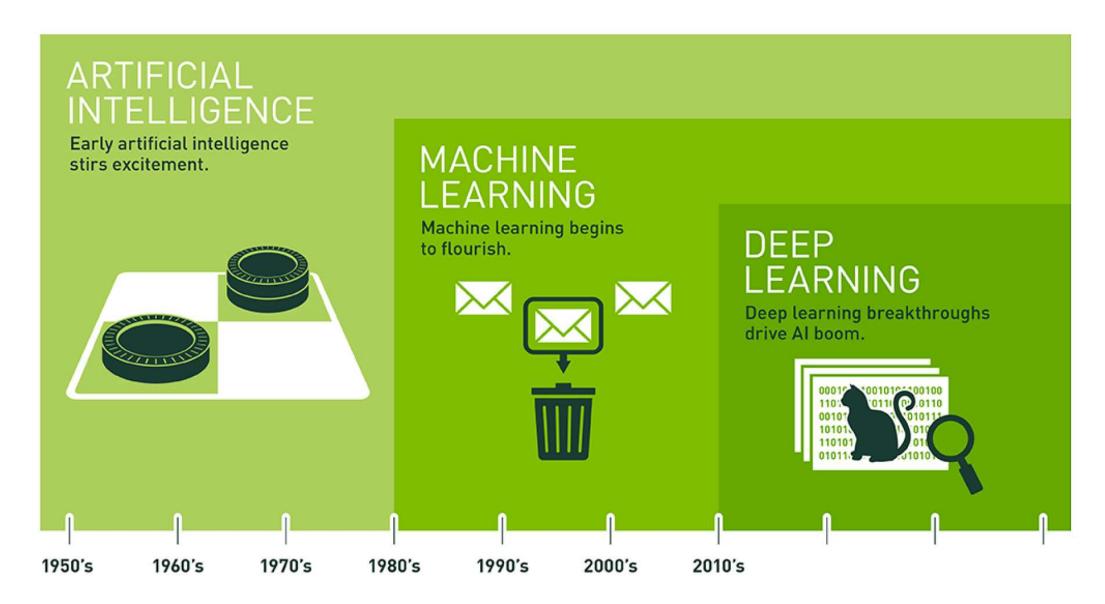




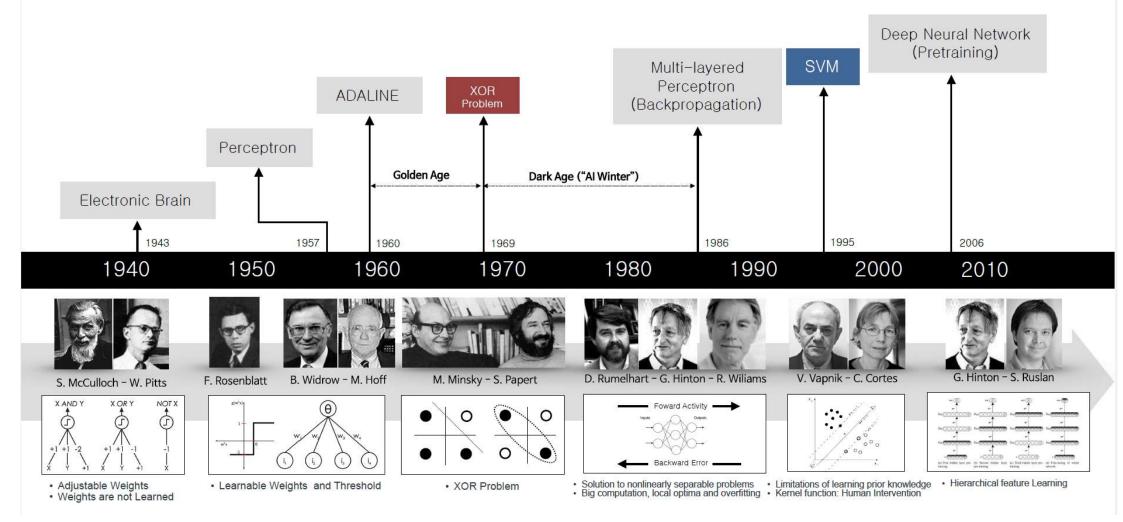




feedback from validation



Since an early flush of optimism in the 1950s, smaller subsets of artificial intelligence – first machine learning, then deep learning, a subset of machine learning – have created ever larger disruptions.



#### \* AlphaGo (DeepMind)



## ⋆ TPU (Google)



## Google claims its Tensor Processing Unit (TPU) is 7 years into the future ahead of Moore's Law

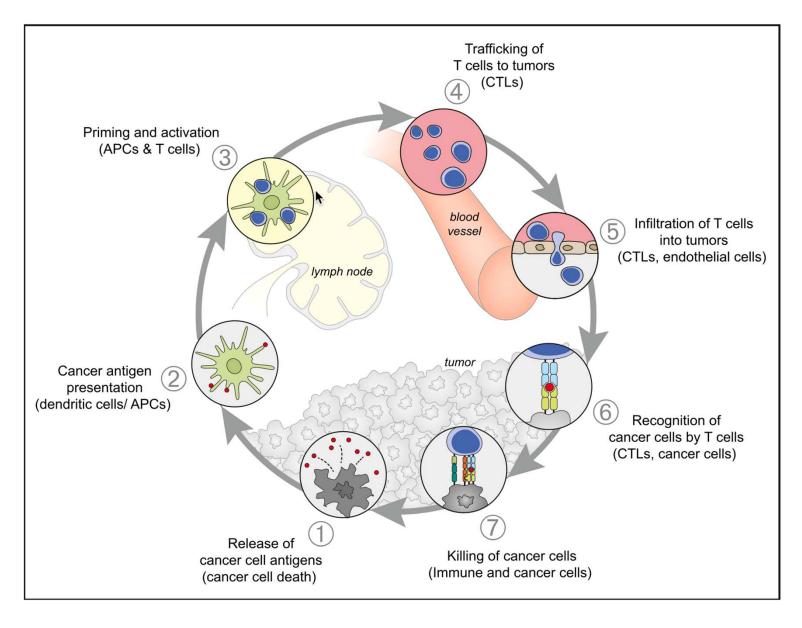
05/18/2016 - 23:03 | Norm Jouppi



iTunes: <u>identification of Tumor ne</u>oantigens from NG<u>S</u> data

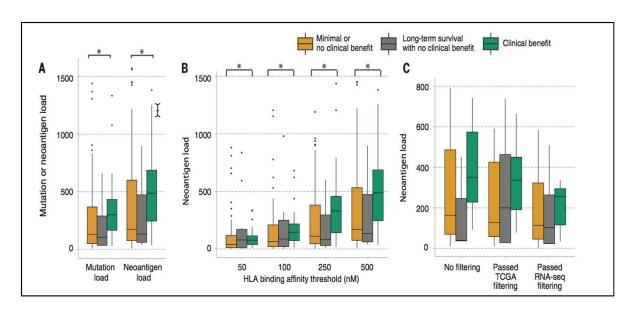
#### **Background and Significant**

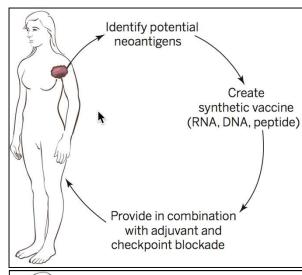


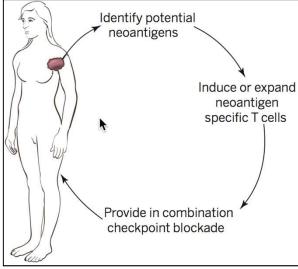


## 1

#### **Background and Significant**









#### **Background and Significant**

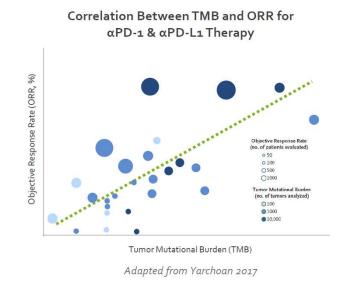


#### Neoantigens Represent Ideal Tumor Targets



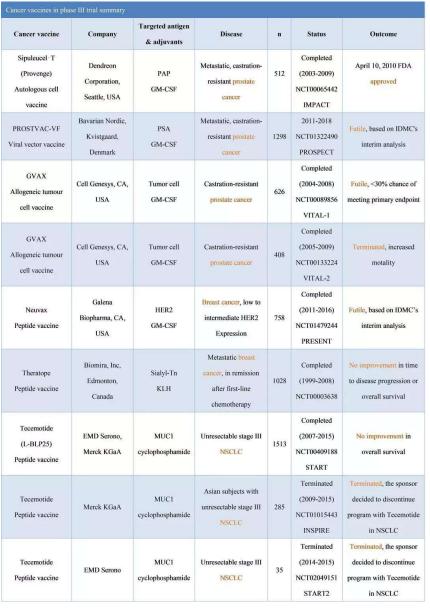
## NEOANTIGENS ARE FUNDAMENTAL TO IMMUNE CHECKPOINT ACTIVITY

(van Rooij et al 2013, Gubin et al 2014, Rizvi et al 2015)





## Cancer vaccine development







#### **HHS Public Access**

Author manuscript

Nature. Author manuscript; available in PMC 2018 January 13.



Nature. 2017 July 13; 547(7662): 217-221. doi:10.1038/nature22991.









## 1

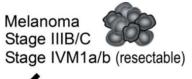
#### **Background and Significant**



a

Tumor procurement

Peripheral blood

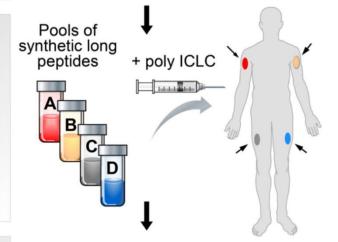


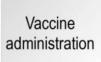
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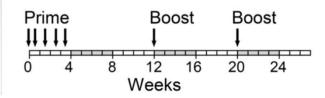
Target selection

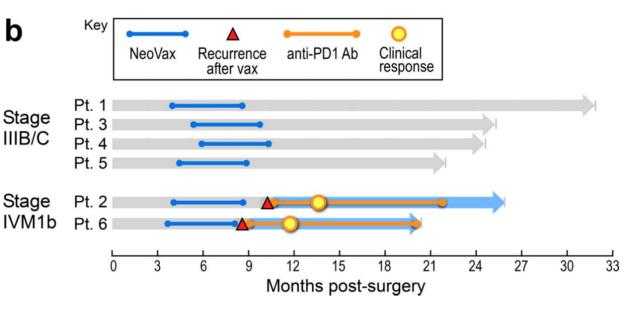
- DNA and RNA sequencing to identify tumor-specific mutations
- HLA-typing
- Prediction of personalized HLAbinding peptides

Personal vaccine manufacture

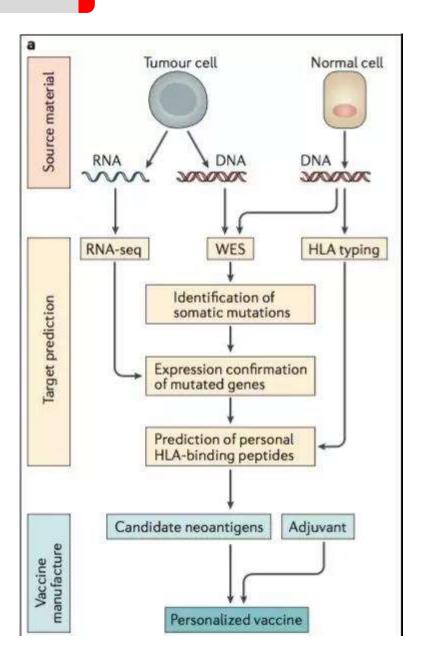






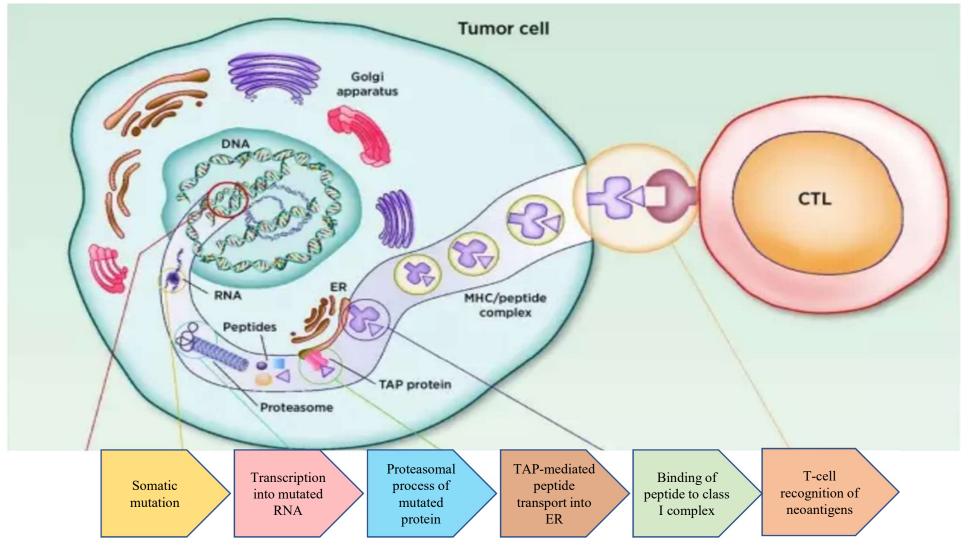




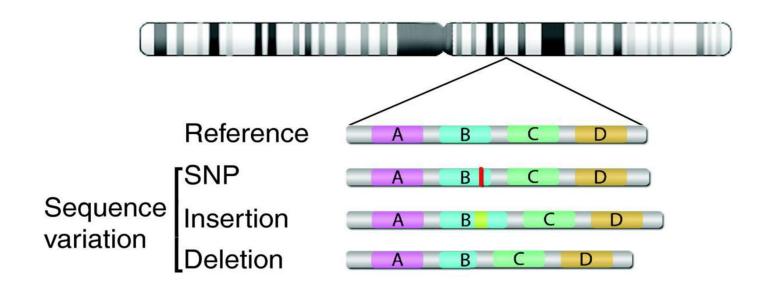




## Big picture

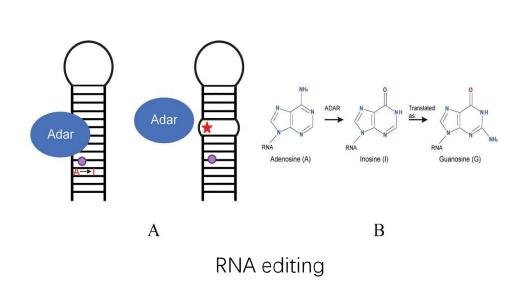


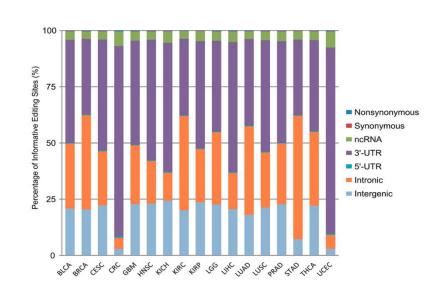




**Neoantigen sources: Mutations** 







RNA editing distribution

Neoantigen sources: Transcriptome modification



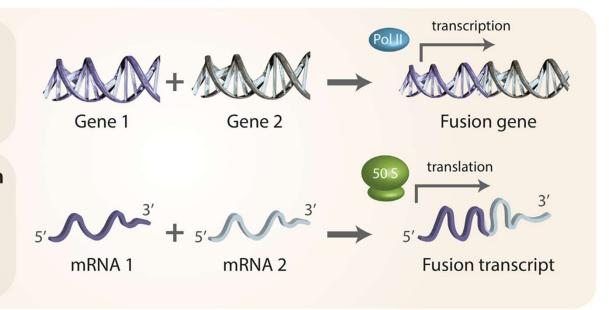
#### Gene fusion formation

## A Fusion by structural rearrangements

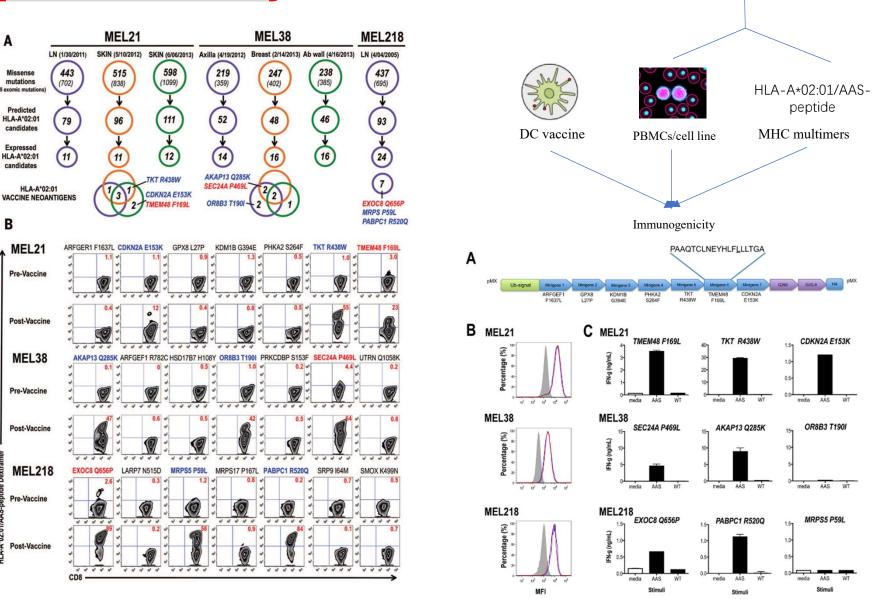
Translocations, inversions, deletions and insertions

## B Fusion by transcription or splicing

Transcription read-through, mRNA *trans*-splicing or *cis*-splicing



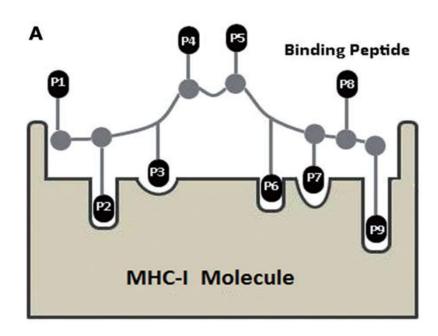
Neoantigen sources: Gene fusion





Spontaneous Immunity





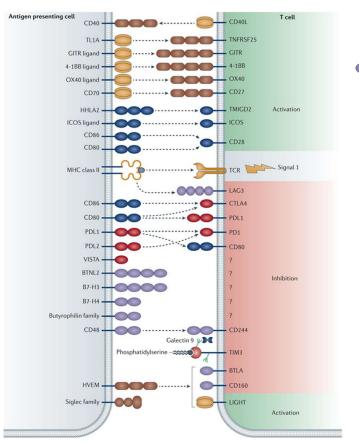
Peptide:8-11bp

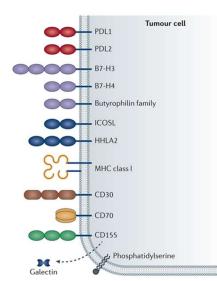
MHC-I type

Similarity between mutant peptides and normal peptides

Peptide\_MHC-I binding affinity



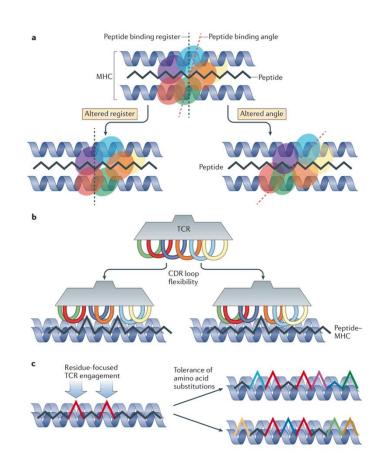


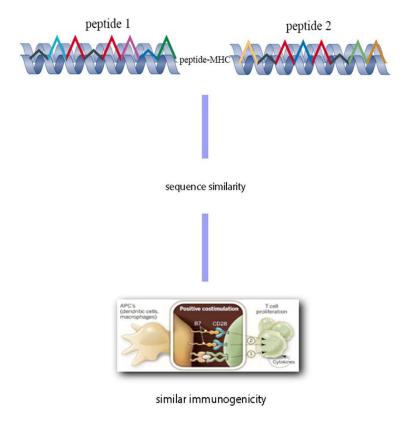


- 1. Many co-receptors
- 2. Lower binding affinity
- 3. Long TCR sequence

pMHC-T cell recognition

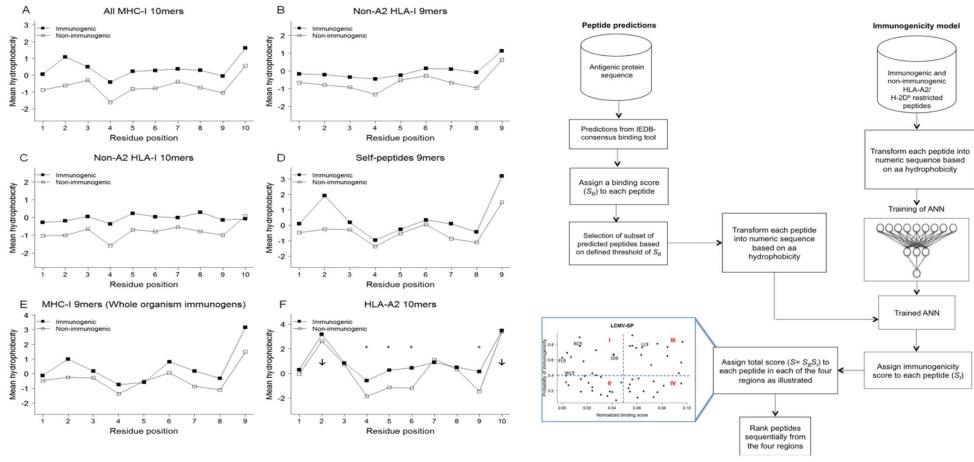






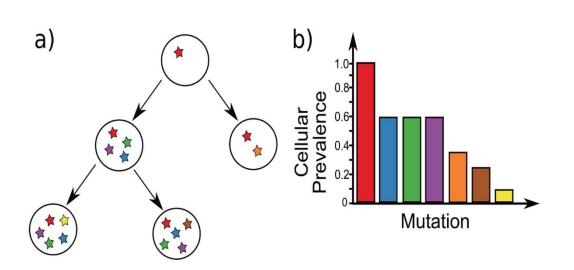
Sequence similarity-based T cell recognition probability

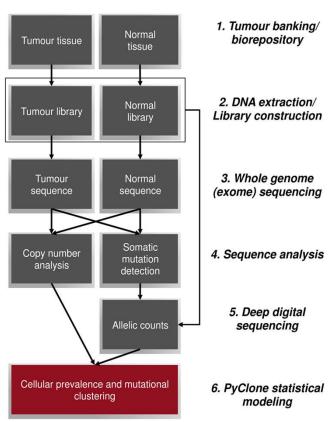




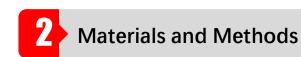
Hydrophobicity





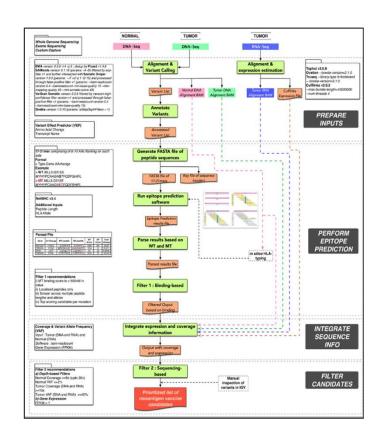


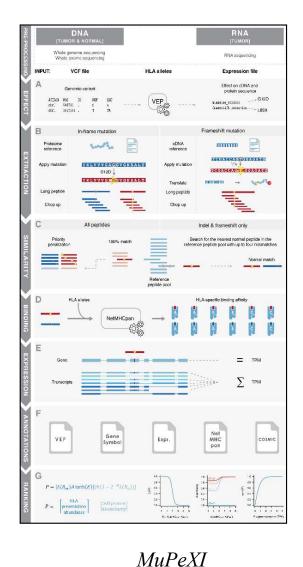
Cellular prevalence

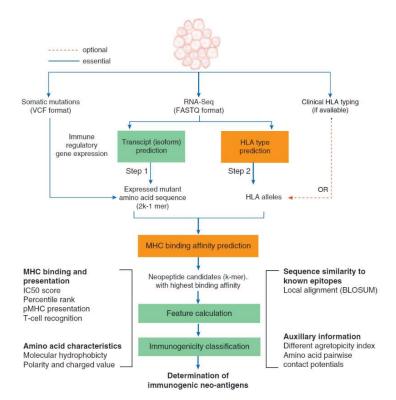


## Available tools









pvac-seq

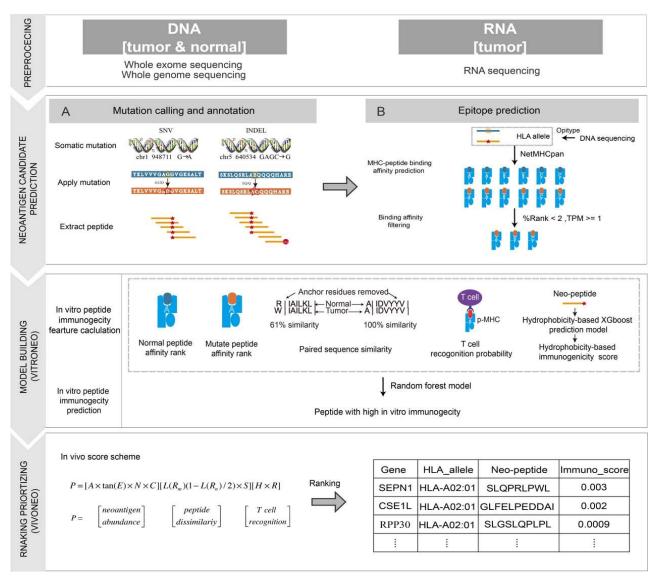
Cancer Immunology Immunotherapy, 2017

Neopepsee

Annals of Oncology, 2018

Genome Medicine, 2016

## **iTunes**







#### **Acknowledgement**



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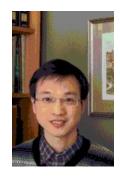
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@Mass Medical School



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@East Hospital



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国家重点研发计划慢病专项 2016

国家重点研发计划精准医学专项 2017

# From Data to Therapy, A Long but Prospective Way to Go

