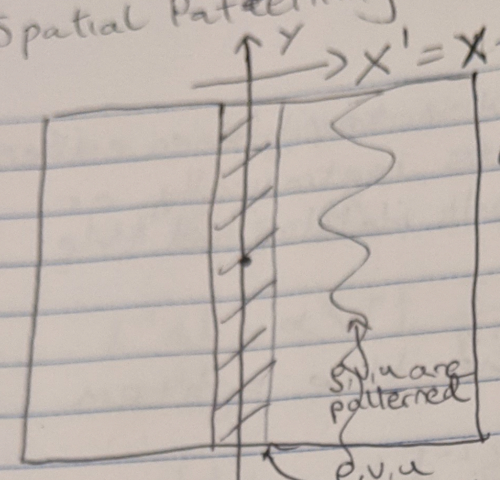
Spatial Patterning

speed of MF

$x' = x - vt$ MF @ $x=0$

$\Rightarrow$ we are in ref frame of furrow.

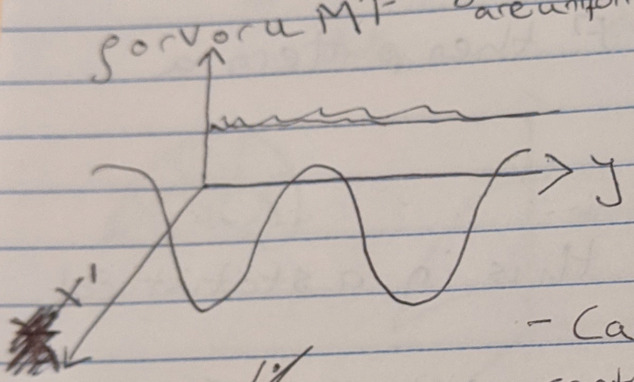


We have the following field measurement.

1) ρ, density

2) v, velocity

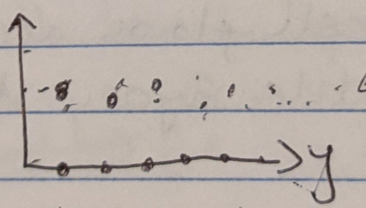
3) u, fate.



~~we will treat x' as the~~

- Can I treat x' as the control parameter?
- Is the system invariant, statistically in $x' = x - vt$ ref. frame?

consider $u(y)|_{x'}$



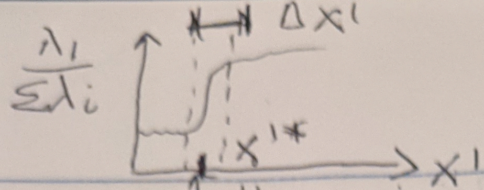
each time pt gives a different set of us and vs.

- Two ways to look at the data.
  1) PCA 2) Fourier

Option 1: PCA

@ each x' $\rightarrow$ PCA of $\{u(y)\}$ $\rightarrow$ which pts. along y covary

- expect ~~that~~ at $x' \approx 0$ you will have an evalue spectrum with no gap $\rightarrow$ at some x' I expect a gap to open up



↳ the region where the uniform solution looses stability.

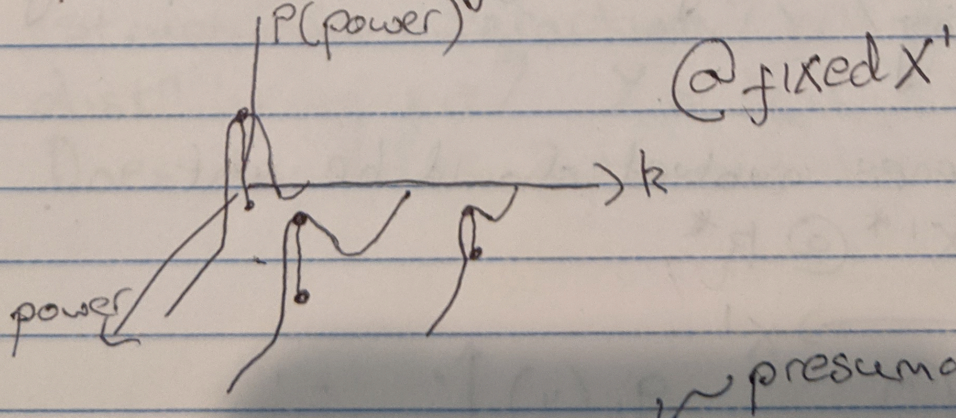
Q: Do we see this in A (area), V (velocity), or U (gate)? Do they all have a similar signature in the same region?

If yes then maybe we are in business.
→ then pursue option 2.

Option 2: Fourier:

- Within a $\Delta x'$ window around x'^* perform a Fourier analysis. Q: what does this mean?

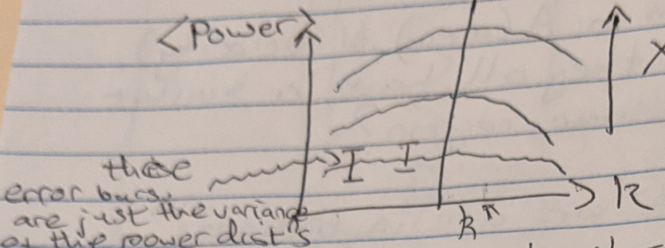
- At each value of x' calculate the power at a wavemode k. Since we have many renditions of the system (different time points of the movie) we will get a distⁿ of power at a given x' and k.



presumably close to x'^*

- I expect @ some x' a band of k will have substantially more power.

- So what do we plot?



Q: is this what we see?

- A: Does the PC1 at $x' = x'^*$ correspond to the k^* seen through the Fourier analysis?

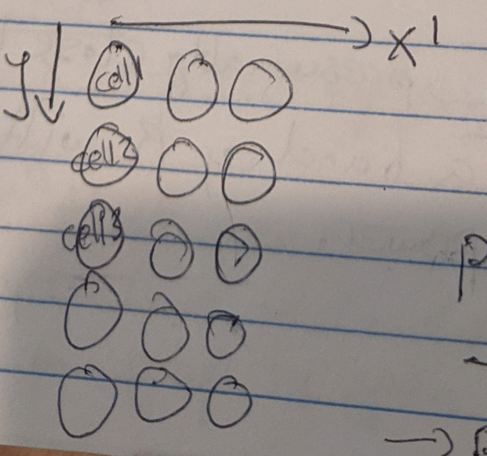
Q: What does this look like in the Sca mutant?

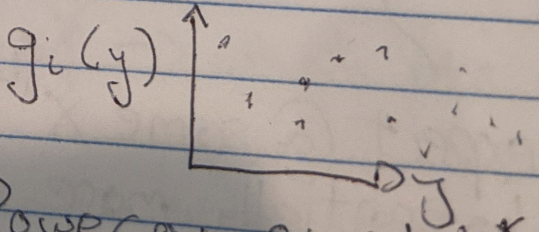
Q: What does the above plot look like for the different fields?

Q: Now what if we had high dimensional gene expression data, and wish to identify the genes participating in this patterning?

A: loosely, the genes involved should be most variable ~~@~~ @ x'^* @ k^*.

$\Rightarrow$





Power of g_i ~~at~~ k^* @ x'^*

$\rightarrow p_i^* \rightarrow Cov(p_i^*, p_j^*)$

$\rightarrow PC_1$