AI based portable Hospital

Team Members:

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2. Sidik Mohamed Hassan---Zhejiang university of science and technology
3. Angel---Tsinghua University

Team Members

- Abdul Etibaroghlu

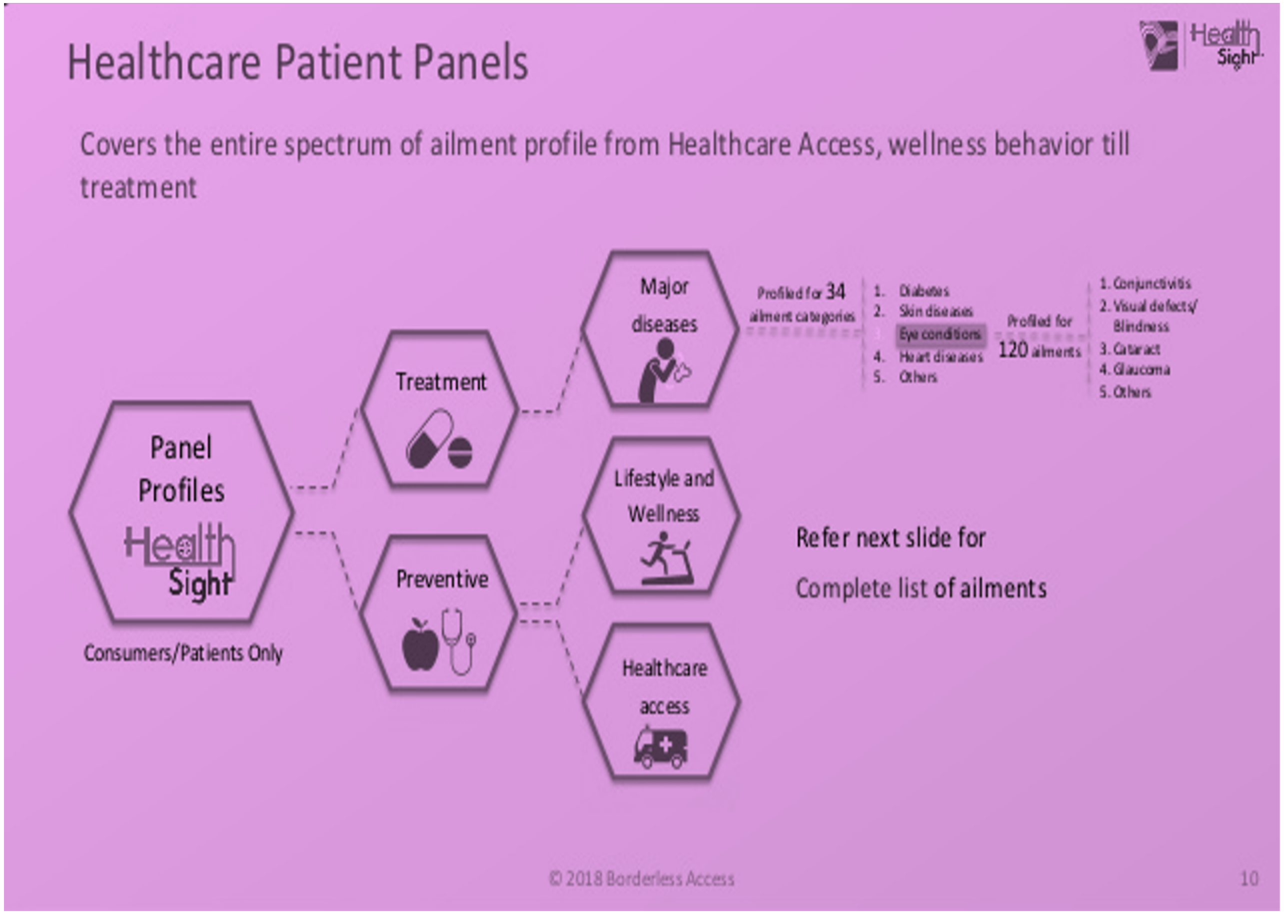
Azerbaijan,

Zhejiang Normal University,

Master of Biology

What we designed?

Portable Hospital, let AI decides:

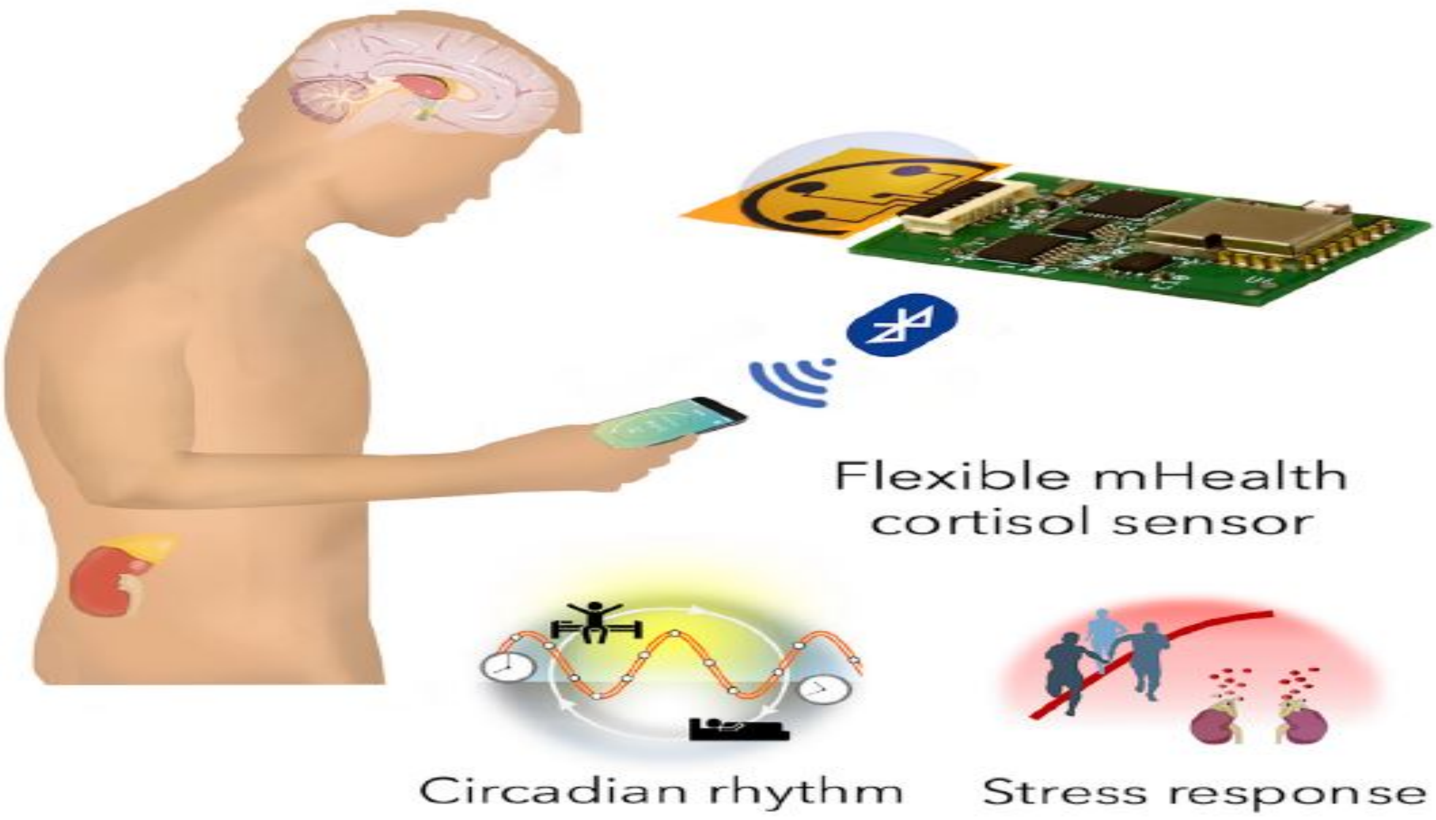


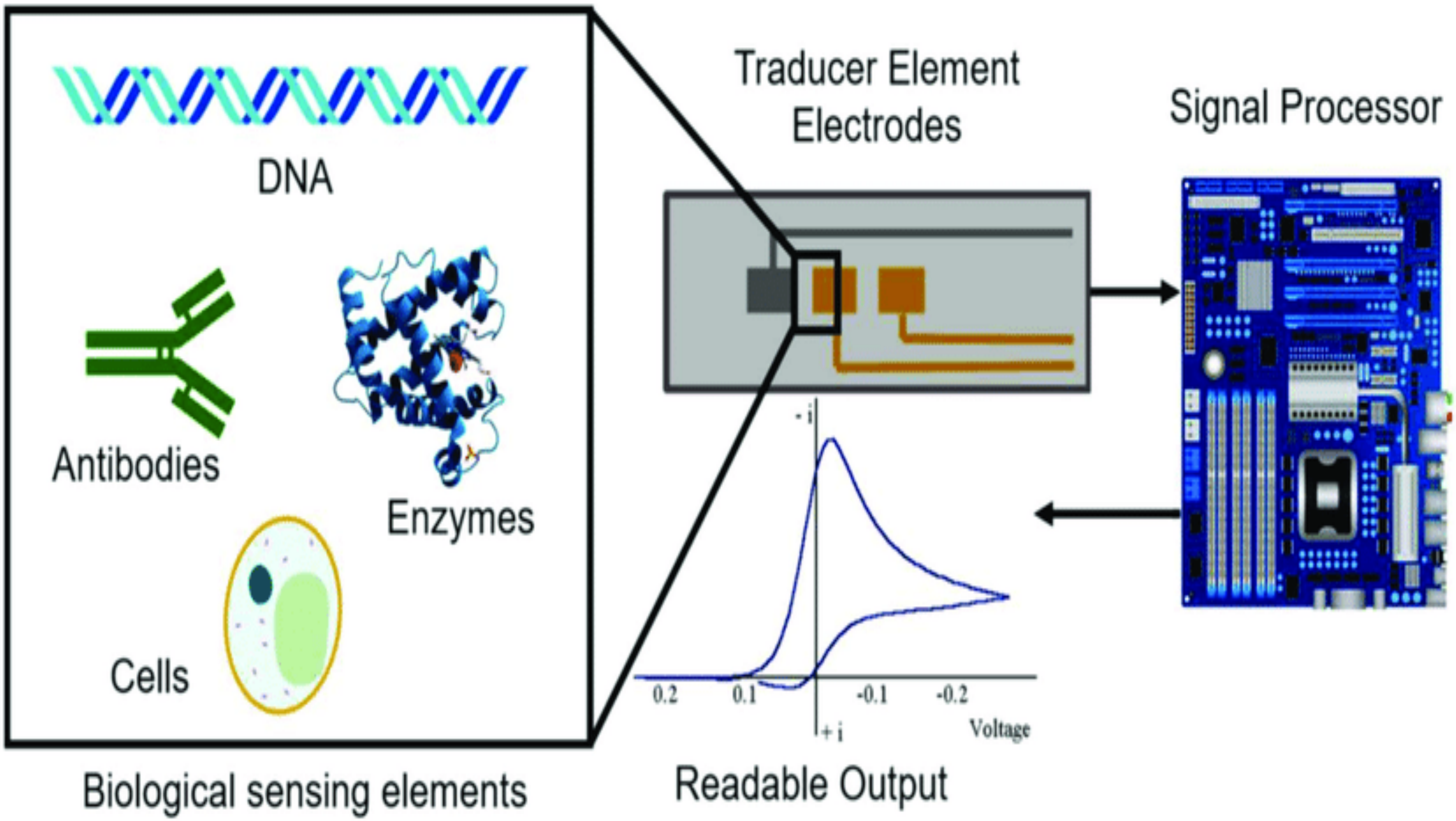
Decides based on your daily routine and health status history:

Tracks: blood pressure, melatonin level in blood, testosterone level, sweat analysis,

How it works?

Electrochemical Biosensors




DNA
Antibodies
Enzymes
Cells
Biological sensing elements
Traducer Element
Electrodes
Signal Processor
- i
+ i
0.2
0.1
-0.1
-0.2
Voltage
Readable Output

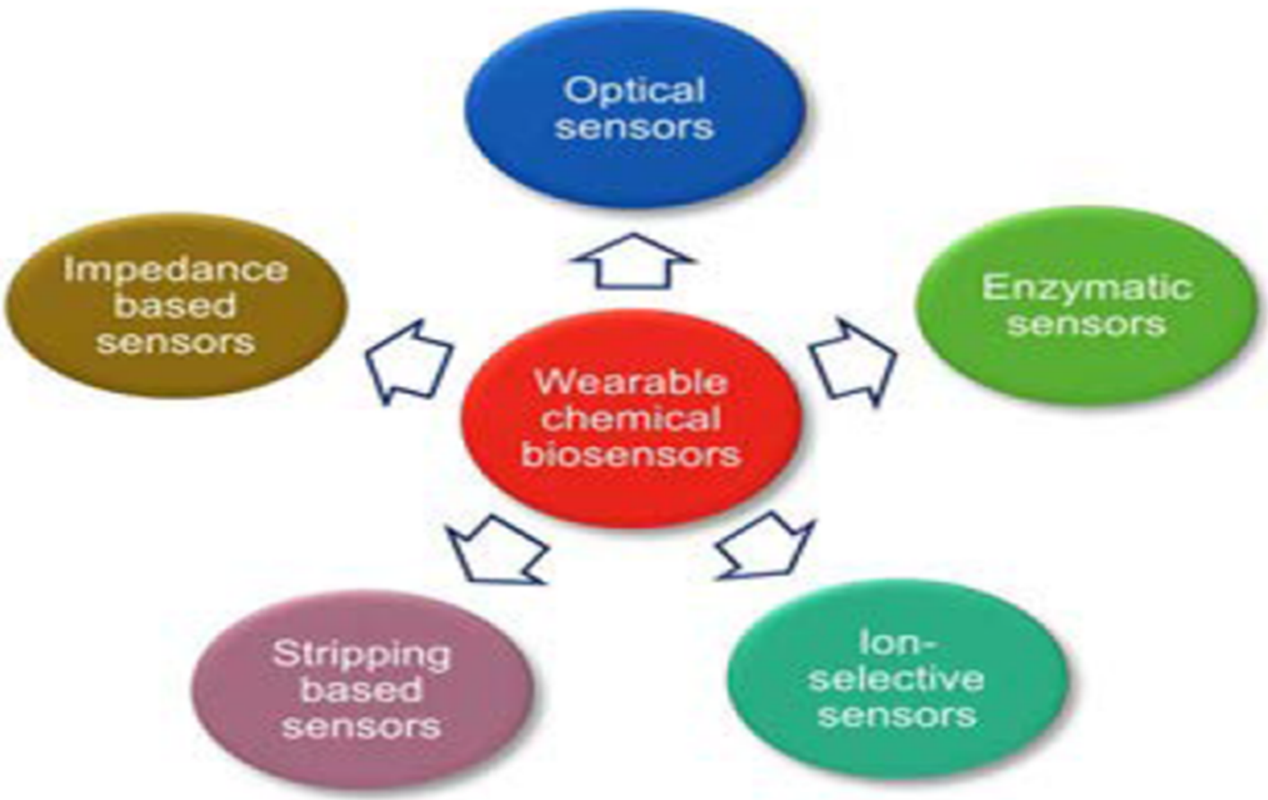
Team member

- Name: Sidik Mohamed Hassan
- School : Zhejiang university of science and technology
- Master of chemical engineering

Sweat biosensor

- Human sweat, a very important bio fluid, consists of water (99%), ions (Na^+, K^+, Ca^{2+}, etc.), metabolites (glucose, lactate, ethanol, etc.), hormones, small proteins and peptides, providing a wealth of chemical information about physiological and metabolic status.

DETECTION TECHNIQUES

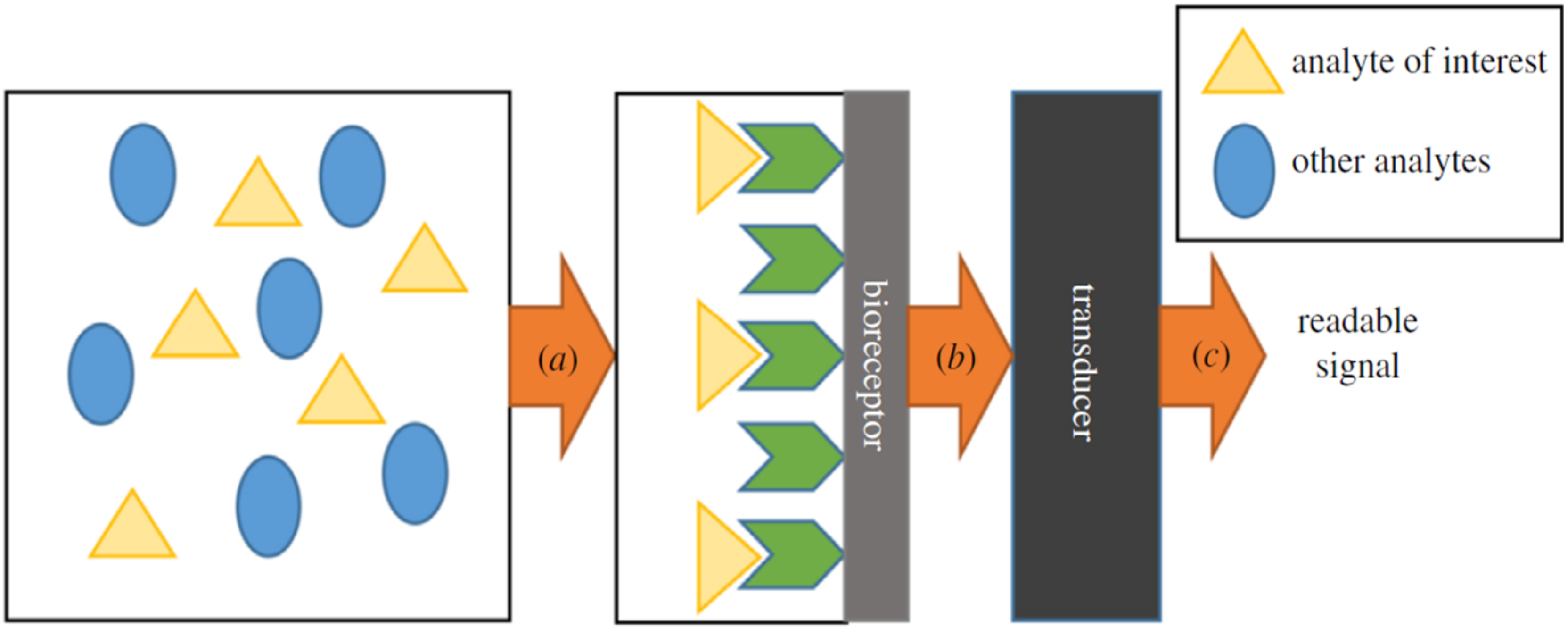


Types of biosensor and the analytes they can detect in sweat

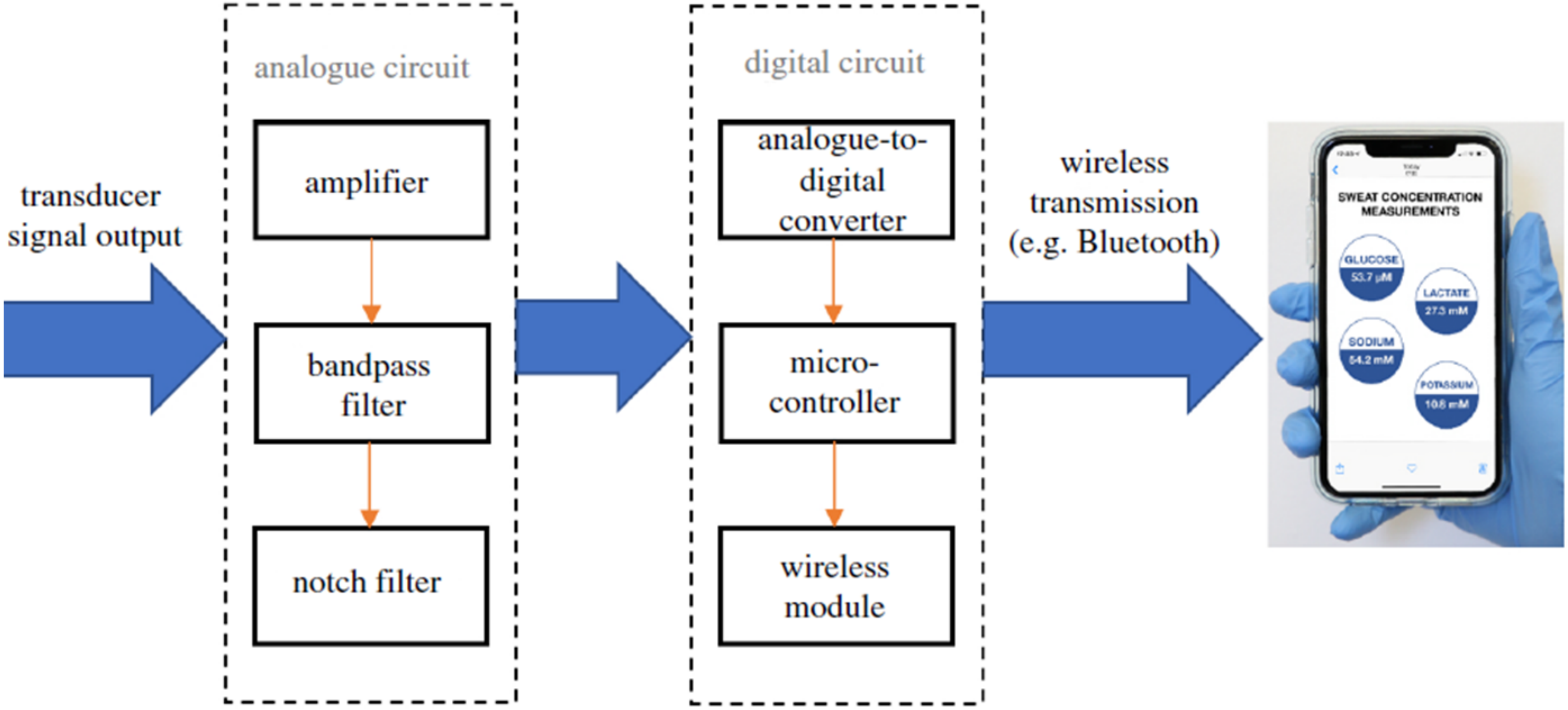
sensor	analyte/data of interest
optical	sweat rate pH level OH^-, H^+, Cu^+, Fe^{2+}
impedance-based	sweat rate sweat conductivity
ion-selective electrodes (ISEs)	pH level Na^+, H^+, K^+, NH_4^+, Cl^-, Mg^{2+}, Zn^{2+}, Ca^{2+}
enzymatic amperometric	metabolites (glucose, lactate, ethanol, uric acid)
stripping-based	heavy metals (Cu, Zn, Pb, Cd, Hg)

The most common methods of detection are enzymatic amperometric and potentiometric ion-selective electrode (ISE)
sensors .

How To Design Sweat Biosensor



How does it work



Applications

cystic fibrosis	Chloride
hypoglycaemia	glucose
Ischaemia	lactate
Hypokalaemia	Potassium
Hyponatremia	sodium

Team member

- Name: Angel
- School: Tsinghua university
- Master degree of Mathematics Statistics

Data analysis of blood sugar data

- Brief statement: This data is about 27 diabates patients'health conditions. Serum total cholesterol(x1), glycerine(x2), fasting insulin(x3), glycated haemoglobin(x4), fasting blood sugar(y). We need to analysis how x1,x2,x3,x4 impact y

- Calculation:
- > mydata<-read.table("clipboard",header=T)
- > mydata

	No	x1	x2	x3	x4	y
1	1	5.68	1.90	4.53	8.2	11.2
2	2	3.79	1.64	7.32	6.9	8.8
3	3	6.02	3.56	6.95	10.8	12.3
4	4	4.85	1.07	5.88	8.3	11.6
5	5	4.60	2.32	4.05	7.5	13.4
6	6	6.05	0.64	1.42	13.6	18.3
7	7	4.90	8.50	12.60	8.5	11.1
8	8	7.08	3.00	6.75	11.5	12.1
9	9	3.85	2.11	16.28	7.9	9.6
10	10	4.65	0.63	6.59	7.1	8.4
11	11	4.59	1.97	3.61	8.7	9.3
12	12	4.29	1.97	6.61	7.8	10.6
13	13	7.97	1.93	7.57	9.9	8.4
14	14	6.19	1.18	1.42	6.9	9.6
15	15	6.13	2.06	10.35	10.5	10.9
16	16	5.71	1.78	8.53	8.0	10.1
17	17	6.40	2.40	4.53	10.3	14.8
18	18	6.06	3.67	12.79	7.1	9.1
19	19	5.09	1.03	2.53	8.9	10.8
20	20	6.13	1.71	5.28	9.9	10.2
21	21	5.78	3.36	2.96	8.0	13.6
22	22	5.43	1.13	4.31	11.3	14.9
23	23	6.50	6.21	3.47	12.3	16.0
24	24	7.98	7.92	3.37	9.8	13.2
25	25	11.54	10.89	1.20	10.5	20.0
26	26	5.84	0.92	8.61	6.4	13.3
27	27	3.84	1.20	6.45	9.6	10.4

- > lm.health<-lm(y~x1+x2+x3+x4,data=mydata) ## linear regression of y for the variables x1,x2,x3,x4
- > summary(lm.health) ## read the result of the linear regression

```
Call:
lm(formula = y ~ x1 + x2 + x3 + x4, data = mydata)

Residuals:
    Min      1Q  Median      3Q     Max
-3.6268 -1.2004 -0.2276  1.5389  4.4467

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   5.9433     2.8286   2.101   0.0473 *
x1            0.1424     0.3657   0.390   0.7006
x2            0.3515     0.2042   1.721   0.0993 .
x3           -0.2706     0.1214  -2.229   0.0363 *
x4            0.6382     0.2433   2.623   0.0155 *
---
Signif. codes:
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 2.01 on 22 degrees of freedom
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Multiple R-squared:  0.6008,	Adjusted R-squared:  0.5282

F-statistic: 8.278 on 4 and 22 DF,  p-value: 0.0003121
```

Conclusion

- As the analysis shows, the p-value of x3 and x4 is smaller than 0.05, and the p-value of x1 and x2 is bigger than 0.05, so fasting insulin(x3) and glycated haemoglobin(x4) have the bigger impact on fasting blood sugar(y), serum total cholesterol(x1) and glycerine(x2) have the smaller impact. That is to say, fasting insulin(x3) and glycated haemoglobin(x4) are two main influence factors of fasting blood sugar(y).

Use the cluster to cluster the patients

- If the patients are in the same category, then they have the similar health conditions.

- Calculation:
- d<-dist(mydata,method="euclidean",diag=T,upper=F,p=2)
- KM<-kmeans(mydata,4,nstart=20,algorithm="Hartigan-Wong") ## Use K-means to cluster 4 category.
- KM

```
K-means clustering with 4 clusters of sizes 10, 3, 7, 7

Cluster means:
         No       x1       x2       x3        x4
1 12.500000 5.434000 2.580000 8.635000  8.240000
2 24.000000 8.673333 8.340000 2.680000 10.866667
3 21.714286 5.501429 1.678571 4.952857  9.200000
4  4.142857 5.438571 2.018571 5.271429  9.542857
         y
1  9.71000
2 16.40000
3 12.57143
4 12.52857

Clustering vector:
 [1] 4 4 4 4 4 4 1 4 1 1 1 1 1 1 1 1 3 1 3 3 3 3 2 2 2 3
[27] 3

Within cluster sum of squares by cluster:
[1] 362.48049  56.61493 155.88397 162.13403
 (between_SS / total_SS =  70.9 %)

Available components:

[1] "cluster"      "centers"      "totss"
[4] "withinss"     "tot.withinss" "betweenss"
[7] "size"         "iter"         "ifault"
>
```

Conclusion of the cluster

- As the result show, if we cluster these 27 diabates patients into 4 categories, then these four categories have 10, 3, 7, 7 patients, respectively.
- First category: Number 7, 9~16, 18 (10 patients)
- Second category: Number 23~25 (3 patients)
- Third category: Number 17, 19~22, 26~27 (7 patients)
- Forth category: Number 1~6, 8 (7 patients)