字符串的模糊匹配

- 基本概念
- 字符串的编辑距离
- 最长公共子序列

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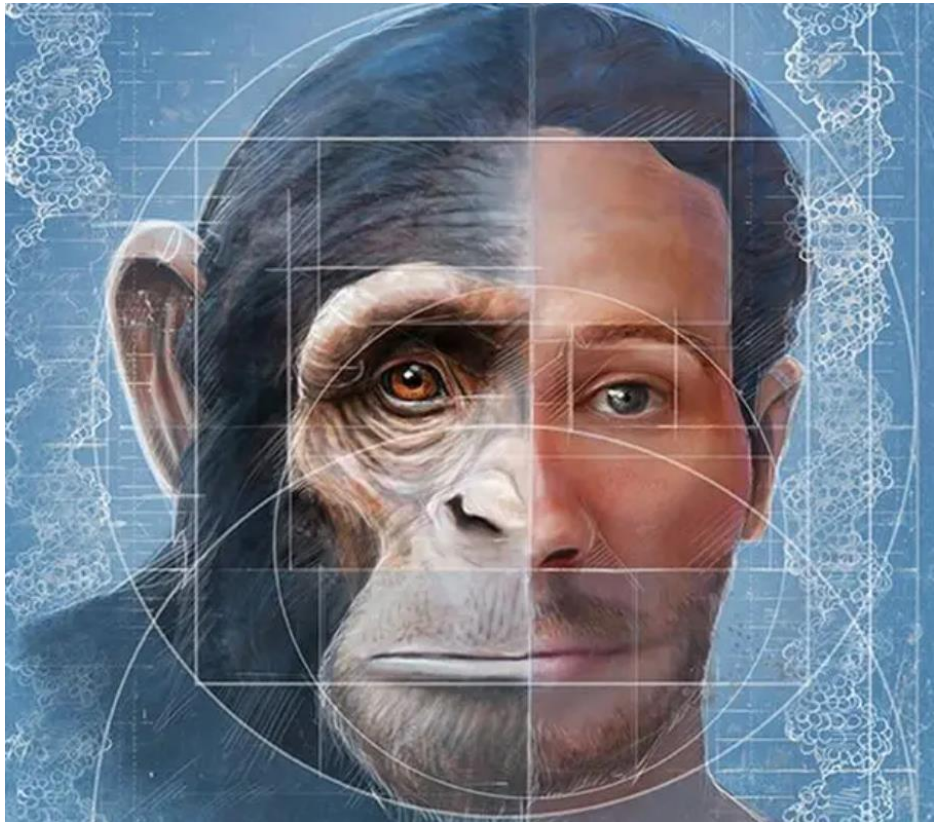
字符串的模糊匹配

- 模糊匹配：降低精确匹配的要求：*S*和*P*之间只要有一定程度的相似，就认为匹配成功。
- 用于衡量两个字符串之间的相似程度。

应用举例：基因序列比对



Answers Research Journal 4 (2011):233–241.
www.answersingenesis.org/arj/v4/human-chimpanzee-genome.pdf

ARJ

Genome-Wide DNA Alignment Similarity (Identity) for 40,000 Chimpanzee DNA Sequences Queried against the Human Genome is 86–89%

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Abstract

To provide a fresh and less-biased global set of analyses, large-scale comparative DNA sequence alignments between the chimpanzee and human genomes were performed with the BLASTN algorithm. One group of experiments was conducted with query and subject low-complexity sequence masking enabled while the second set had masking parameters disabled. Each group of sub-experiments tested fifteen combinations of three different word sizes (7, 11, and 15) and five different e-values (1000, 10, 0.1, 0.001, and 0.00001) for a total of 1.2 million attempted genome-wide alignments. Individual BLASTN query jobs each involved a data set of 40,000 chimpanzee whole genome shotgun sequences (WGSS) obtained from the National Center for Biotechnology (NCBI) and queried against four different human genome assemblies (GRCH37, GRCH36, Alternate SNP Assembly, and the Celera Assembly).

The use of low complexity sequence masking had the effect of decreasing computational time about 5–6 fold, lengthening the alignments slightly, lowering the number of database hits, and lowering the percent nucleotide identity slightly. Depending on the BLASTN parameter combination, average sequence identity for the 30 separate experiments between human and chimp varied between 86 and 89%. The average chimp query sequence length was 740 bases and depending on the BLASTN parameter combination, average alignment length varied between 121 and 191 bases.

The chimp sequences were subsequently implicated by personal correspondence with NCBI staff and supporting data from this study to be pre-screened for some level of homology to the human genome. Nevertheless, excluding data for the large amount of chimp sequence that did not align, a very conservative estimate of human-chimp DNA similarity genome-wide is 86–89%. Results from this study unequivocally indicate that the human and chimpanzee genomes are at least 10–12% less identical than is commonly claimed. These results are more clearly in line with the large anatomical and behavioral differences observed between human and chimp.

Keywords: human chimpanzee similarity, genome comparison, DNA alignment, BLASTN algorithm

Tomkins J. Genome-Wide DNA Alignment Similarity (Identity) for 40000 Chimpanzee DNA Sequences Queried against the Human Genome is 86-89%. Answers Research Journal, 4(2011): 233-241.

应用举例：论文/代码查重

```
int T;
scanf("%d", &T);
for (int i = 0; i < T; i++)
{
        int n;
        scanf("%d", &n);
        int tmp, cnt = 1;
        for (int j = 0; j < n; j++)
        {
                scanf("%d", &tmp);
                arr[tmp] = cnt++;
        }
        for (int j = 1; j <= n; j++)
        {
                int index = 2;
                while (index * j <= n)
                {
                        if (arr[index * j] < arr[j])
                        {
                                ans[ptr_t]++;
                        }
                        index++;
                }
        }
```

```
    int T; scanf("%d", &T);
    for(int i = 0; i < T; i++){
        int n; scanf("%d", &n);
        int tmp, cnt = 1;
        for(int j = 0; j < n; j++){
            scanf("%d", &tmp);
            a[tmp] = cnt++;
        }
        for(int j = 1; j <= n; j++){
            int p = 2;
            while(p * j <= n){
                if(a[p * j] < a[j]){
                    b[x]++;
                }
                p++;
            }
        }
        x++;
    }
    for(int i = 0; i < T; i++){
        printf("%d\n", b[i]);
    }
    return 0;
}
```

字符串的编辑距离

- 如何量化两个字符串之间的相似程度？
- **字符串编辑距离：**将一个字符串转化成另一个字符串，需要的最少编辑操作次数。
- 编辑操作：增加一个字符、删除一个字符、替换一个字符。
- 编辑距离越大，说明两个字符串的相似程度越小；编辑距离越小，说明两个字符串的相似程度越大。对于两个完全相同的字符串，编辑距离为 0。

字符串的编辑距离

- FOOD转换成MONEY：
- 编辑距离4：第1位F替换为M，第3位O替换为N，第4位插入E，第5位D替换为Y。

F O O D

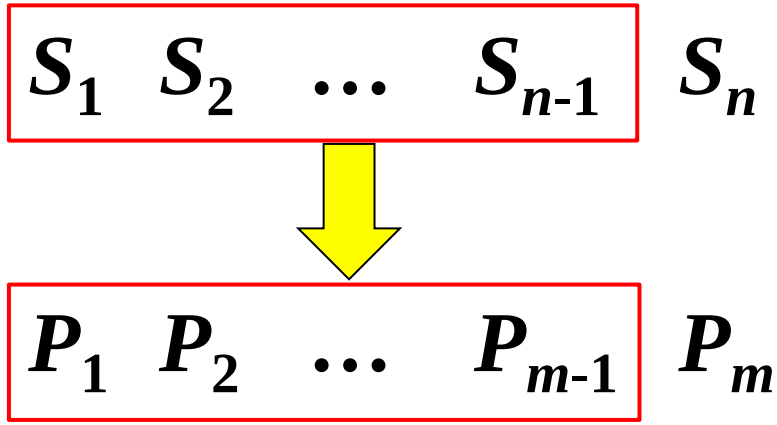
M O N E Y

- 给定两个字符串$S_1 \ldots S_n$和字符串$P_1 \ldots P_m$，计算S和P的编辑距离。【LanqiaoOJ1507、LeetCode72】

Dist(n, m)

S和P的编辑距离Dist(n, m)

- 将S变换为P：若$S_n = P_m$

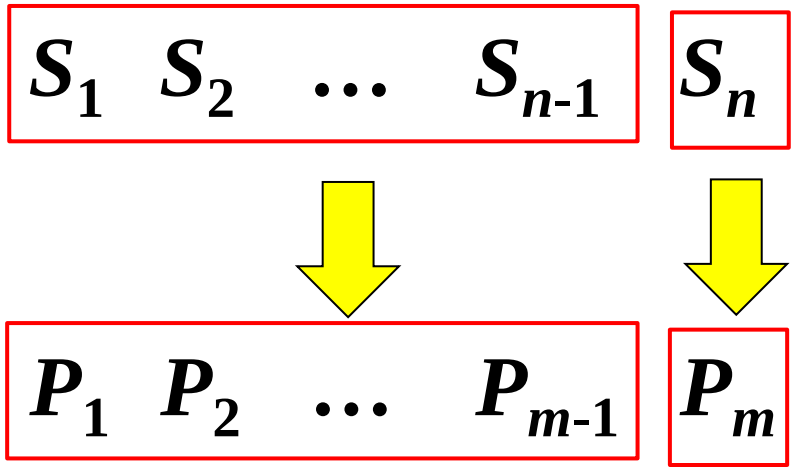


- 只需将$S_1 \ldots S_{n-1}$变换为$P_1 \ldots P_{m-1}$，即

$$\text{Dist}(n, m) = \text{Dist}(n\text{-}1, m\text{-}1)$$

S和P的编辑距离Dist(n, m)

- 将S变换为P：若$S_n \neq P_m$

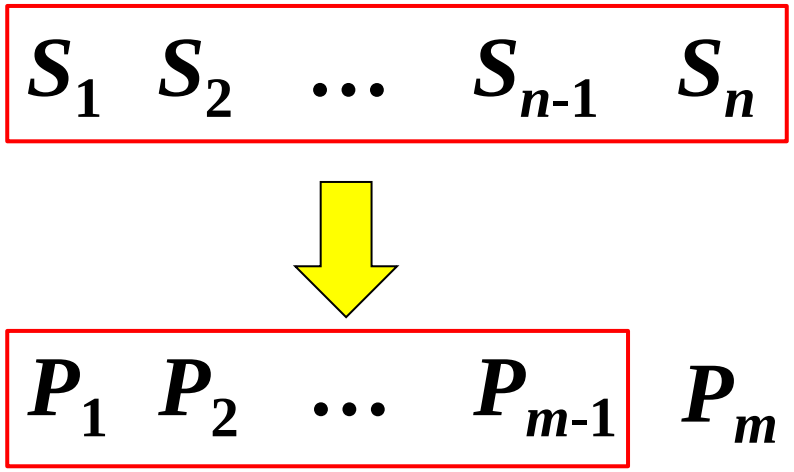


- 方案1：先把$S_1 \ldots S_{n-1}$变换为$P_1 \ldots P_{m-1}$，再将S_n替换为P_m.

$$\text{Dist}(n, m) = \text{Dist}(n\text{-}1, m\text{-}1)+1$$

S和P的编辑距离Dist(n, m)

- 将S变换为P：若$S_n \neq P_m$

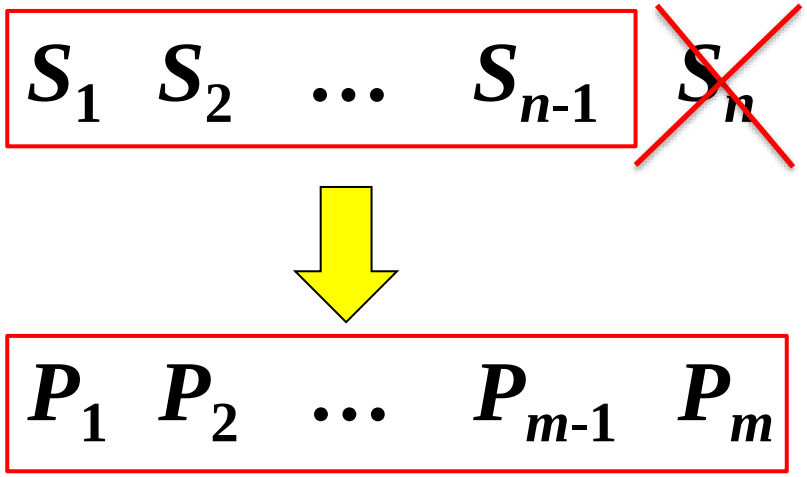


- 方案2：先把$S_1 \ldots S_n$变换为$P_1 \ldots P_{m-1}$，再插入P_m.

$$\text{Dist}(n, m) = \text{Dist}(n, m\text{-}1)+1$$

S和P的编辑距离Dist(n, m)

- 将S变换为P：若$S_n \neq P_m$



- 方案3：先把$S_1 \ldots S_{n-1}$变换为$P_1 \ldots P_m$，再删去S_n.

$$\text{Dist}(n, m) = \text{Dist}(n\text{-}1, m)+1$$

S和P的编辑距离Dist(n, m)

$$Dist(n,m)=\begin{cases} Dist(n-1,m-1), & S_n = P_m \\ \min\{Dist(n-1,m-1), Dist(n,m-1), Dist(n-1,m)\}+1, & S_n \neq P_m \end{cases}$$

m

			Dist[*n*-1][*m*-1]	**Dist[*n*-1][*m*]**
n			**Dist[*n*][*m*-1]**	**Dist[*n*][*m*]**

S和P的编辑距离Dist(n, m)

$$Dist[i][j]=\begin{cases} Dist[i-1][j-1], & S_i = P_j \\ \min\{Dist[i-1][j-1], Dist[i][j-1], Dist[i-1][j]\}+1, & S_i \neq P_j \end{cases}$$

Dist[i][j]: $S_1...S_i$和$P_1...P_j$的编辑距离

j

i

	Dist[*i*-1][*j*-1]	Dist[*i*-1][*j*]	
	Dist[*i*][*j*-1]	Dist[*i*][*j*]	

字符串S和P的编辑距离

$$Dist[i][j]=\begin{cases} Dist[i-1][j-1], & S_i = P_j \\ \min\{Dist[i-1][j-1], Dist[i][j-1], Dist[i-1][j]\}+1, & S_i \neq P_j \end{cases}$$

		“ ”	B	C	D
	“ ”	0	1	2	3
	A	1	1	2	3
	B	2	1	2	3
	C	3	2	1	2

字符串S和P的编辑距离

$$Dist[i][j]=\begin{cases} Dist[i-1][j-1], & S_i = P_j \\ \min\{Dist[i-1][j-1], Dist[i][j-1], Dist[i-1][j]\}+1, & S_i \neq P_j \end{cases}$$

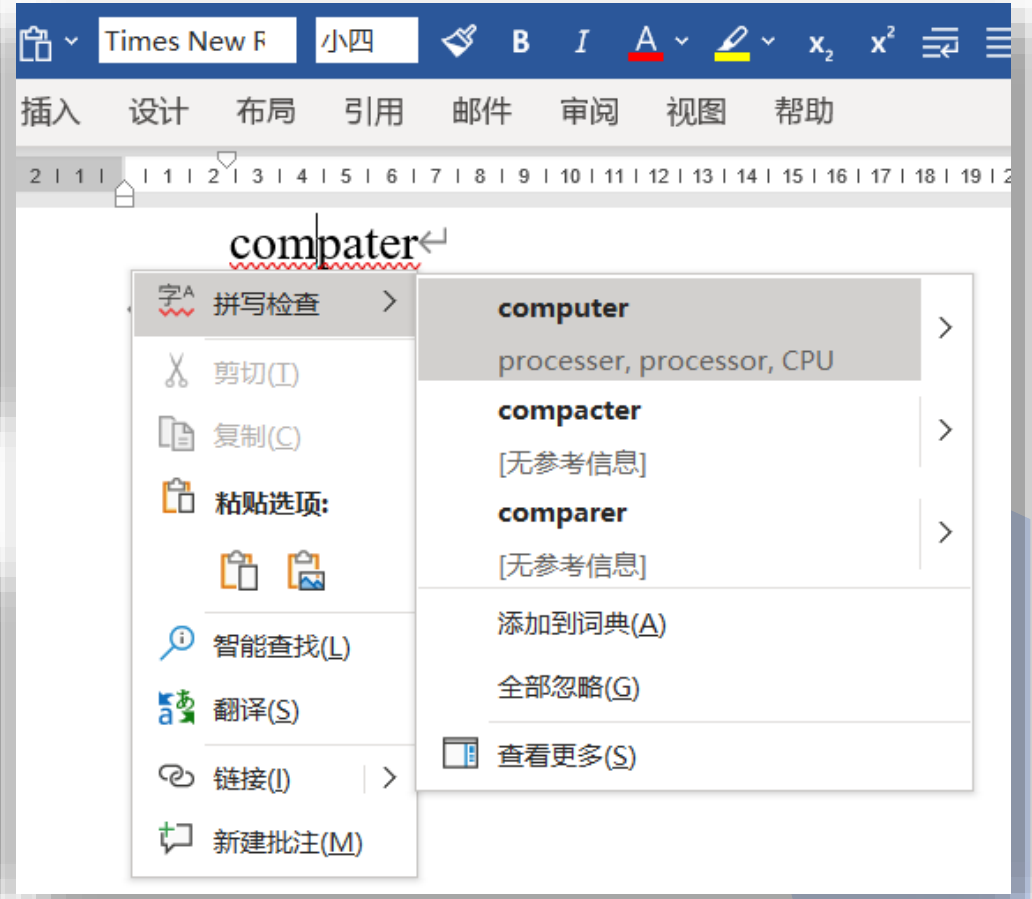
```
const int N=110;
int EditDistance(char *s, char *p, int n, int m) {
    int i, j, D[N][N];
    for(i=0; i<=n; i++) D[i][0]=i; //填第0列
    for(j=0; j<=m; j++) D[0][j]=j; //填第0行
    for(i=1; i<=n; i++)
      for(j=1; j<=m; j++)
        if(s[i-1]==p[j-1]) D[i][j]=D[i-1][j-1];
        else D[i][j]=1+min(D[i-1][j-1],D[i][j-1],D[i-1][j]);
    return D[n][m];
}
```

0	1	2	3
1			
2	D[*i*-1][*j*-1]	D[*i*-1][*j*]	
3	D[*i*][*j*-1]	D[*i*][*j*]	

时间复杂度 $O(nm)$

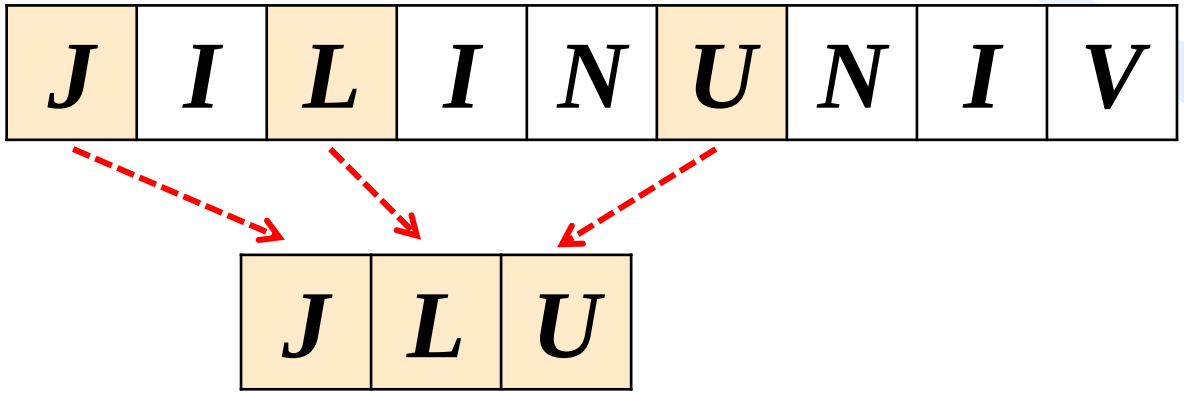
$Dist[n][m]$表示$S_1...S_n$和$P_1...P_m$的编辑距离

字符串S和P的编辑距离



最长公共子序列（LCS, Longest Common Sequence）

- 可用两个字符串的最长公共子序列长度衡量其相似程度。
- 子序列：由字符串中若干字符按原相对次序构成



- 最长公共子序列：两个字符串的公共子序列中的最长者。
- 例：*S* = "HelloWorld" ， *P* = "loop"
- *S*和*P*的最长公共子序列为loo

最长公共子序列（LCS, Longest Common Sequence）

给定两个字符串S和P，长度分别为n和m，要求找出它们最长的公共子序列长度。【LanqiaoOJ1189、LeetCode1143】

- 考察$S_1 \ldots S_i$和$P_1 \ldots P_j$
- 令LCS(i, j)表示$S_1 \ldots S_i$和$P_1 \ldots P_j$的最长公共子序列长度。
- 若$S_i = P_j$，则LCS(i, j)=LCS$(i\text{-}1, j\text{-}1)+1$

$$\underbrace{S_1 \quad \cdots \quad S_{i-1}} \quad S_i$$

$$\underbrace{P_1 \quad \cdots \quad P_{j-1}} \quad P_j$$

最长公共子序列（LCS, Longest Common Sequence）

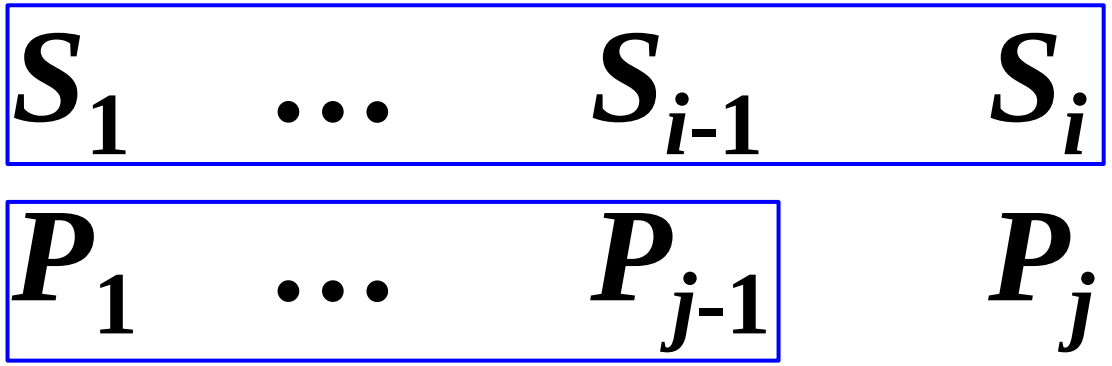
- 若$S_i \neq P_j$，则LCS(i, j)=max{LCS(i-1, j), LCS(i, j-1)}

$$S_1 \quad \cdots \quad S_{i-1} \qquad S_i$$

$$P_1 \quad \cdots \quad P_{j-1} \qquad P_j$$

最长公共子序列（LCS, Longest Common Sequence）

- 若$S_i \neq P_j$，则LCS(i, j)=max{LCS(i-1, j), LCS(i, j-1)}



最长公共子序列（LCS, Longest Common Sequence）

- 若$S_i \neq P_j$，则LCS(i, j)=**max**{LCS(i-1, j), LCS(i, j-1)}

$$\begin{array}{cccc} S_1 & \cdots & S_{i-1} & S_i \\ P_1 & \cdots & P_{j-1} & P_j \end{array}$$

最长公共子序列（LCS, Longest Common Sequence）

$$LCS[i][j]=\begin{cases} LCS[i-1][j-1]+1, & S_i = P_j \\ \max\{LCS[i][j-1], LCS[i-1][j]\}, & S_i \neq P_j \end{cases}$$

***LCS*[*i*][*j*]:$S_1...S_i$和$P_1...P_j$的最长公共子序列长度**

j

i

	LCS[*i*-1][*j*-1]	**LCS[*i*-1][*j*]**	
	LCS[*i*][*j*-1]	**LCS[*i*][*j*]**	

最长公共子序列（LCS, Longest Common Sequence）

$$LCS[i][j]=\begin{cases} LCS[i-1][j-1]+1, & S_i = P_j \\ \max\{LCS[i][j-1], LCS[i-1][j]\}, & S_i \neq P_j \end{cases}$$

$LCS[i][j]$:$S_1...S_i$和$P_1...P_j$的最长公共子序列长度

		" "	B	C	D
	" "	0	0	0	0
	A	0	0	0	0
	B	0	1	1	1
	C	0	1	2	2

最长公共子序列（LCS, Longest Common Sequence）

$$LCS[i][j]=\begin{cases} LCS[i-1][j-1]+1, & S_i = P_j \\ \max\{LCS[i][j-1], LCS[i-1][j]\}, & S_i \neq P_j \end{cases}$$

$LCS[n][m]$表示$S_1...S_n$和$P_1...P_m$的最长公共子序列长度

```
const int N=1010;
int longestCommonSubsequence(char *s,char *p,int n,int m){
    int i, j, LCS[N][N];
    for(i=0; i<=n; i++) LCS[i][0]=0; //填第0列
    for(j=0; j<=m; j++) LCS[0][j]=0; //填第0行
    for(i=1; i<=n; i++)
      for(j=1; j<=m; j++)
        if(s[i-1]==p[j-1]) LCS[i][j]=LCS[i-1][j-1]+1;
        else LCS[i][j]=max(LCS[i][j-1], LCS[i-1][j]);
    return LCS[n][m];
}
```

0	0	0	0
0			
0			
0			

时间复杂度 $O(nm)$

最长公共子序列——变形问题

给定两个字符串S和P，长度分别为n和m，编写程序计算最少去掉几个字符可使二者相等。【LeetCode583】

例：$S = a\ x\ b\ c\ e$，$P = a\ b\ c\ f\ e$. S应去掉1个字符x, P应去掉1个字符f，合计2个字符

S	a	x	b	c	e
P	a	b	c	f	e

- S和P去掉最少的字符后，若剩下的字符串相等，则剩下的字符串一定是S和P的最长公共子序列；
- 若最长公共子序列长度为k，则S应删去$n-k$个字符，P应删去$m-k$个字符。

最长公共子序列——变形问题

给定一个字符串S，计算其最长回文子序列长度。【LeetCode516】

- S和其逆序S^{-1}的最长公共子序列，即为最长回文子序列

S	x	a	b	y	c	k	b	a
S^{-1}	a	b	k	c	y	b	a	x

最长公共子序列——变形问题

给定一个长度为n的字符串S，计算最少删除几个字符，能使剩下的子序列成为回文。

- n - 最长回文子序列长度

S	x	a	b	y	c	k	b	a