# Chemical and Linguistic Considerations for Encoding Chinese Characters: An Embodiment Using Chain-End Degradable Sequence-Defined Oligourethanes Created by Consecutive Solid Phase Click Chemistry

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# TABLE OF CONTENTS

I. General procedure and equipment	1
II. Synthesis and characterization	2
III. Sequencing experiments	8
IV. User manual for Python scripts	77

## I. General procedure and equipment

All materials used in the synthesis of each compound and related tests, were purchased from Sigma-Aldrich Chemical Co., Acros Organics, Tokyo Chemical Industry, Chem Impex International, etc. and used without further purification. Solvents (DCM, NMP, chloroform, DMSO, DMF, MeOH, MeCN, Isopropanol) were of reagent grade or HPLC grade quality and purchased from Fischer Scientific. NMR solvents (CDCl<sub>3</sub>-*d*, MeOD-*d*<sub>4</sub>) were purchased from Cambridge Isotope Laboratories.

**Column chromatography** was performed using silica gel 60 ( $230 \pm 400$  mesh,  $0.040 \pm 0.063$  mm) from Dynamic Adsorbents.

**TLC** analyses were carried out using Silica TLC Plates Glass Backing 20 by 20 cm sheet UV active at 254 nm.

**Reverse phase column chromatography** and **HPLC** purifications were performed on Shimadzu Prominence HPLC system equipped with Zorbax SB-C18 preparatory column (21.2 x 250 mm) with 7.0 µm packing material. Analytical HPLC traces were also carried out using a Zorbax SB-C18 analytical column (4.6 x 250 mm) with 5.0 µm packing material. 5-95% gradient elution (MeCN/H<sub>2</sub>O with 0.1% formic acid). Hydrophobic urethanes utilized 30-95% gradient elution (MeCN/H<sub>2</sub>O with 0.1% formic acid).

<sup>1</sup>H and <sup>13</sup>C spectra were recorded on Bruker AVIII with a BBFO Prodigy liquid nitrogen CryoProbe 600 MHz NMR spectrometers. The NMR spectra were referenced to solvent and the spectroscopic solvents were purchased from Cambridge Isotope Laboratories.

**Liquid Chromatography/Mass spectra** were recorded on an Agilent Technologies 6120 Single Quadrupole or 6125B Single Quadrupole mass spectrometer interfaced with an Agilent 1200 series liquid chromatography system equipped with a diode-array detector. Column: Agilent ZORBAX Eclipse Plus S2 C18 narrow bore column; 2.1 mm internal diameter; 50 mm length; 5 micron particle size; P.N. 959746-902. Resulting spectra were analysed using Agilent LC/MSD ChemStation. Separations were achieved

with a gradient elution from 5 to 95% organic, using MeCN and Water w/ 50 mM ammonium acetate as the eluents. **High resolution mass spectrometry** was performed by the UT-Austin Mass Spectrometry Facility using an Agilent Technologies 6530 Accurate-Mass Q-TOF (G6530A) with an Agilent Technologies Jet Stream ESI source, interfaced with an Agilent Technologies 1260 Infinity liquid chromatography system (G1312B). An Agilent Technologies 6546 Accurate-Mass Q-TOF (G6546A) with an Agilent Technologies Dual Jet Stream ESI source, interfaced with an Agilent Technologies 1260 Infinity liquid chromatography system (G7112B), was used.

#### II. Synthesis and characterization

#### II(a). Synthesis and characterization of the monomer



To a stirred solution of Fmoc-*L*-azidolysine (1.972 g, 5 mmol) in anhydrous THF (19 mL) was added N,N-carbonyldiimidazole (1.08 g, 6.7 mmol) at room temperature. The reaction stirred for at least 10 minutes and was then cooled to 0 °C. Next, a solution of NaBH<sub>4</sub> (311.7 mg, 8.24 mmol) in H<sub>2</sub>O (8.32 mL) was added. The solution was stirred for at least 30 minutes, up to 1.5 hours. The reaction was quenched by addition of 1M HCl and extracted with EtOAc (3 x 65 mL). The combined organics were washed 1x with brine, dried over Na<sub>2</sub>SO<sub>4</sub>, and concentrated under vacuum. The crude product was purified by silica gel chromatography (1:1 Hexanes:EtOAc) to furnish a white solid (1.69 g, 89%). <sup>1</sup>H NMR (600 MHz, MeOD-*d*<sub>4</sub>)  $\delta$  7.79 (d, *J* = 12 Hz, 2H), 7.66 (d, *J* = 12 Hz, 2H), 7.38 (t, *J* = 12 Hz, 2H), 7.30 (t, *J* = 12 Hz, 2H), 4.40-4.43 (m, 1H), 4.30-4.34 (m, 1H), 4.21 (t, *J* = 6 Hz, 1H), 3.56-3.59 (m, 1H), 3.43-3.50 (m, 2H), 3.27 (t, *J* = 6 Hz, 2H), 1.55-1.64 (m, 3H), 1.35-1.49 (m, 3H). <sup>13</sup>C NMR (125 MHz, MeOD-*d*<sub>4</sub>)  $\delta$  159.13, 145.70, 145.62, 142.93, 129.05, 128.42, 126.52, 126.47, 121.21, 67.82, 65.70, 54.45, 52.65, 49.83, 32.02, 30.03, 24.56. HRMS +ESI: calculated (C<sub>21</sub>H<sub>24</sub>N<sub>4</sub>O<sub>3</sub>Na<sup>+</sup>) 403.1746, found 403.1741. [M<sup>+</sup>Na].



To a stirring solution of **1** (1.69 g, 4.45 mmol) in anhydrous DCM (22 mL) was added pyridine (378  $\mu$ L, 4.67 mmol) dropwise. Next, 4-nitrophenyl chloroformate (1.08 g, 6.67 mmol) was added, and the reaction left to stir overnight. Reaction was monitored by TLC (2:1 Hexanes:EtOAc) and upon consumption of the starting material, was diluted excessively in DCM and transferred to a separatory funnel. The organic layer was washed with 1M NaHSO<sub>4</sub> (2x), then 1M Na<sub>2</sub>CO<sub>3</sub> (3x), and finally brine. The organic layer was dried over Na<sub>2</sub>SO<sub>4</sub>, filtered, and concentrated in vacuo. The product was purified by silica gel chromatography (2:1 Hexanes:EtOAc) and isolated as a white solid (1.75 g, 3.20 mmol). <sup>1</sup>H NMR (600 MHz, CDCl<sub>3</sub>-*d*)  $\delta$  8.25 (d, *J* = 12 Hz, 2H), 7.78 (d, *J* = 6 Hz, 2H), 7.59 (d, *J* = 12 Hz, 2H), 7.41 (t, *J* = 12 Hz, 2H), 7.36 (d, *J* = 12 Hz, 2H), 7.31 (t, *J* = 12 Hz, 2H), 4.82 (d, *J* = 6 Hz, 1H), 4.43-4.50 (m, 2H), 4.31-4.34 (m, 1H), 4.21-4.26 (m, 2H), 3.99-4.05 (m, 1H), 3.30 (t, *J* = 6 Hz, 2H), 1.44-1.67 (m, 6H). <sup>13</sup>C NMR (125 MHz, CDCl<sub>3</sub>-*d*)  $\delta$  156.17, 155.50, 152.62, 145.60, 143.92, 143.88, 141.50, 127.93, 127.22, 125.50, 125.11, 125.08, 121.89, 120.20, 70.78, 66.89, 51.26, 50.02, 47.40, 31.05, 28.64, 23.19. HRMS +ESI: calculated (C<sub>28</sub>H<sub>27</sub>N<sub>5</sub>O<sub>7</sub>Na<sup>+</sup>) 568.1808, found 568.1799. [M<sup>+</sup>Na].





#### II(b). General procedure for the solid-supported synthesis of oligourethanes

**Coupling**: Phenyalaninol loaded (0.44 mmol/gram, 200-400 mesh) 2-chlorotrityl polystyrene resin (40 mg, 0.0176 mmol) was added to a small fritted solid phase synthesis apparatus (5mL). The apparatus was then evacuated and backfilled with argon. The resin was suspended in 0.5 mL of anhydrous N-methyl-2-pyrrolidinone (NMP) and left to swell for 10 minutes. Next, Hunig's base (4.4  $\mu$ L, 0.025 mmol) was added, followed by hydroxybenzotriazole (13.4 mg, 0.10 mmol). The suspension was swirled for 30 seconds until everything was dissolved. Finally, the activated amino alcohol **2** (33.2 mg, 0.05 mmol) was added. Reaction was shaken for 8 hours on a shaker at room temperature. Resin was washed with NMP (5x3 mL), then DCM (5x3 mL), and finally Et<sub>2</sub>O (3x2 mL). Resin was dried overnight under vacuum. Test cleavages were effected with 1% TFA in DCM (5x0.2 mL) for 20 seconds each. Coupling efficiency was checked by LC/MS. NOTE: depending on the cleavage times and amounts of TFA used, the trifluoroacetic ester (presumably on the terminal alcohol) was observed by LC/MS. This ester was readily hydrolyzed by dissolving the sample in DCM and shaking with saturated NaHCO<sub>3</sub>.

**Solid phase CuAAC click chemistry**: To the oligourethanes on the resin (about 40 mg resin, 0.0176 mmol) in the 5 mL fritted solid phase synthesis apparatus, a terminal alkyne (5.0 eq.), sodium ascorbate (1.0 eq.), TBTA (1.0 eq.) and copper iodide (0.5 eq.) were added along with 0.7 mL DMF. The solid phase synthesis apparatus was sealed with a septum and purged with N<sub>2</sub> gas for 15 minutes. After degassing, parafilm was used to seal the septum on the solid phase synthesis apparatus to prevent oxygen from going into the apparatus. The reaction was placed on the shaker and agitated for 18 hours at room temperature. The resin was then collected by vacuum filtration and washed with NMP (5x3 mL), then DCM (5x3 mL), and finally Et<sub>2</sub>O (3x2 mL).

**Deprotection:** Resin loaded with terminal Fmoc-protected oligocarbamates (0.0176 mmol) suspended in 20% piperidine in DMF (3 mL) and shaken for 2 hours at room temperature. Cleavage of the dibenzofulvene-piperidine adduct was calculated by absorbance at 301 nm using Beer's Law. The resin was washed with DMF (5x3 mL), DCM (5x3 mL), Et<sub>2</sub>O (3x2 mL), and dried overnight under vacuum.

General procedure for labelling of the terminal amine with a NBD-Fluoride (on resin): To a fritted reaction vessel was added the oligomer (dimer, trimer or tetramer) on resin (0.0176 mmol). Vessel was evacuated and backfilled with argon. The resin was suspended and swelled in anhydrous DMF (2.4 mL) for 5 minutes. Next, DIPEA (41.76  $\mu$ L, 0.24 mmol) was added, followed by 4-fluoro-7-nitrobenzofurazan (33 mg, 0.179 mmol). Reaction was left to shake overnight. Resin was washed with DMF (5x16 mL), DCM (5x16 mL), and Et<sub>2</sub>O (3x8 mL).

**Cleavage procedure:** Cleavages were effected with 1% TFA in DCM (5x1 mL) for 20 seconds each at room temperature. Resin was filtered off, and cleaved product was concentrated. Oligomer was purified by reverse-phase preparatory HPLC (5-95% MeCN/H<sub>2</sub>O, 0.1% formic acid gradient elution).

#### II(c). Determination of Conversions of Synthesized Oligourethanes



Oligomer 1: #6027

Oligomer 2: #8fd1



 $HO \xrightarrow{H}_{O} \xrightarrow{N}_{N} \xrightarrow{O}_{N} \xrightarrow{N}_{O} \xrightarrow{N}_{N} \xrightarrow{O}_{N} \xrightarrow{N}_{O} \xrightarrow{N}_{N} \xrightarrow{O}_{N} \xrightarrow{N}_{O} \xrightarrow{N}_{N} \xrightarrow{N}_{O} \xrightarrow{N}_{N} \xrightarrow{N}_{O} \xrightarrow{N}_{N} \xrightarrow{N}_{N$ 

Oligomer 3: \*BDRW





Oligomer 5: #9060







Oligomer Z1: \*YI



Oligomer Z2: \*YT





Oligomer Z3: \*UMC

Oligomer Z4: \*PDW



Oligomer Z5: \*FLVV

Oligomer Z6\_1: #4e5f

Oligourethane	Conversion <sup>a</sup>	Oligourethane	Conversion <sup>a</sup>
1	38%	Z1	80%
2	81%	Z2	90%
3	63%	Z3	83%
4	77%	Z4	65%
5	55%	Z5	65%
6	48%	Z6	68%

Table 1. The conversions of 12 synthesized oligourethanes

<sup>a</sup>Conversions were determined by the ratio of the peak area of product to the total peak area in LC trace.

## **III. Sequencing experiments**

### III(a). General procedure for self-degradation (sequencing)

The sequencing procedure is adapted from previous work.<sup>1</sup> The oligomer (measured to be at a final concentration between 0.5-1 mM) was dissolved in methanol and added to a vial. Next, potassium phosphate tribasic monohydrate was dissolved in water and then added to the reaction solution. The final concentration of base was approximately 30 mM. The final ratio of methanol and water was 1:2.5, respectively. Before placing the vial on the heated shaker, the reaction was sampled for LC/MS by taking 50  $\mu$ L of the reaction mixture and diluted into 50  $\mu$ L of a 1:1 methanol: water mixture. The reaction was ramped quickly to 70 °C in the heated shaker and held at the temperature. The reaction was sampled every 60 minutes.

### III(b). Oligomer Sequencing Data:























769 C65H93N21O13

1381.746

MS Zoo





(M+H)-

310.1872			2446588			
1275.6845	1275.6858	1	164259	C61H86N20O11	(M+H)+	0.99
1276.6870	1276.6886	1	121823	C61H86N20O11	(M+H)+	1.24
1277.6888	1277.6912	1	48473	C61H86N20O11	(M+H)+	1.89
1278.6911	1278.6938	1	11885	C61H86N20O11	(M+H)+	2.15
1279.6918	1279.6964	1	3160	C61H86N20O11	(M+H)+	3.58
1280.6949	1280.6989	1	757	C61H86N20O11	(M+H)+	3.09
End Of Report						

















296.2078			2679292				
1406.6970	1406.6996	1	20946	C66H92CIN21012	(M+H)+	1.85	
1407.6988	1407.7024	1	17367	C66H92CIN21O12	(M+H)+	2.51	
1408.6981	1408.7010	1	14207	C66H92CIN21O12	(M+H)+	2.03	
1409.6972	1409.7018	1	7920	C66H92CIN21O12	(M+H)+	3.25	
1410.7031	1410.7036	1	3249	C66H92CIN21012	(M+H)+	0.34	
End Of Report							



























	ODS. III/2	Calc. m/2	Charge	Abundance	Formula	Ton Species	rge mass Error (ppin)
	255.1451	255.1452	1	176362	C11H18N4O3	(M+H)+	0
	256.1477	256.1479	1	22645	C11H18N4O3	(M+H)+	0
	257.1550	257.1501	1	2804	C11H18N4O3	(M+H)+	-19
	258.1715	258.1524	1	421	C11H18N4O3	(M+H)+	-73
3	293.1010			1625527			
	End Of Repo	ort					

Chemical Formula: C11H18N4O3 Exact Mass: 254.14



Chemical Formula:  $C_{15}H_{18}N_4O_2$ Exact Mass: 286.14





Chemical Formula: C<sub>15</sub>H<sub>24</sub>N<sub>4</sub>O<sub>2</sub> Exact Mass: 292.19













Chemical Formula: C<sub>31</sub>H<sub>46</sub>N<sub>12</sub>O<sub>6</sub> Exact Mass: 682.37

O -N \\



Chemical Formula: C<sub>19</sub>H<sub>25</sub>N<sub>7</sub>O<sub>4</sub> Exact Mass: 415.20



MassHunter Qual 10.0 (End of Report)












Exact Mass: 446.20









After 60 minutes of sequencing, all the following molecules are observed in the solution and analyzed via High-Res MS.











Exact Mass: 177.08



MS Spectrum	i Peak List					
Obs. m/z	Calc. m/z	Charge	Abundance	Formula	Ion Species	Tgt Mass Error (ppm)
330.1927			1516400			
502.0829	502.0833	1	14174	C20H20BrN7O4	(M+H)+	0.78
503.0860	503.0860	1	3568	C20H20BrN7O4	(M+H)+	-0.03
504.0814	504.0815	1	16105	C20H20BrN7O4	(M+H)+	0.14
505.0830	505.0841	1	3865	C20H20BrN7O4	(M+H)+	2.07
506.0834	506.0865	1	1086	C20H20BrN7O4	(M+H)+	6.12
End Of Rep	ort					

End of hepoire



mo opecaram	I Curt List					
Obs. m/z	Calc. m/z	Charge	Abundance	Formula	Ion Species	Tgt Mass Error (ppm)
200.0680	200.0682	1	52132	C10H11NO2	(M+Na)+	0.88
201.0714	201.0714	1	5911	C10H11NO2	(M+Na)+	0.04
202.0780	202.0737	1	628	C10H11NO2	(M+Na)+	-21.08
330.1926			1735902			
End Of Repo	ort					

\_\_\_\_



O´ Chemical Formula: C<sub>17</sub>H<sub>23</sub>N<sub>5</sub>O<sub>2</sub> Exact Mass: 329.19

١H

MS Spectrum	Peak List					
Obs. m/z	Calc. m/z	Charge	Abundance	Formula	Ion Species	Tgt Mass Error (ppm)
330.1927	330.1925	1	1631610	C17H23N5O2	(M+H)+	-0.83
331.1958	331.1953	1	329494	C17H23N5O2	(M+H)+	-1.67
332.1980	332.1979	1	36961	C17H23N5O2	(M+H)+	-0.44
333.2098	333.2003	1	5255	C17H23N5O2	(M+H)+	-28.5
334.2105	334.2028	1	1033	C17H23N5O2	(M+H)+	-23.2

--- End Of Report ---





After 60 minutes of sequencing, all the following molecules are observed in the solution and analyzed via High-Res MS.













After 60 minutes of sequencing, all the following molecules are observed in the solution and analyzed via High-Res MS.





Exact Mass: 979.51



Exact Mass: 177.08

--- End Of Report ---





After 60 minutes of sequencing, all the following molecules are observed in the solution and analyzed via High-Res MS.













After 60 minutes of sequencing, all the following molecules are observed in the solution and analyzed via High-Res MS.









End Of Re



Exact Mass: 1002.55





Exact Mass: 177.08

End Of Report --







After 60 minutes of sequencing, all the following molecules are observed in the solution and analyzed via High-Res MS.





MS Zoomed Spectrum





f Chemical Formula: C<sub>65</sub>H<sub>83</sub>ClN<sub>20</sub>O<sub>10</sub> Exact Mass: 1338.63



Obs. m/z	Calc. m/z	Charge	Abundance	Formula	Ion Species	Tgt Mass Error (ppm)
296.2077			2549357			
1339.6363	1339.6362	1	274774	C65H83CIN20O10	(M+H)+	-0.06
1340.6388	1340.6390	1	218795	C65H83CIN20O10	(M+H)+	0.16
1341.6371	1341.6376	1	178187	C65H83CIN20O10	(M+H)+	0.36
1342.6375	1342.6384	1	93068	C65H83CIN20O10	(M+H)+	0.66
1343.6379	1343.6402	1	34085	C65H83CIN20O10	(M+H)+	1.69
1344.6396	1344.6424	1	10338	C65H83CIN20O10	(M+H)+	2.12
1345.6400	1345.6447	1	3456	C65H83CIN20O10	(M+H)+	3.52
End Of Repo	ort			·		





1044.4349	1044.4354	1	57102	C51H58CIN15O8	(M+H)+	0.47
1045.4371	1045.4382	1	34677	C51H58CIN15O8	(M+H)+	1.08
1046.4348	1046.4358	1	28709	C51H58CIN15O8	(M+H)+	0.93
1047.4359	1047.4369	1	13870	C51H58CIN15O8	(M+H)+	0.92
1048.4386	1048.4389	1	4234	C51H58CIN15O8	(M+H)+	0.37
1049.4423	1049.4413	1	1288	C51H58CIN15O8	(M+H)+	-1.03
End Of Rep	ort					

---- End C





MS Spectrum	Peak List					
Obs. m/z	Calc. m/z	Charge	Abundance	Formula	Ion Species	Tgt Mass Error (ppm)
296.2074			2117257			
343.0932	343.0932	1	19791	C15H17CIN4O2	(M+Na)+	0.01
344.0967	344.0961	1	3716	C15H17CIN4O2	(M+Na)+	-1.85
345.0903	345.0908	1	6641	C15H17CIN4O2	(M+Na)+	1.29
346.0925	346.0934	1	1370	C15H17CIN4O2	(M+Na)+	2.61
End Of Repo	ort					



## References

 Dahlhauser, S. D.; Escamilla, P. R.; Vandewalle, A. N.; York, J. T.; Rapagnani, R. M.; Shei, J. S.; Glass, S. A.; Coronado, J. N.; Moor, S. R.; Saunders, D. P.; Anslyn, E. V. *J. Am. Chem. Soc.* **2020**, *142* (6), 2744–2749.



## III(c). Sequencing the oligomers with overlapping truncated oligomers of similar polarities in LC



The sequencing of Oligomer 4 (#7fd2) is a scenario where multiple peaks overlap. In this case, it can be difficult to identify what peaks are overlapping, and what is the order in which these peaks show up in LC-MS. The MS data can help in deconvolute that. The process is shown below:

At 0 min, there is only one peak in the LC trace and the corresponding MS for that peak is shown below:



At 60 min, there are two peaks in the LC trace, and the corresponding MS for these peaks are shown below:



At 120 min, there are three peaks in the LC trace, and the corresponding MS for these peaks are shown below:


As we keep observing the LC trace and the corresponding MS peaks for the 180 and 240 minutes, we can confidently say what peaks are overlapping and what is the order of their appearance and disappearance. From this observation, the accurate sequence of the given oligomer can be determined.



## III(d). The oligomers and corresponding Chinese characters.



















(1) Unicode encoding





















(2) Zhengma encoding







## IV. User manual for Python scripts

To use this program, download the zip file, which can be located by clicking on "Code" on the GitHub website.

위 main → 위 1 branch 下 0 tags		Go to file Code	•
<b>bobtodd</b> Added all Zheng Ma code	Local	Codespaces	
code Added	▶ Clone	(	?
data Added	HTTPS GitHub CLI		
drafts Added	https://github.com/LingRes	sCtr/zhengmadificati	
img Added	Use Git or checkout with SVN usin	g the web URL.	
aw Added	다. Open with GitHub Desktop		
🗋 .gitignore Added	Δ	- 1-	_
🗋 README.md Update	🖁 Download ZIP		

# - To convert from Chinese characters to Zhengma codes

## 1. Go to the "code" folder.

<b>E</b>	bobtodd Added all Zheng Ma code and data files current as of 2023/06/21 a@cdb20 3 week		a0cdb20 3 weeks ago	🕑 4 commits
	code	Added all Zheng Ma code and data files current as of	2023/06/21	3 weeks ago
	data	Added all Zheng Ma code and data files current as of	2023/06/21	3 weeks ago
	drafts	Added all Zheng Ma code and data files current as of	2023/06/21	3 weeks ago
	img	Added all Zheng Ma code and data files current as of	2023/06/21	3 weeks ago
	raw	Added all Zheng Ma code and data files current as of	2023/06/21	3 weeks ago
Ľ	.gitignore	Added MacOS file .DS_Store to .gitignore		3 weeks ago
Ľ	README.md	Update README.md		3 weeks ago

2. Open the "4\_converter.ipynb" file.

Name	Last commit message	Last commit date
•		
1_background.ipynb	Added all Zheng Ma code and data files current as of 2023/06/21	3 weeks ago
2_data.ipynb	Added all Zheng Ma code and data files current as of 2023/06/21	3 weeks ago
3_tests.ipynb	Added all Zheng Ma code and data files current as of 2023/06/21	3 weeks ago
4_converter.ipynb	Added all Zheng Ma code and data files current as of 2023/06/21	3 weeks ago
🗋 zm_helpers.py	Added all Zheng Ma code and data files current as of 2023/06/21	3 weeks ago

### 3. Load and run the codes 1-4 shown below.

In [1]:	<pre># If running in Google Colab #from google.colab import drive #drive.mount('/content/gdrive') # #path_prefix = "/content/gdrive/My Drive/Colab Notebooks/zhengma/raw/" #data_prefix = '/content/gdrive/My Drive/Colab Notebooks/zhengma/data/'</pre>
In [2]:	<pre># If running on local system path_prefix = "/raw/" data_prefix = '/data/'</pre>
In [3]:	<pre>import pickle # Load pickLe with open(data_prefix + 'df_zm_merged.pkl', 'rb') as pickle_file:     df_zm_merged = pickle.load(pickle_file)</pre>
In [4]:	<pre>def characters_to_codes_simplistic(cjk_string, zm_dataframe, db_column='RIME Characters', zm_column='ZM Codes'):     # Input:     # string of CJK characters     # database of Zheng Ma codes as a pandas DataFrame     # name of column to check for characters     # name of column containing Zheng Ma codes     # Output:     # list (dictionary?) of Zheng Ma codes     # - In case of multiple code correspondences, choose the longest     characters = cjk_string.strip().replace(' ', '')     codes = []     for characters in characters:</pre>
	<pre>for character in characters:     # Find any rows in the desired column that have the desired character     # Take the ZM codes in those rows as a list     possible_codes = zm_dataframe[zm_dataframe[db_column] == character][zm_column].tolist()      # Choose the **longest code** in that list of ZM codes     max_code = max(possible_codes, key=len) if possible_codes else None     # There could be several, so order alphabetically and pick the first     desired_codes = [c for c in possible_codes if len(c) == len(max_code)] if max_code else None     desired_code = sorted(desired_codes)[0] if desired_codes else 'N/A: no match'     codes.append([character, desired_code]) return codes</pre>

4. In code line 5, enter the Chinese characters to be encoded, encased in quotation marks as shown in the red box. The example below reads "Zhengma Method" in Chinese.



5. Run code 6 to obtain the Zhengma codes that correlate to the Chinese characters.

```
In [6]: new_test_codes_output1 = characters_to_codes_simplistic(new_test_string1, df_zm_merged)
print(new_test_codes_output1)
[('郑', 'uagy'], ['码', 'gxvv'], ['输', 'heqk'], ['入', 'oda'], ['法', 'vbzs']]
```

## - To convert from Zhengma codes to Chinese characters

#### 1. Go to the "code" folder.

<b>E</b>	bobtodd Added all Zheng Ma code and	data files current as of 2023/06/21	a0cdb20 3 weeks ago	🕄 4 commits
	code	Added all Zheng Ma code and data files current as of	2023/06/21	3 weeks ago
	data	Added all Zheng Ma code and data files current as of	2023/06/21	3 weeks ago
	drafts	Added all Zheng Ma code and data files current as of	2023/06/21	3 weeks ago
	img	Added all Zheng Ma code and data files current as of	2023/06/21	3 weeks ago
	raw	Added all Zheng Ma code and data files current as of	2023/06/21	3 weeks ago
Ľ	.gitignore	Added MacOS file .DS_Store to .gitignore		3 weeks ago
Ľ	README.md	Update README.md		3 weeks ago

#### 2. Open the "4\_converter.ipynb" file.

Name	Last commit message	Last commit date
🖿		
1_background.ipynb	Added all Zheng Ma code and data files current as of 2023/06/21	3 weeks ago
2_data.ipynb	Added all Zheng Ma code and data files current as of 2023/06/21	3 weeks ago
3_tests.ipynb	Added all Zheng Ma code and data files current as of 2023/06/21	3 weeks ago
4_converter.ipynb	Added all Zheng Ma code and data files current as of 2023/06/21	3 weeks ago
zm_helpers.py	Added all Zheng Ma code and data files current as of 2023/06/21	3 weeks ago

#### 3. Load and run the codes 1-3 and 8 shown below.

```
In [1]: # If running in Google Colab
          #from google.colab import drive
          #drive.mount('/content/gdrive')
          #path_prefix = "/content/gdrive/My Drive/Colab Notebooks/zhengma/raw/"
          #data_prefix = '/content/gdrive/My Drive/Colab Notebooks/zhengma/data/'
In [2]: # If running on local system
          path_prefix = "../raw/"
data_prefix = '../data/'
In [3]: import pickle
          # Load pickle
          with open(data_prefix + 'df_zm_merged.pkl', 'rb') as pickle_file:
              df_zm_merged = pickle.load(pickle_file)
In [8]:
         def codes_to_characters_simplistic(code_list, zm_dataframe, db_column='RIME Characters', zm_column='ZM Codes'):
             # Input:
             # list of ZM codes
             # database of Zheng Ma codes as a pandas DataFrame
             # name of column to check for characters
                 name of column containing Zheng Ma codes
             #
             # Output:
                string of CJK characters
                   - In case of multiple character correspondences for a code, choose...
             #
             cjk_string = ''
             for code in code_list:
                 # Make sure the code is a valid ZM code:
# - fewer than 5 letters
                 # - no spaces
if ' ' not in code:
                     if len(code) < 5:</pre>
                          # Get the characters for that code
                          possible_characters = zm_dataframe[zm_dataframe[zm_column] == code][db_column].tolist()
                          # Remove any empty strings
                         viable_characters = [x for x in possible_characters if (len(x) > 0)]
                          # Add the smallest string (hopefully 1 character)
                          # ... watch out: there might be more than one minimum..
                          # ... what does min() do? return the first it finds in the list?
                         cjk_string += min(viable_characters, key=len)
                     else:
                         print('Code too long: {}'.format(code))
                  else:
                     print('Code should not contain spaces: {}'.format(code))
             return cjk_string
```

4. In code line 10, enter the Zhengma codes to be decoded back to Chinese characters as shown in the red box below. Each Zhengma code should be encased in quotation marks as well as separated from the other Zhengma codes by commas. Then, all Zhengma codes should be encased in a pair of brackets. Running this code will return the Chinese characters correlating to the Zhengma codes.

