

1 **A new paradigm for numerical simulation of microneedle based drug delivery**
2 **aided by histology of microneedle pierced skin**

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7 **Abstract**

8 Microneedle (MN) is a relatively recent invention and an efficient technology for transdermal
9 drug delivery (TDD). Conventionally, the mathematical models of MNs drug delivery define the
10 shape of the holes created by the MNs in the skin as the same as their actual geometry.
11 Furthermore, the size of the MN holes in the skin is considered to be either the same or a
12 certain fraction of the lengths of the MNs. However, the histological images of the MN treated
13 skin indicate that the real insertion depth is much shorter than the length of the MNs and the
14 shapes may vary significantly from one case to another. In addressing these points, we propose
15 a new approach for modelling MN based drug delivery, which incorporate the histology of MN
16 pierced skin using a number of concepts borrowed from image processing tools. It is expected
17 that the developed approach will provide better accuracy of the drug diffusion profile. A new
18 computer program is developed to automatically obtain the outline of the MNs treated holes and
19 import these images into computer software for simulation of drug diffusion from MN systems.
20 This method can provide a simple and fast way to test the quality of MNs design and modelling,
21 as well as simulate experimental studies, e.g., permeation experiments on MN pierced skin
22 using diffusion cell. The developed methodology is demonstrated using two dimensional (2D)
23 numerical modelling of flat MNs (2D). However, the methodology is general and can be
24 implemented for 3D MNs if there is sufficient number of images for reconstructing a 3D image
25 for numerical simulation. Numerical modelling for 3D geometry is demonstrated by using
26 images of an ideal 3D MN. The methodology is not demonstrated for real 3D MN as there are
27 not sufficient numbers of images for the purpose of this paper.

28 **Keywords:** Transdermal drug delivery, microneedles, numerical modelling and simulation,
29 histological image, diffusion, Canny edge detection

30 1. Introduction

31 Transdermal drug delivery (TDD) methods, which intend to deliver various drugs through the
32 skin, need to conquer the outermost layer of the skin, namely, the *stratum corneum* (SC) [1].
33 Mathematical modelling of drug transport through the skin can provide important insights into
34 TDD and it is considered to be important for analysing TDD as indicated by a large number of
35 studies [2, 3]. This paper aims to report a new paradigm for numerical simulation of microneedle
36 (MN) based drug delivery aided by histology of the MN treated skin.

37 The importance of the physicochemical properties of solutes for transdermal permeation has
38 been known since the early 1940s. But, it is only since the 1960s, i.e., when Higuchi first related
39 these properties to passive diffusion in percutaneous absorption of drug molecules [4] using
40 Fick's first law of diffusion that modelling diffusion of drugs for TDD has been seriously
41 attempted. Based on the diffusion law, many researchers have now simulated drug transport
42 from different technologies that can enhance the TDD [5]. MN technology is a promising method
43 and it is increasingly being explored for controlled enhancement of TDD of different molecules
44 [6, 7].

45 The first MN modelling paper aimed to aid design of hollow MNs for fluid extraction [8]. Since
46 then, various researchers have focussed on improving the accuracy of simulation by
47 incorporating important fundamental features of the behaviour of MNs for drug delivery, thereby,
48 achieving better prediction of the drug diffusion behaviour [9, 10]. For example, the geometry
49 and size of the MNs, which are important factors, have been considered in a number of
50 previous modelling studies because they determine the drug diffusion rate and flux from the
51 MNs [11]. Consequently, optimization of the MNs geometry, shape and size of the MNs has
52 been attempted by many researchers, so that the desired TDD rate can be identified for specific
53 case [12]. These frameworks demonstrate that the patterns of MNs and alignment of these MNs
54 on the patch are important to provide a sufficient delivery rate of drugs [13].

55 Overall, it seems that the simulations for MNs based drug delivery are helpful for design of MNs
56 and understanding how they function but these require results of high quality and accuracy.
57 Generally, the current researches on MNs modelling idealize the size and shapes of the MN
58 holes (i.e., the computational domain) which are created by the MNs and often it is assumed
59 that the size of the holes are the same as the MNs themselves or a certain fraction of the
60 lengths of the MNs. However, the histological images of these holes indicate that the shapes of
61 MNs and their associated holes may be very different [14]. Not only the lengths of the MNs
62 pierced holes vary in length from case to case but also their shapes may vary. From the point of
63 view of TDD, this implies that the drug delivery rate should vary from case to case. This can
64 become a crucial factor that causes inaccuracy in the simulation results. For these reasons, this

65 paper aims to develop a new paradigm in numerical simulation for drug delivery by MNs which
66 can incorporate the shapes and sizes of the MNs holes as determined from the histological
67 images of MNs treated skin. It is hypothesised that more realistic simulated drug transport
68 behaviour (e.g., transient drug concentration profile) can be obtained by averaging simulation
69 results from a number of cases given by different histological images for the same circumstance
70 (e.g., the same skin, MN length and drug molecule), coupled with experimental data (e.g.,
71 diffusion coefficient of the drug or drug permeability) for the corresponding case.

72 In addressing this issue, this paper introduces a new approach that should improve the
73 simulation accuracy of MNs based drug delivery. We present a numerical model based on the
74 histological images of MNs treated skin instead of using the conventional method [15] which
75 considers the geometry of MNs in conjunction with a correction factor to determine the lengths
76 of the holes. There are several advantages of using these images, as discussed below.

77 When we consider the histological images and couple them with experimentally determined
78 parameters (e.g., drug diffusion coefficient) for modelling the drug transport, the deformation of
79 the skin due to insertion of MN [9, 16], which affects the drug transport behaviour, will be
80 directly accounted for. Most MN drug delivery simulations tend to ignore the effects of skin
81 deformation as it is governed by the geometry of the MNs, force exerted on the MN patch and
82 viscoelastic properties of the skin, thereby, making skin deformation and its effect on drug
83 transport a difficult quantity to determine. However, there are several researches which focused
84 on studying the factors that can cause skin deformation, e.g., the MN insertion force has been
85 decomposed into several components to increase the accuracy of the simulation [16]. Similarly,
86 the viscoelastic properties of the skin layers have been considered [17]. The histological images
87 provide a view of the holes created by MNs on skins. For the same cases, experimental data on
88 drug permeation and effective diffusion coefficient can be obtained. The accuracy of the
89 information can also be increased by acquiring a number of these images and experimental
90 data. As stated earlier, it is hypothesised in this paper that these information can then be used
91 to carry out more accurate numerical simulations for MN based drug delivery.

92 The histological image can provide an efficient way to evaluate the practicability of the MNs
93 modelling and, the images may be acquired irrespective of the source or the method of
94 acquiring them. For example, the cross-sectional view of the MNs treated skin can be acquired
95 by using a cryotome and then viewed under a microscope [18]. Similarly, technologies such as
96 optical coherence tomography (OCT) [19, 20] and micro-CT [21] have been useful in obtaining
97 images of MN pierced skin. These images can show whether the pathways (holes) created by
98 the MNs are adequate in overcoming the SC and for a target drug molecules to pass through.

99 In order to analyse the drug transport behaviour based on the histological images, a MATLAB
100 program has been developed in this work which can automatically acquire the coordinates of
101 various points of the image of the skin sample. These coordinates (i.e., not the image) can then
102 be imported into a simulator (e.g., commercially available software COMSOL [22]) to carry out
103 the desired simulations for drug transport.

104 **2. Histology of MNs treated skin as computational domain for numerical simulation**

105

106 **2.1 Acquisition of images of MNs pierced skin**

107 In this work, the computational domain for the numerical simulation is based on the histological
108 images which can expose the cross-sectional views of MNs treated skin. The images are
109 collected using porcine ear skin purchased from local abattoir [23]; however, the developed
110 methodology is general and it would work with images collected via any other means.

111 The skin samples are freshly harvested and flash frozen using liquid nitrogen after sectioning
112 and kept in the freezer at -20°C if they are not used immediately after collection. The sample
113 are wrapped in aluminium foil and left in room temperature to defrost for 2 hr before an
114 experiment. The skin are cautiously separated from the underneath cartilage using a surgical
115 scalpel.

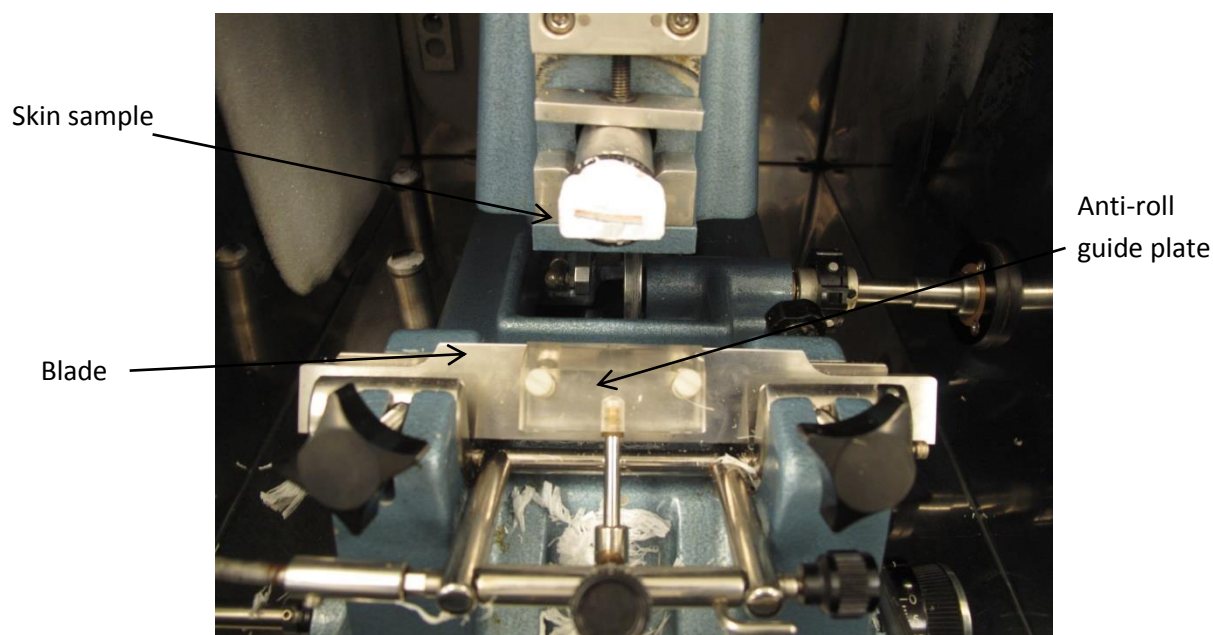
116 1100µm/1400µm long MN patches which are purchased from nanoBioSciences (Sunnyvale, CA,
117 USA) are used to pierce the skin. The insertion depths of these commercial MNs patches (~
118 400 – 500 µm) are much shorter than the actual lengths of the MN as the insertion depths
119 depend not only the actual MN lengths but also the force of insertion, MN density of the patches
120 and viscoelasticity of the skin. These have been demonstrated in our previous paper [24] and
121 are not discussed here.

122 A MNs patch is pushed with a relatively high thumb pressure to ensure that all the needles are
123 pierced into the skin and then mounted to a pneumatic pump with a constant 1MPa pressure for
124 10min. The sectioning protocol for the prepared skin sample using cryotome (Fig. 1) is
125 consistent with our previous study and is not discussed in detail in this paper [25]. The sample
126 of sliced skin is then analysed under a microscope and a number of images are taken using a
127 camera which is attached to the microscope. The acquired images are processed for numerical
128 simulation as discussed below.

129

130 2.2 Processing of skin histological images for numerical simulations

131 An image of the skin histology cannot be directly used as a computational domain for numerical
132 simulations as the skin layers/surfaces needs to be identified in terms of co-ordinate points.
133 Furthermore, due to the possibility of a number of other factors which affect the quality of the
134 original image for simulation purpose, the developed algorithm is designed to eliminate these
135 factors. These are discussed separately in the latter part of the paper.

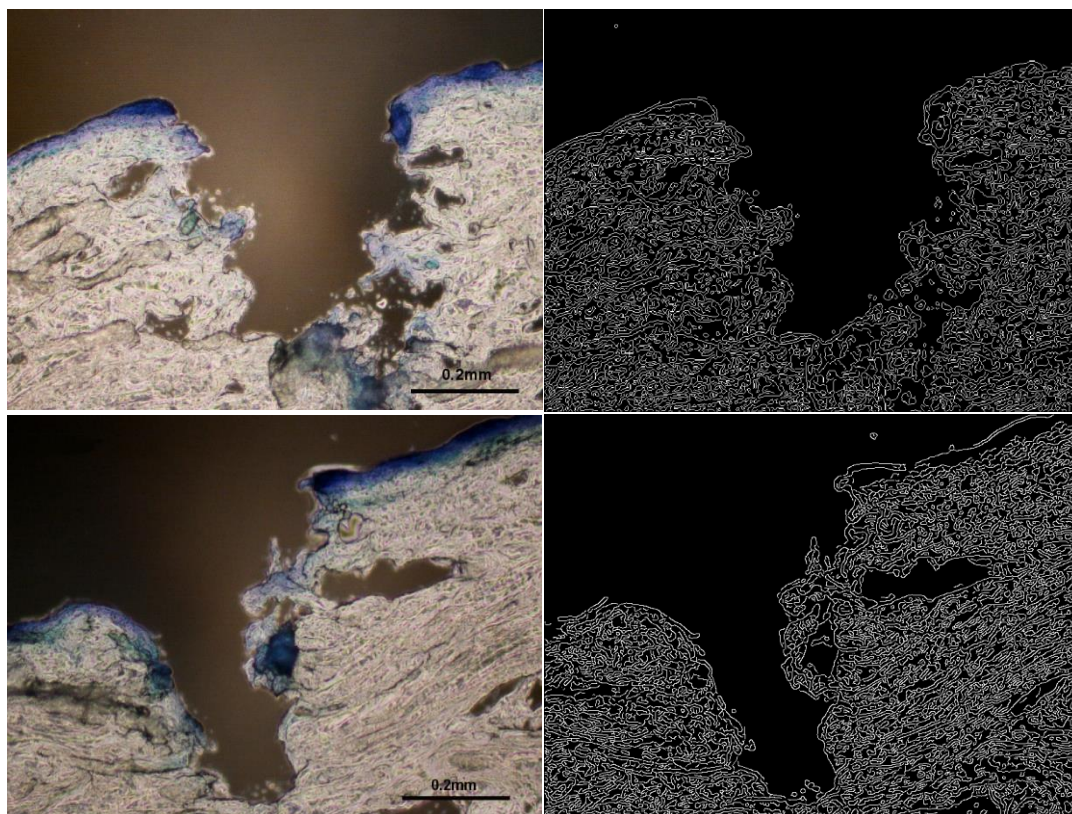


136

137 Fig. 1 A cryotome setup which was used to acquire the histological images of the MN pierced
138 skin. The skin sample is wrapped in glue, fixed on the sample holder between the blade and
139 anti-roll guide plate, and sliced into think sections.

140 Once the images of the cross-sectional view of the MN pierced skin samples are captured, all
141 the images are imported into MATLAB (Natick, MA, USA) for processing [26]. In this work, an
142 in-house MATLAB program was developed to process these images. The first step of this
143 program is to acquire all the edges of the image. To achieve this, all RGB images (conventional
144 format using red, green and blue added on each other to reproduce all colours) need to be
145 converted into grayscale images. A Canny edge detection algorithm [27] is then applied on the
146 grayscale images to acquire the edges of the individual images. A Canny algorithm is an
147 advanced image filter based on a Gaussian filter [28]. It involves four stages, namely, (i) noise
148 reduction, (ii) edge detection, (iii) edge thinning, and (iv) thresholding with any hysteresis, which
149 provide high quality edges of computational domain in a black and white map. Two examples of
150 images of skin pre-treated with MN, which have been processed with the Canny algorithm using
151 the developed MATLAB code, are shown in Fig. 2. From the figure we can see that the edges of
152 the original images are acquired with high quality details. However, in reality, we do not need all

153 the details in different skin layers as well as the debris outside the skin which do not have any
154 significance for the drug transport. Furthermore, the presence of debris may influence the
155 numerically determined transport behaviour. Therefore, the images obtained are further
156 processed by specific algorithms to acquire smoother profiles of the skin layers/surfaces.



157

158 Fig. 2 Two examples of histological images of skin pierced with MNs (images on the right)
159 which are treated with the Canny edge detection algorithm (images on the left) for further
160 processing and numerical simulations.

161

162 **2.2.1 Different steps adopted for smoothing the images of skin histology for numerical** 163 **simulation**

164 The algorithm for preparing the geometry of the computational domain for numerical simulation
165 is consisted of four stages: (i) the image dilation and fill, (ii) debris identification, (iii) debris
166 elimination and (iv) importing domain as computational domain for numerical simulation. When
167 all four stages are finished, the acquired geometry of the domain is expected to be ready as a
168 computational geometry for numerical simulations.

169 **2.2.1.1 Dilation and filling**

170 Firstly, the edges acquired from the edge detection process need to be dilated to connect any
171 gaps on the skin surfaces. It is a necessary step to accomplish an intact domain for numerical
172 simulation from discrete lines as shown in Fig. 2 [29]. From a number of trials we have

173 concluded that a 5 pixels×5 pixels dilation matrix is sufficient to connect all the gaps in the
174 images that we have collected. However, this matrix may be different in another case where the
175 image of the skin histology is significantly more complicated and requires significant amount of
176 dilation and filling. To achieve higher accuracy, the size of the matrix, represented as 'se' in this
177 paper, can be modified in the developed program. After all the gaps have been connected,
178 there may be still some undesired sections (e.g., holes or unconnected parts) left in the image,
179 which need to be filled, as otherwise they would impede the process of the skin layer acquisition
180 and numerical simulations. The boundary of the domain also needs to be defined according to
181 the profile of skin surface before the 'image fill' process.

182 **2.2.1.2 Debris identification**

183 As discussed above, after the computational domain (an image) has been confirmed, there may
184 still be some undesired skin debris in it. The debris can be hard to predict in the images
185 because they can be constituted by loose debris of the skin sample (e.g., generated while the
186 skin is pierced) as well as by other impurities or bubbles in the embedding compounds (e.g.,
187 gels used for acquiring cryotome images). The MATLAB program has been developed to
188 automatically identify all kinds of debris so as to smooth the images irrespective of their sources.

189 For the purpose of debris identification, the debris in the image is discriminated from the main
190 body of the skin sample and the debris is identified individually by the program. After the debris
191 is identified, an elimination program is launched to remove the debris. This stage of the
192 developed program is designed to remove debris from the image without causing any damage
193 to the computational domain of interest. Our method shows great advantages comparing to
194 other filtration methods (such as using rank or Gaussian filtering methods to remove debris)
195 which can cause great damage to the outline of the skin [30]. Fuller details of the debris
196 elimination program will be introduced in section 2.2.1.3.

197 **2.2.1.2.1 Specifying corners of the debris in terms of co-ordinates**

198 The debris identification stage is based on the assumption that the debris has closed
199 edges/boundaries. In other words, if a point on the edge of debris moves along its edge, it will
200 eventually come back to the same point where it started. This is an important factor in the
201 developed algorithm so as to discriminate the debris from the skin sample and confirm which of
202 the target debris is to be eliminated. If we choose a corner of the debris as the starting point,
203 this point will then go from corner to corner and finally reach the original corner. Therefore, we
204 need to classify the moving patterns between the corners. To explain this process a logic
205 diagram is shown in the Fig. 3. In the figure, the capital letters L/R/U/D/T/B/P/N represent the
206 initial alphabets of words left/right/up/down/top/bottom/positive/negative, respectively, which
207 represent how a position moves in the algorithm to identify the debris. For example, the

208 combination of LTP indicates the following: (1) the current point is on one of the left (L) top (T)
209 corners of the image; (2) the points on its lower right have their pixel intensity values equal to
210 positive (P) 1.0; and (3) positive represents the direction of the edge detecting process passing
211 this point is clockwise (while negative represents counter-clockwise). In contrast, the LTN points
212 satisfy the inverse of the above three conditions for LTP points. A schematic diagram to explain
213 the differences between the LTP and LTN points has been shown in Fig. 4.

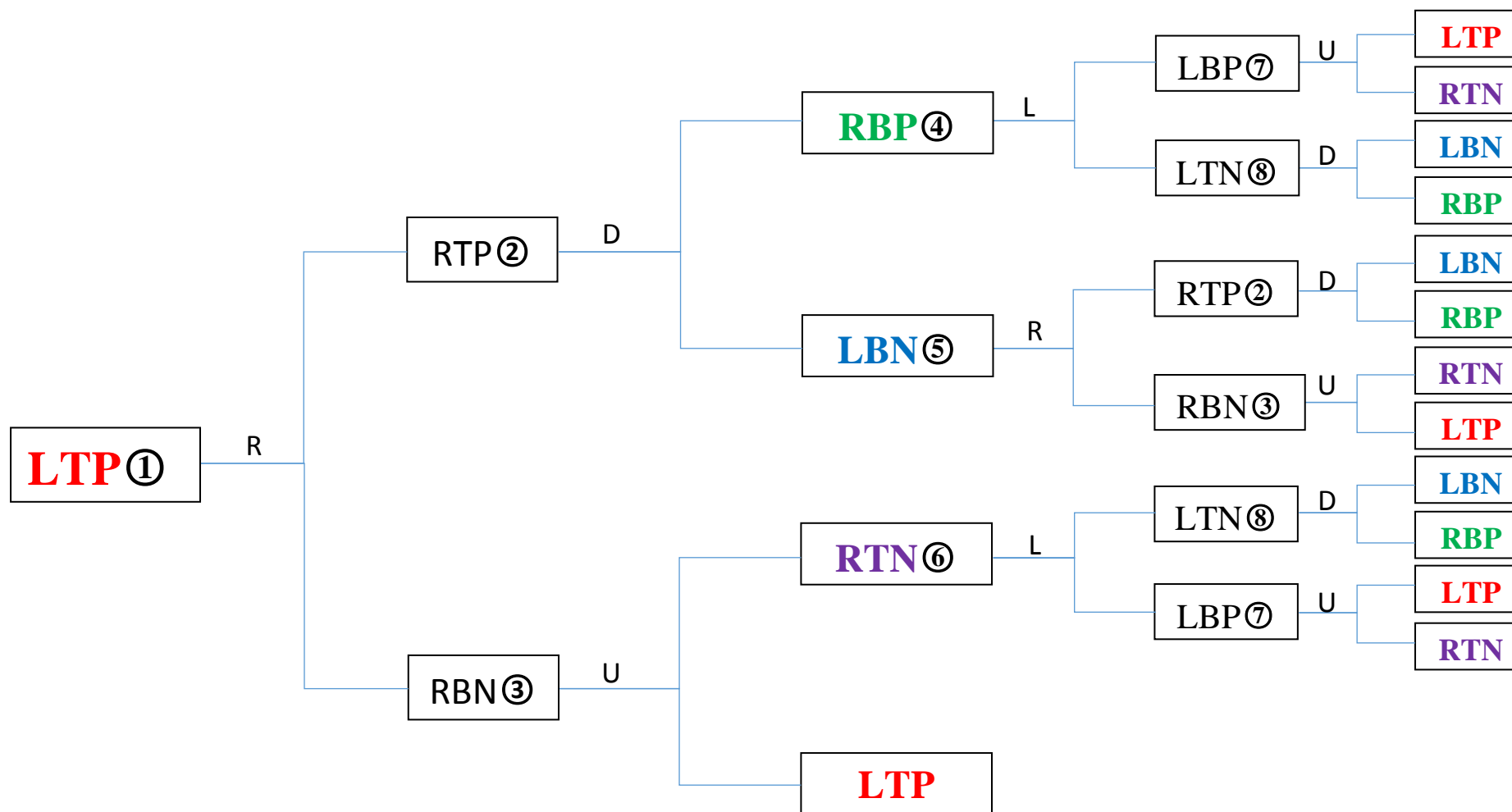
214 **2.2.1.2.2 Principles for the identification of debris**

215 In this section, we discuss the principles and the mechanism of the debris identification process
216 in more detail. The developed MATLAB program starts from LTP which could be a positive left
217 top corner of a domain of any shape. To define a corner in an image, we define that a minimum
218 number of four points are required. In this specific case at point (x,y) , a LTP can be confirmed if
219 it satisfies the following four conditions: $(x+1,y-1)=0$; $(x,y-1)=0$; $(x-1,y-1)=0$ and $(x-1,y)=0$ (for a
220 800×600 image, the coordinate from left top to left bottom is $x=0$ to $x=600$, from left top to right
221 top is $y=0$ to $y=800$). Once a LTP point is chosen, there are two initial conditions that should be
222 satisfied for this program. Firstly, LTP is chosen as the only criterion being both the starting
223 point and terminal point, and secondly, it is defined that the first move from LTP is always to the
224 right direction (clockwise). From Fig. 3 we can see that there are only two destinations if a LTP
225 point moves to the right following the edges, i.e., RTP and RBN. If a point reaches the RTP,
226 then it can only move downward to either RBP or LBN. An example edge detection process has
227 been shown in Fig. 5.

228 Although there are 8 different corners involved according to Fig. 3, they are all connected to the
229 four terminals which are marked with different colours. They are LTP/RTN/LBN/RBP marked
230 with red/purple/blue/green, respectively. However, only the red LTP is the real terminal. . When
231 the process reaches red LTP, a check must be made to compare the current point to the
232 original one. If they are the same point, it indicates that the edge detection process has been
233 done because the selected point has travelled the entire surface of the debris and back to its
234 original position again. If not, the process will go back to LTP^① and continues until it reaches
235 the original point. The circle enclosed number represents pathway 1 which is connecting LTP to
236 either corner RTP or RBN. These pathways can keep the edge detection process to stay on the
237 edge. Otherwise, the process may never move from one corner to another.

238 When the edge detection process reaches other three terminals, it will jump back to the
239 previous junction that has the same colour with that terminal, for example, all purple RTN
240 terminals will jump back to junction purple RTN^②. An illustration of a simple loop starting from
241 junction RTN^③, which moves to terminal RTN following the edge of the shape and then jumps

242 back to junction RTN[⊙], has been shown in Fig. 6. Where the blue and black arrows represent
243 the process conducted in logic diagram and reality, respectively. When the process jumps back
244 to the junction RTN[⊙], the point will move to the left again until it reaches the terminal LTP. All
245 three coloured junctions connect to a LTP terminal to avoid falling into infinite loops.

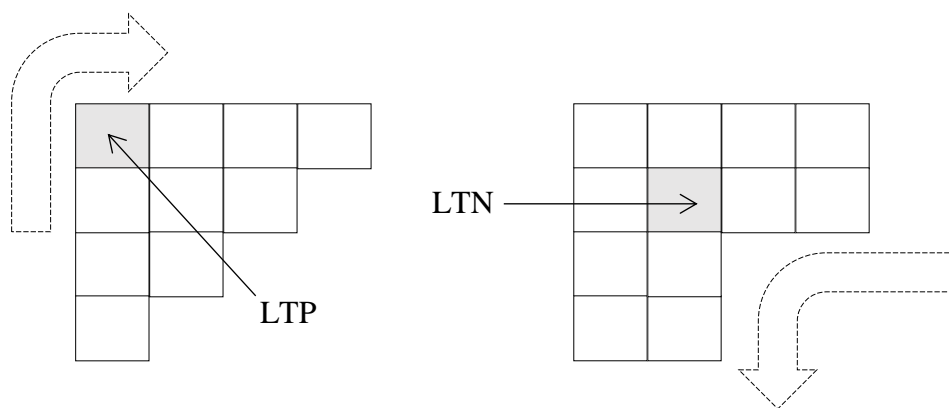


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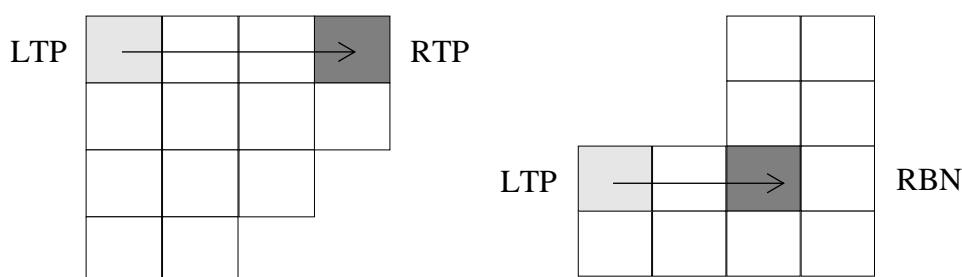
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Fig. 3 A logic diagram of edge detection algorithm: L=left, R=right, U=up, D= down, T=top, B= bottom, P=positive, N=negative. Circle enclosed number represents pathways connected to specific corners.



249
250 Fig. 4 A schematic diagram to demonstrate the differences between a LTP point and a LTN point
251 (each square in the diagram represents one pixel in the image).

252



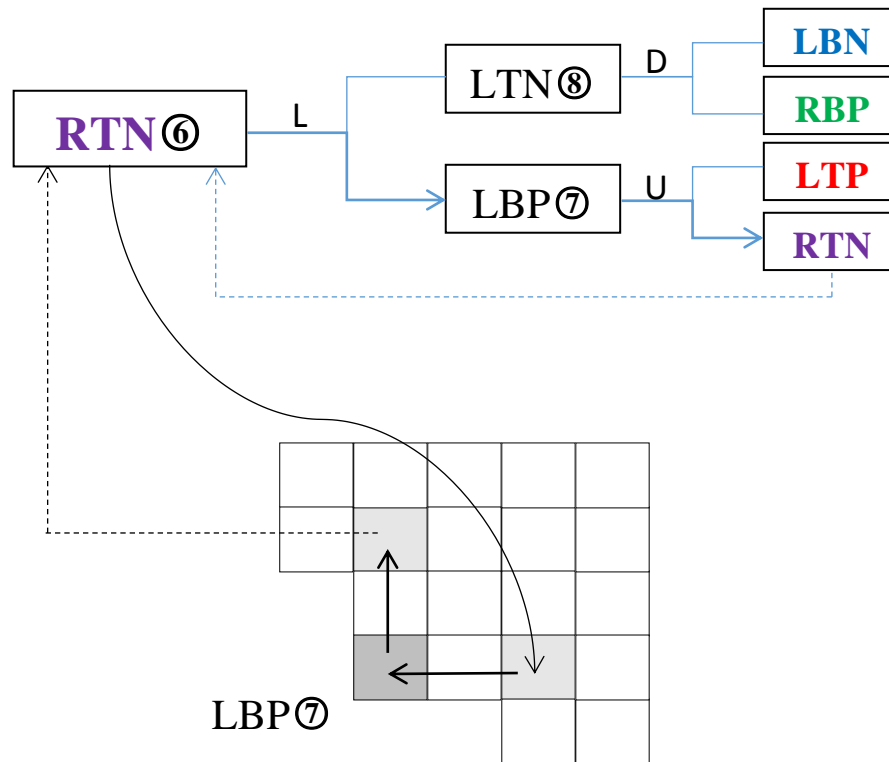
253
254 Fig. 5 A schematic diagram which shows two possibilities for a point while moving from LTP to
255 either RTP or RBN (each square in the diagram represents one pixel in the image).

256 2.2.1.2.3 The definition of hidden corners

257 In some cases, there are corners which are not easy to distinguish from the shape because the
258 definition of a corner in this program and it may not be possible to assign co-ordinates precisely
259 to each point. This is because these corners are concealed in the shape or overlapped with other
260 points. However, they can be found by the edge detection process. The reason for the existence
261 of these hidden corners is that the trajectory of the edge detection process is not always straight.
262 When the trajectory is terraced, the corner will appear as irregular. An illustration of hidden
263 corners RBN and RTN in edge detection process has shown in Fig. 7.

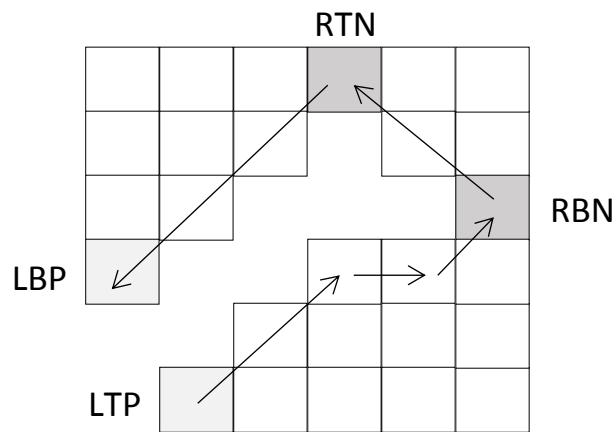
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266

267 Fig. 6 An example of a typical case in which the debris identification process reaches a terminal
 268 (see Fig. 3) where it will automatically jump back to its corresponding junction (each square in
 269 the diagram represents one pixel in the image).



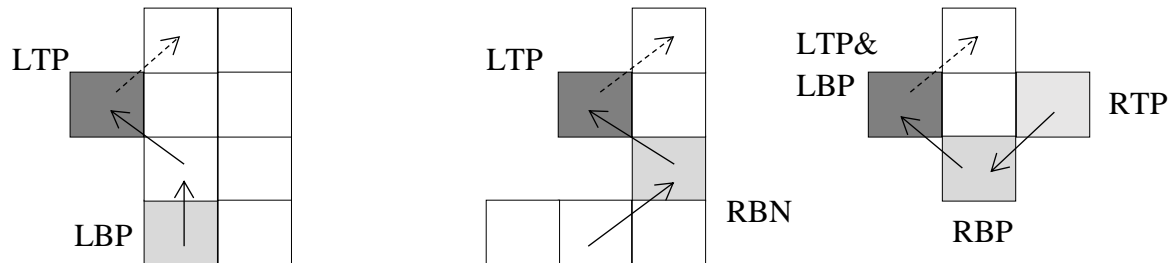
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271 Fig. 7 Illustration of two hidden corners existing in this example figure, which are RTN and RBN
 272 formed due to terraced edge (each square in the diagram represents one pixel in the image).

273 The corners LTP and LBP are easy to identify but the corners of RBN and RTN are likely to be
 274 anomalous. Nevertheless, the RBN and RTN can be recognized by the program, and therefore,
 275 the developed MATLAB code will ensure that the edge detection process will not be affected.

276 2.2.1.2.4 Special cases in the process of identifying corners

277 A special circumstance needs to be clarified when the edge detection process runs back to LTP
 278 from the only two possible corners: LBP and RBN. Three representative cases have been shown
 279 in Fig. 8:

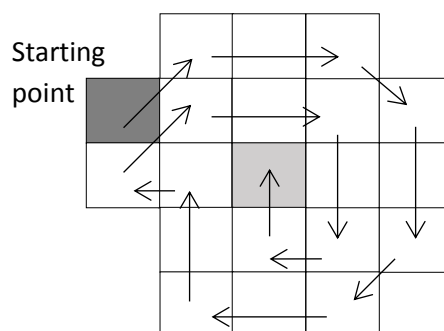


280
 281 Fig. 8 Three special cases in the edge detection process which need to be identified individually
 282 in the program by the user (each square in the diagram represents one pixel in the image).

283 The first and second cases in Fig. 8 show that when the edge detection process moves up from
 284 LBP and RBN to LTP corner, the program will not be able to recognize the LTP corner according
 285 to the logic diagram. The program will ignore the LTP corner and move on to follow the dashed
 286 arrow. The third case shows an extreme circumstance in which the LTP corner overlaps the LBP
 287 corner and the program will go on following the dashed arrow. The reason for this situation is due
 288 to the fact that when we define the LTP corner, we have used four points. However, only three
 289 points have been used to profile the pathways. The problem for all other corners has been solved
 290 by applying the 'hidden corner' concept which has been mentioned previously. But the LTP
 291 corner is different because the program may have to be terminated here. To solve this special
 292 case, an additional step must be introduced to compare the current LTP corner to the original
 293 one. Once the left top corner is confirmed as the same one of the original corner, it indicates that
 294 one of the debris has been identified so that the corresponding elimination process will be
 295 triggered.

296 2.2.1.3 Debris elimination

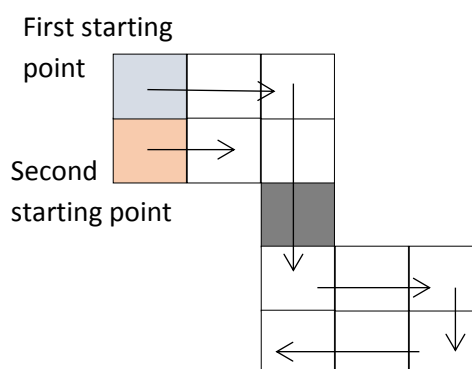
297 Once all the debris has been identified, the program will jump to the elimination stage
 298 automatically to remove the skin debris. As mentioned before, a conventional image filter cannot
 299 be applied here due to the inaccuracy [31]. Therefore, the elimination process is specially
 300 designed which shares the same logical diagram with the debris identification process. However,
 301 the elimination process will erase every point that the moving point Y has passed through.
 302 Therefore, the program will not stop until the last point of the debris is eliminated because the
 303 starting point has already been erased at the beginning. The elimination program peels off the
 304 debris shape layer by layer and jumps back to the debris identification program once the process
 305 is finished. An illustration of the elimination process is shown in Fig. 9.



306

307 Fig. 9 An illustration of the debris elimination process (each square in the diagram represents
308 one pixel in the image).

309 The elimination process begins from the starting point which is a LTP corner of the shape and
310 will be at the middle point of the shape that marked in light grey colour. However, the elimination
311 process may not be able to finish in one go because sometimes the shape will be broken into
312 several small blocks. It happens when the connection point is erased so that the moving point Y
313 cannot go back to the original block to finish the elimination process. To solve this problem, the
314 identification process is always scanning line by line from top to bottom. Once the first starting
315 point is identified, the program will jump to elimination process to remove the debris. After the
316 elimination, the identification program will scan the next line and find the second starting point to
317 remove the remaining part of the debris. The illustration is shown in Fig. 10.



318

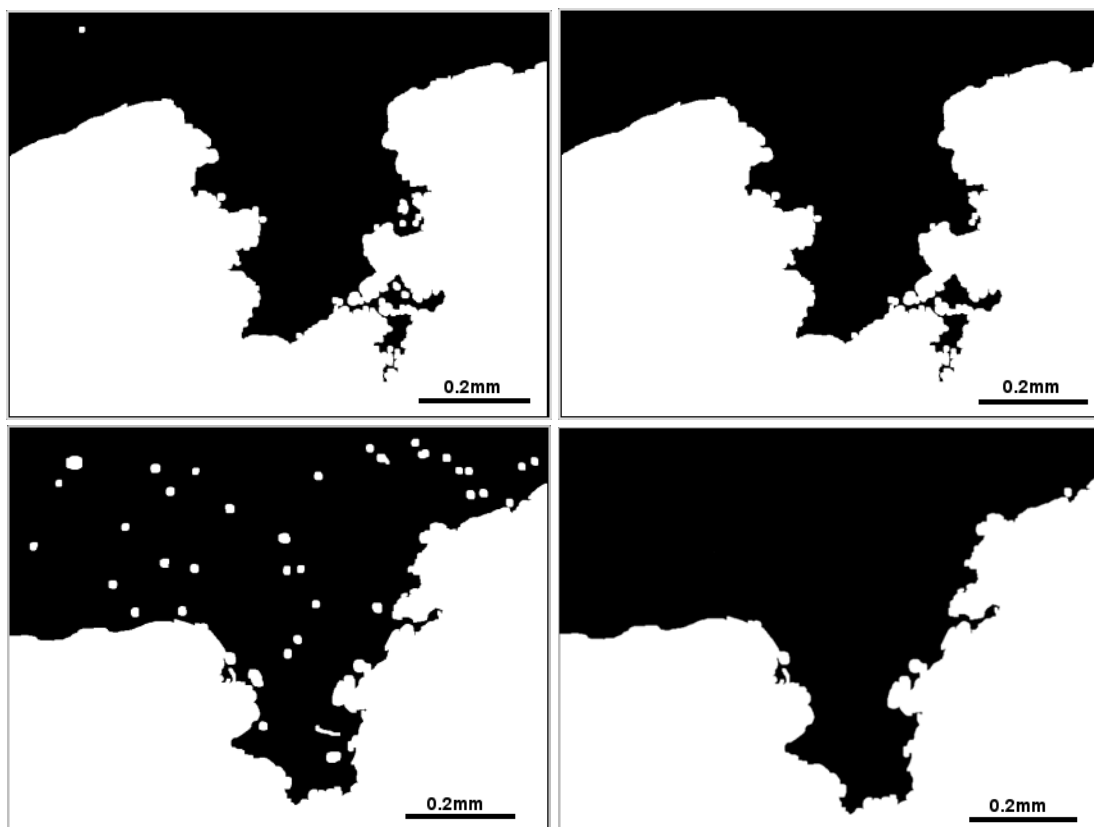
319 Fig. 10 An illustration for the special elimination case, first starting point, second starting point
320 and the connection points are marked with light blue, pink and grey, respectively (each square in
321 the diagram represents one pixel in the image).

322 To increase the speed of the program, a global parameter 'si' is set to describe the maximum
323 size of debris. The 'si' parameter is pre-set to 30 in this work, which means that the maximum
324 size of debris in an image is equal to or smaller than 30x30 pixels. After all debris are identified
325 and eliminated, the program will move to the next stage and the treated image compared to the
326 untreated image is shown in Fig. 11.

327 3 Numerical simulations using processed image

328 3.1 Acquiring processed image in numerical simulator

329 After the debris identification and elimination process, the image shows clear outline of the skin
330 sample without the interference of the debris. The program then captures the profile of the skin
331 by picking up all the points on the boundary. The thickness of the profile is defined to be one
332 pixel and the acquired profile will be saved in a matrix.

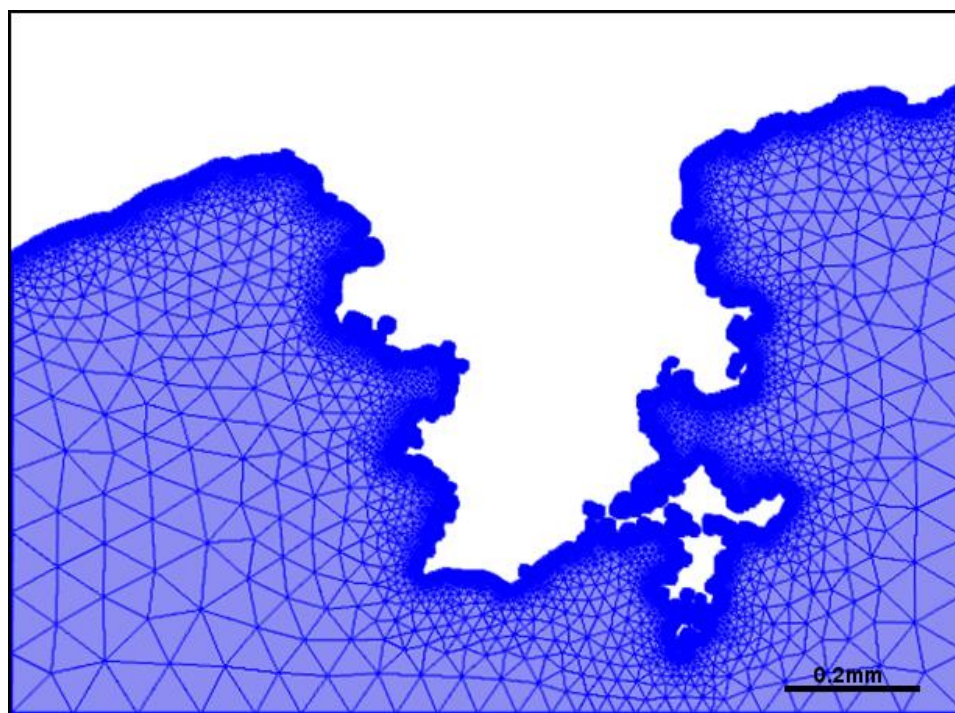


333
334 Fig.11 Two pairs of typical images before (left) and after (right) treating with debris identification
335 and elimination stages. The two images on the right hand (top and bottom images) side are now
336 ready to be used as computational domains for numerical simulation.

337 To carry out the diffusion analysis, the profile of the skin is imported into a commercially available
338 FEM software (COMSOL) in this work. However, it can be imported to any numerical software or
339 environment. All the coordinates of the points that are required for geometry are saved in a [n,2]
340 matrix and the order of the coordinate of points are also properly reorganized. To achieve the
341 same geometry between the computational domain in the FEM software and the imported
342 domain, the rearranged coordinate in the matrix must represent adjacent points in the image.

343 After the profile of the skin surface has been acquired, the computational domain is converted
344 into computational geometry whose boundary is consisted by coordinate of points (instead of

345 boundary lines as seen in an image). This imported geometry is then meshed for numerical
346 simulation. An example of a numerical mesh is shown in Fig. 12. The coordinates of all points in
347 the mesh are saved in a .txt file by the program, so the simulation can be done using any
348 software. There is only one task that needs to be done by the users themselves, which is to find
349 the ratio between the pixel and scale of the actual image. This requires user to set up a scale
350 when they obtain an image using camera, micro-scope, OCT or micro-CT or any other source.
351 After the scale is known, the ratio can be easily calculated by an image processing software.



352
353 Fig. 12 A typical image of a histological image which is meshed for numerical simulation

354 3.2 Governing equations

355 As discussed earlier in our papers, an effective skin thickness can be defined for MN treated skin
356 which represents the average path length for drug diffusion through the skin [32, 33]. Using the
357 same concept, we calculate the effective thickness in this work using the images that we have
358 collected. We define that there is negligible change on the diffusion coefficient in viable epidermis
359 due to insertion of MNs and the diffusion profile of drug molecules passing through the skin at
360 steady state is obtained using the Fick's first law:

$$N_i = -D_i \nabla C_i \quad (1)$$

361 Where N_i is the flux, the D_i is diffusion coefficient, C_i is the concentration. In the simulation of
362 MNs treated skin and the thickness of the skin change, so the effective thickness of the skin is
363 introduced in consistent with our previous studies [32, 33]. Therefore, we deduce the diffusion
364 coefficient from the experiment data of passive diffusion and the effective thickness in this study

365 can be simply considered as reduction of the real skin thickness. The real skin thickness is 1.6
 366 mm which is the average over 20 randomly selected samples. An effective thickness of the MNs
 367 treated skin is then calculated using equations (2) and (3) as discussed earlier [33].

$$D_{PD} = \frac{J_{PD}h}{\Delta C} \quad (2)$$

$$h_{eff} = \frac{D_{PD}\Delta C}{J_{MN}} \quad (3)$$

368 Where J_{PD} is the flux from passive diffusion, J_{MN} is the flux from MNs treated diffusion, D_{PD} is the
 369 diffusion coefficient of the skin and h_{eff} is the effective thickness of the MNs treated skin. We use
 370 the steady state model to analyse the experimental data because it is impossible to know the
 371 drug concentration at any position of the skin at any time point. However, the numerical
 372 simulation is able to provide simulated data at any specific time point and depth [34].

373 Once the effective skin thickness has been identified, we apply Fick's second law in order to
 374 build a transient drug diffusion model:

$$\frac{\partial c_i}{\partial t} + \nabla \cdot (-D_i \nabla c_i) = R_i \quad (4)$$

376 Where c_i is the drug concentration, D is the diffusion coefficient, t is the time point and R_i is a
 377 constant.

378 The 1D boundary conditions to solve the differential equations (1) and (4) are:

$$\begin{aligned} 379 \quad C &= C_1 \text{ at } x = 0 \text{ (for all } t \text{ for transient drug transport),} \\ 380 \quad C &= C_2 \text{ at } x = h \text{ (for all } t \text{ for transient drug transport),} \quad (5) \\ 381 \quad C &= 0 \text{ for } 0 < x < h \text{ (at } t = 0 \text{ for transient drug transport)} \end{aligned}$$

382 Where C_1 is the constant drug concentration we give on the skin surface, C_2 is the drug
 383 concentration at the bottom of our skin model, x is the distance between skin surface and a
 384 specific point in the skin, h is the thickness of the skin. For transient simulations, C_2 is set to zero
 385 at the beginning and its cumulative values over time will be calculated using equation (4) until
 386 steady state is reached. In order to solve the differential equations (in 2D or 3D), additional
 387 boundary conditions should be applied to equations (1) and (4):

$$-\mathbf{n} \cdot \mathbf{N}_i = 0 \text{ at plane } y = 0, l \text{ and } z = 0, w \text{ (at all } t \text{ for transient drug transport)} \quad (6)$$

388 Where \mathbf{n} is the normal vector to the plane, \mathbf{N}_i is the flux, y is the length between the front surface
 389 of the model and a specific point in the skin in longitudinal direction and the total length is l , z is

390 the width between the left surface of the model and a specific point in the skin in horizontal
391 direction and the total width is w . The governing equations are implemented in commercial
392 software COMSOL by importing the coordinates of the points on the skin surface and choosing
393 the element sizes for different accuracy scales of FEM mesh. The parameters that are needed
394 for the simulations can be either acquired from experimental data or using the theoretical values
395 (e.g., correlations). If the transient model is applied which refers to equation (4), COMSOL can
396 show the diffusion results at any time point before it reaches the steady state.

397 **4. Results and discussion**

398 **4.1 Calculation of MN insertion depths based on histological images**

399 Four histological images of MNs treated skin samples have been chosen for both 1100 μ m and
400 1400 μ m long MNs. The insertion depth of each image is then calculated using ImageJ software
401 (Bethesda, MA, USA) [35] and the mean insertion depth of each group has been calculated. It is
402 found that the average insertion depth of 1100 μ m and 1400 μ m long MNs are 0.53 ± 0.054 mm
403 and 0.7435 ± 0.099 mm, respectively.

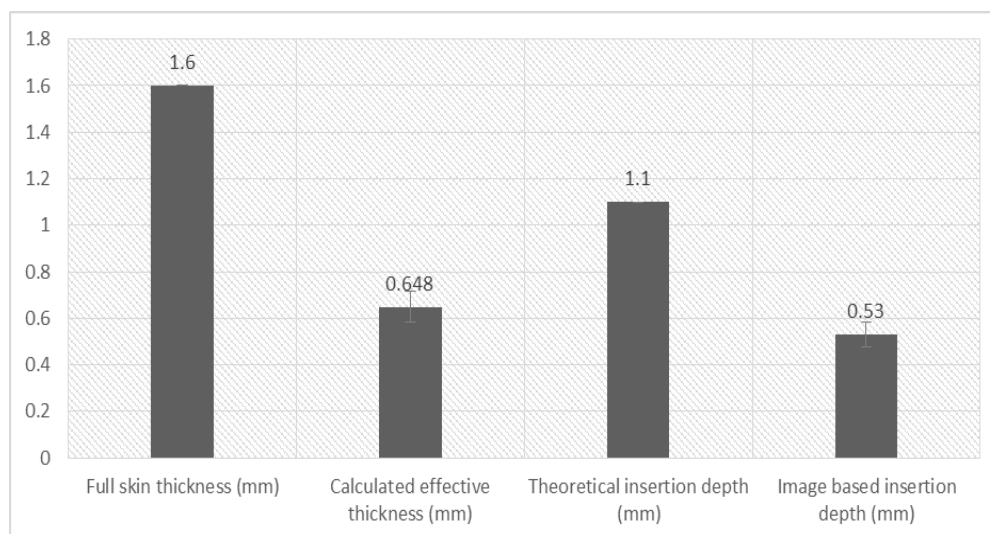
404 The theoretical insertion depth refers to the length of the MNs which are 1.1 mm and 1.4 mm,
405 respectively. The full skin thickness is a constant value of 1.6mm, which is mentioned in the
406 previous section.

407 The experimental data are obtained from our previous study effects of MNs on the permeability
408 of insulin in skin [25]. Since a drug molecule that is larger than 500 Da cannot pass through the
409 SC layer passively [36], we define that the diffusion coefficient for insulin (MW: 5808 Da) in the
410 SC layer is negligible. The histological images also indicate that the MNs partially break the SC
411 layer and mass transfer distance between the drug solution and the receptor compartment in a
412 FDC is reduced. Therefore, the complex situation where the SC layer is involved will not be
413 discussed in this paper and it is defined that the skin layer below the SC is the most relevant for
414 modelling the drug delivery process. For this reason, we consider our skin model as one layer.
415 Furthermore, we compare the passive diffusion in VE and diffusion in MN treated VE by using the
416 diffusion coefficient of the viable epidermis. Based on these assumptions and data from our
417 previous study, the diffusion coefficient (D_{PD}) is calculated as $1.3e-12$ m²/s and the effective
418 thickness of both MNs are deduced accordingly by applying equations (2) and (3), respectively.
419 The insertion depths and skin thickness results acquired for insulin are shown in Fig. 13.

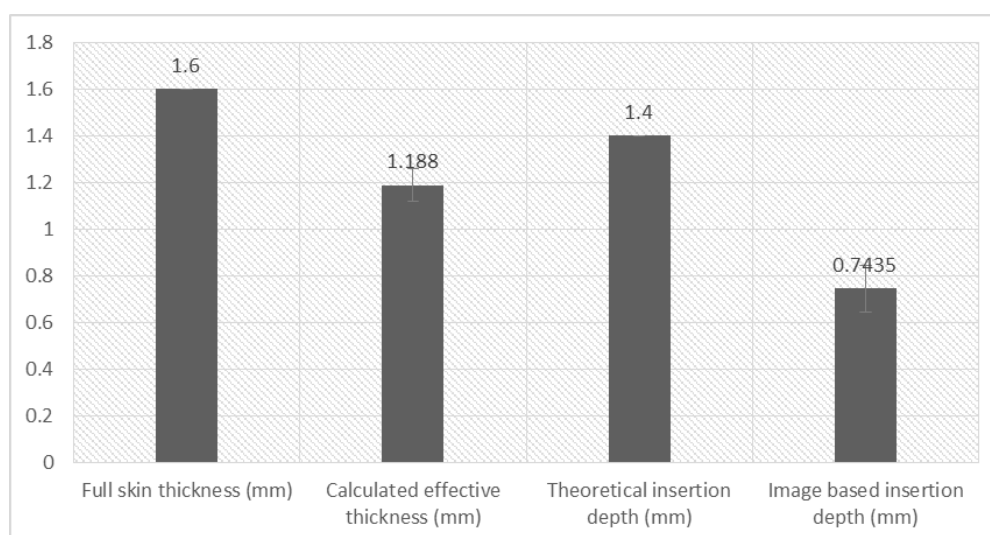
420 As shown in Fig. 13, we compare the full skin thickness with the calculated effective thickness of
421 the skin, theoretical insertion depths (i.e., length of individual MN) and average MN insertion
422 depths based on histological images. The results show that the effective thickness (and hence,

423 the mean path length for drug diffusion) is larger than the MN insertion depths based on the
424 images but smaller than the MN lengths or real skin thickness.

425



426



427 Fig. 13 Two sets of comparison: full skin thickness compared to the effective thickness after MNs
428 insertion. The theoretical insertion relates to the insertion depth calculated from histological
429 images. The effective thicknesses were calculated using data from insulin permeation study for
430 1100µm (top) and 1400µm (bottom) long MNs.

431 4.2 Numerical simulation of drug permeability/diffusion

432 4.2.1 Testing developed scheme for an ideal MN geometry

433 In order to test that the developed algorithm performs, we attempt to simulate an ideal geometry
434 of MN (Fig. 14A) and define that the holes created by them in the skin match their size and
435 shape. Therefore, the MN holes are well defined in terms of shapes and size (Fig. 14) and have
436 no debris in the image, making them a good model to test that the developed scheme is working.
437 As obvious, the modelling does not involve the use of a histological image in this case and the

438 simulation is done using the image of the MN geometry (0.5mm long) with some bends and
439 complex features. We define that such a MN system has been applied according to a 'poke and
440 patch' approach where the MNs have been applied on the skin, removed after creating the MN
441 holes and a drug is then applied on the skin which penetrate into the holes. The drug molecule
442 then diffuses into the skin through the viable epidermis. In effect, we simulate the drug
443 permeation study in a typical Franz diffusion cell as discussed earlier [23].

444 The data for permeation of insulin from our previous experiment using Franz diffusion cells [25]
445 have been chosen to carry out the numerical test. The drug concentration on the skin surface is
446 set to a constant value of 1000ppm and the bottom surface of the skin is set as zero
447 concentration which indicates a static system such as those seen in the receptor compartment in
448 a Franz diffusion cell. The time duration insulin is defined to be 48 hr.

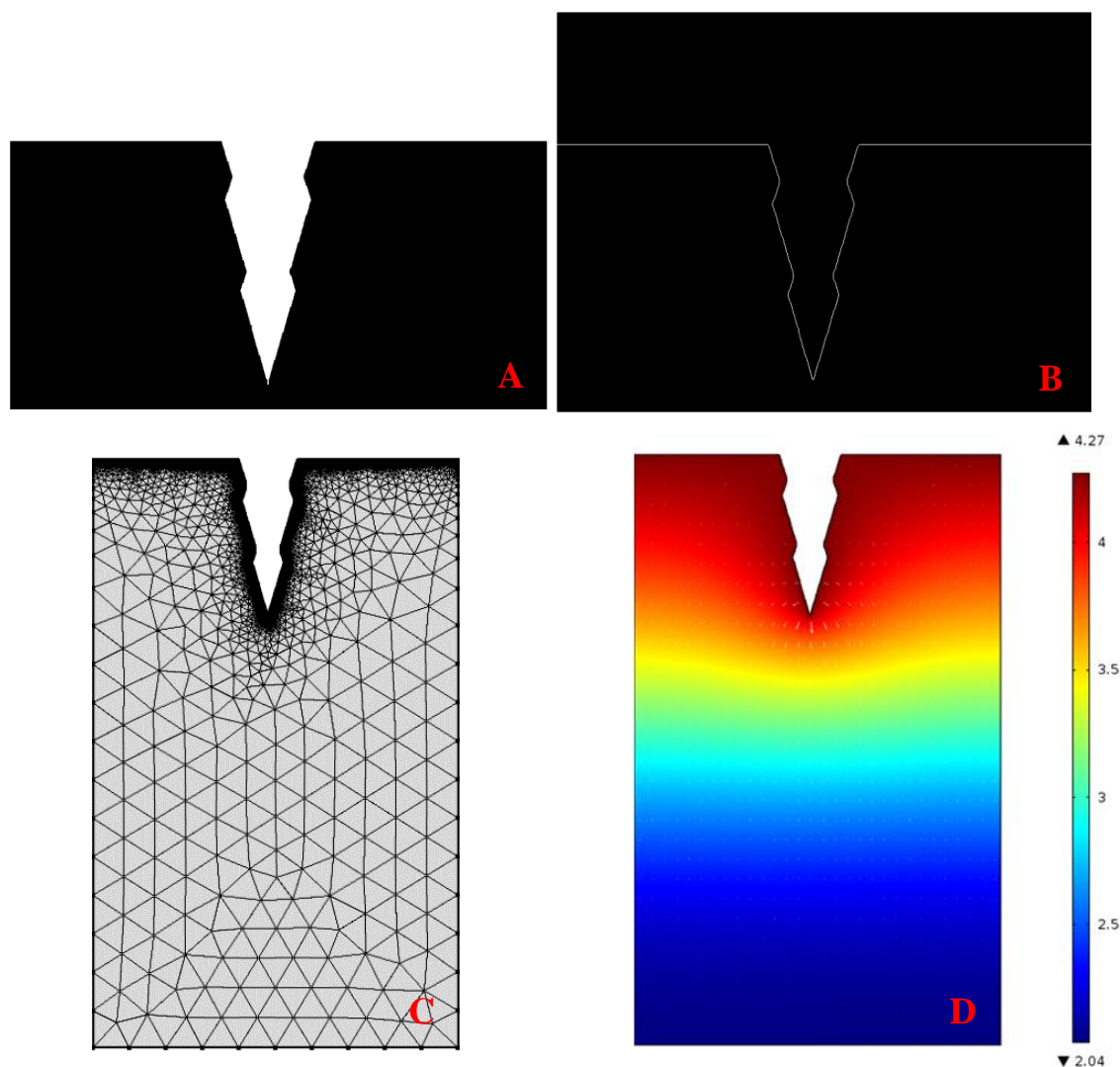
449 Fig. 14 and Fig. 15 show some of the results obtained for the case above. In Fig. 14 (C,D) we
450 show the mesh used for the numerical simulation and concentrations distribution in the MN
451 treated skin at steady state. Figure 15 shows the numerically calculated insulin concentration in
452 the receptor compartment of a Franz diffusion cell with and without MN. The results indicate that
453 insulin (molecular weight: 5808 Da) reaches 10% of its maximum concentration in the receptor
454 compartment in FDC after 48 hr. It has also shown that MNs cause great effects on large size
455 molecules because the trend lines between MNs enhanced diffusion and passive diffusion are
456 distinct.

457 **4.2.2. Numerical simulation of insulin permeation in a Franz diffusion cell**

458 In this section, we will illustrate modelling using the image acquired from cryotome sliced skin
459 sample captured by a microscope camera. The original and processed images are shown in Fig.
460 16. The simulation is then employed based on those 2D histological images. The MNs we
461 applied are flat in structure with negligible thickness; therefore 2D images are sufficient for this
462 study. However, the methodologies are general and therefore they can be applied for MN of any
463 shapes and sizes provided their histological images are available.

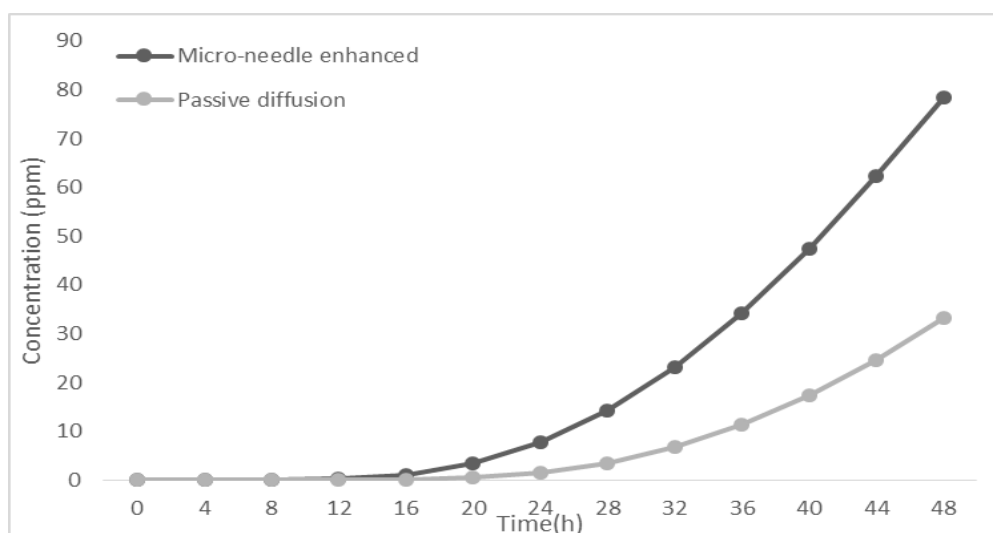
464 The same initial and boundary conditions as discussed earlier are again applied for the purpose
465 of this section. The numerical results for insulin concentration in the receptor compartment of a
466 Franz diffusion cell are shown in Fig. 17. The insulin delivery has been shown higher amount of
467 drug permeated and reduced lag time (time from initiation to the steady state). The simulated
468 data from all the histological images are now averaged and compared with the experimental
469 results of insulin from our previous study [25]. The initial concentration of the drugs and time
470 durations of the simulation remain the same with the experiment condition. The results are

471 shown in Fig. 18. From the figure we can see that that the predicted concentration of insulin
472 resembled well to the experimental results.



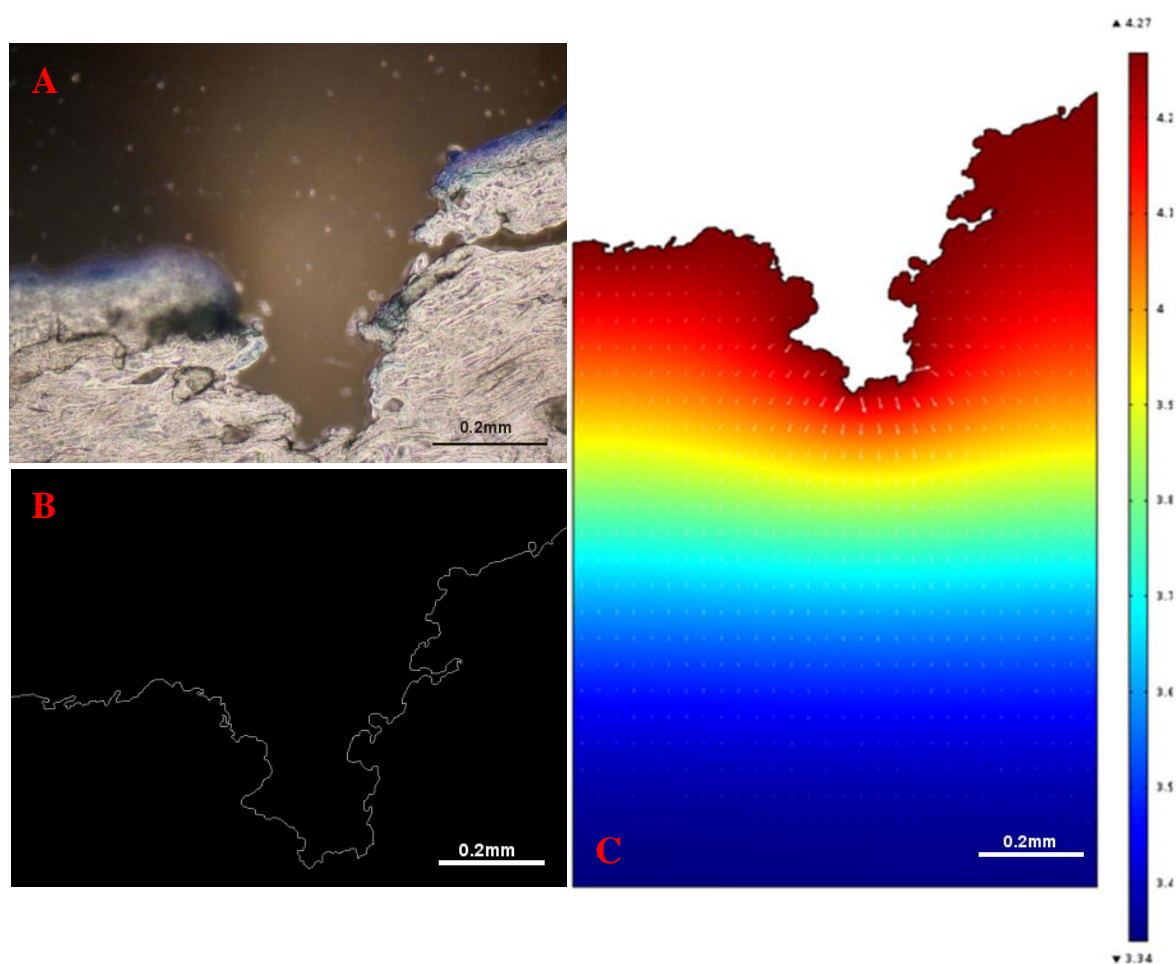
473
474 Fig.14 The process after the image is input into the program. A) The original image; B) The
475 outline of the skin has been captured; C) The skin thickness has been adjusted to 1.6mm and the
476 mesh using FEM has done; D) the simulation of the diffusion profile of the target drug molecule
477 (insulin, in this study)

478



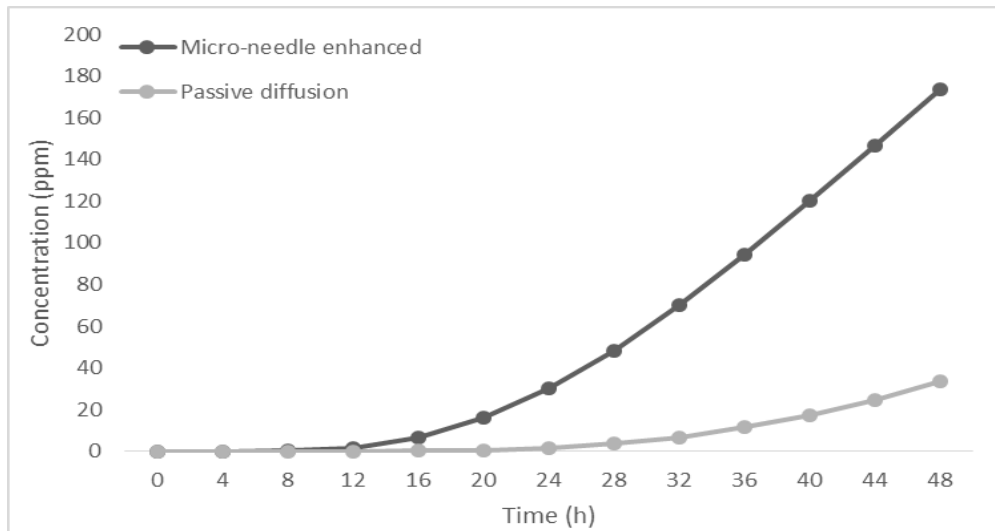
479

480 Fig.15 Insulin concentration profile of the passive diffusion and MNs enhanced diffusion based
481 on the ideal geometry in Fig 14. In both cases, only permeation in viable epidermis is considered.



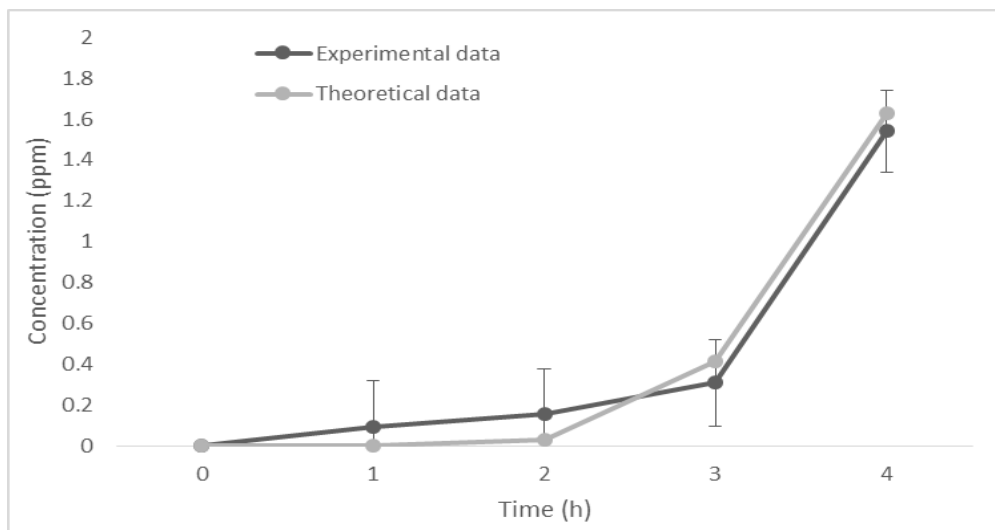
482

483 Fig. 16 The image from cryotome sliced skin is processed by program and simulated in
484 COMSOL. A) The original image; B) The outline of the skin has been captured; C) Simulated
485 diffusion profile of the target drug molecule (insulin, in this paper)



486

487 Fig. 17 The diffusion profile of the passive diffusion and MNs enhanced diffusion based on the
 488 imported model. Insulin concentrations in the receptor compartment of FDC have been
 489 calculated. In both cases, only permeation in viable epidermis is considered.



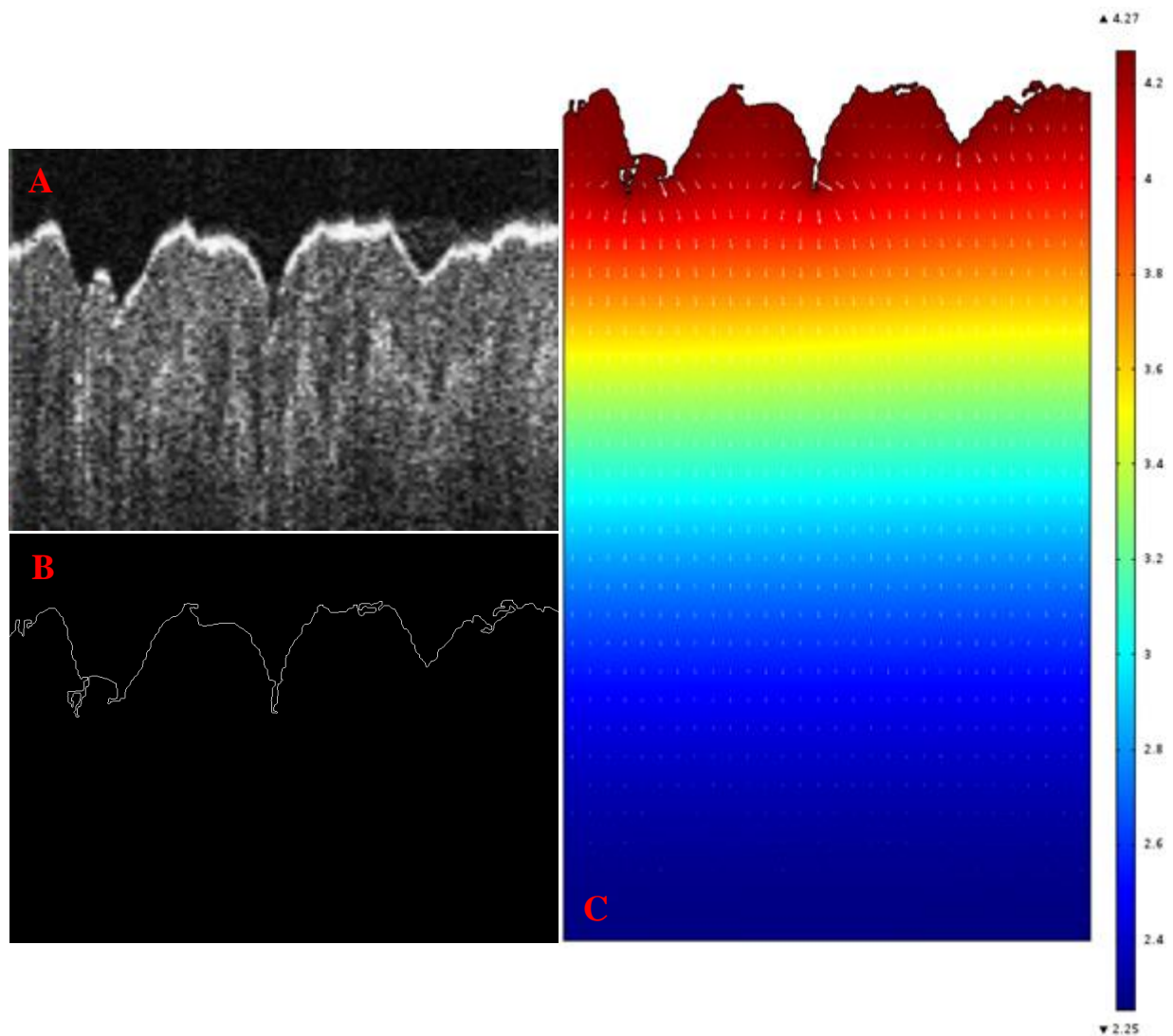
490

491 Fig. 18 Numerical simulation data compared to the experimental results from our previous papers
 492 [25]. The concentration profiles of insulin are presented.

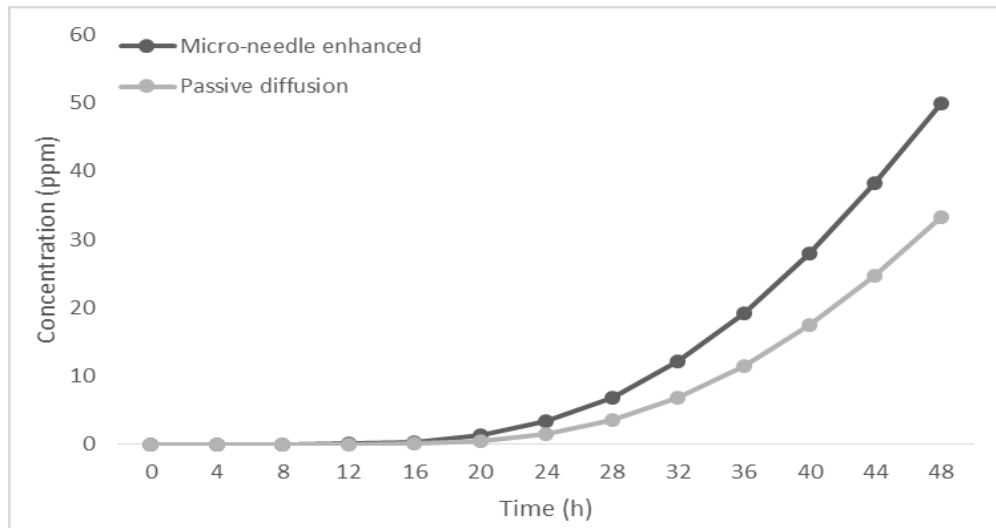
493 4.2.3. Numerical simulation using images obtained from the literature

494 The third modelling scenario is based on a complex OCT image which we have collected from a
 495 published paper [37]. The OCT image has much lower resolution level than the images taken by
 496 the in-house camera in this study. Despite this, it is observed that the developed algorithm can
 497 depict the outline of the skin surface without losing significant details. The numerical modelling
 498 results using these images have been shown in Fig. 19. The image in this case shows that the
 499 MNs create lower insertion depth but more holes than previous images. Assuming that the MNs
 500 in this example are used to carry out an insulin permeation study, the same boundary conditions

501 are applied again on this image. The insulin concentrations in the receptor compartment of a
502 FDC are shown in Fig. 20. The concentration profiles indicate that although the numbers of the
503 holes increased as MNs are pierced into the skin, the diffusion rate is low compare to the passive
504 diffusion. This also suggests that simply increasing the number of the MNs will not greatly
505 increase the permeability in this case. The insertion depth and the geometry of the MNs may
506 present higher impact to the diffusion rate.



507
508 Fig.19 The OCT image is processed by the program and simulated in COMSOL. A) The original
509 OCT image; B) The outline of the skin has been captured; C) the simulation of the diffusion
510 profile of the target drug molecule [37].



511

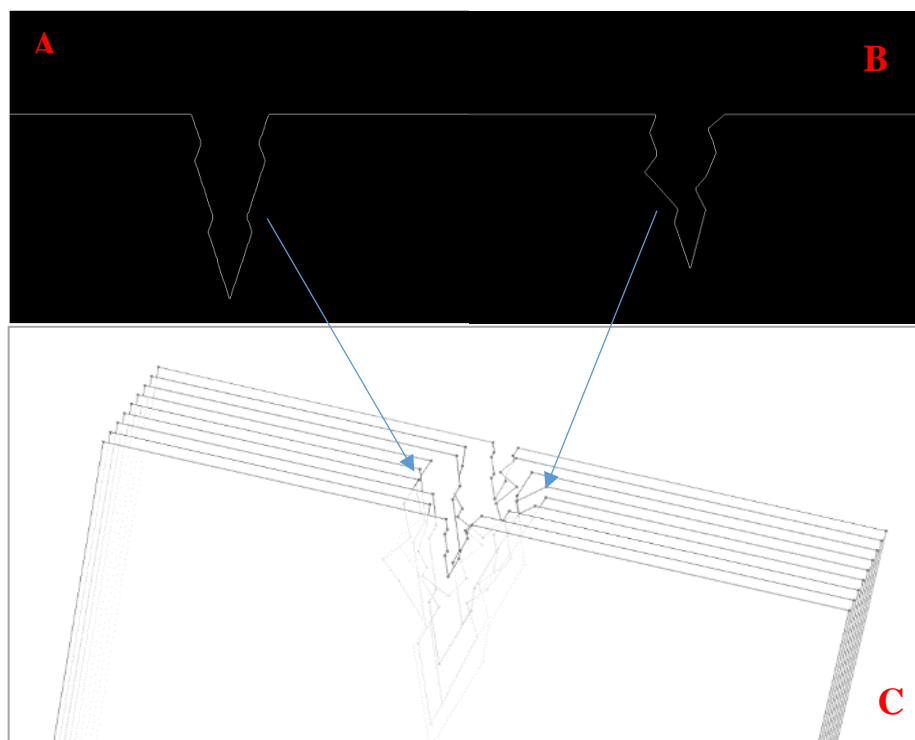
512 Fig. 20 The diffusion profile of the passive diffusion and MNs enhanced diffusion based on the
513 model of Fig. 19. Insulin concentrations at receptor compartment of FDC have been calculated.

514 In both cases, only permeation in viable epidermis is considered so as to have a meaningful
515 comparison.

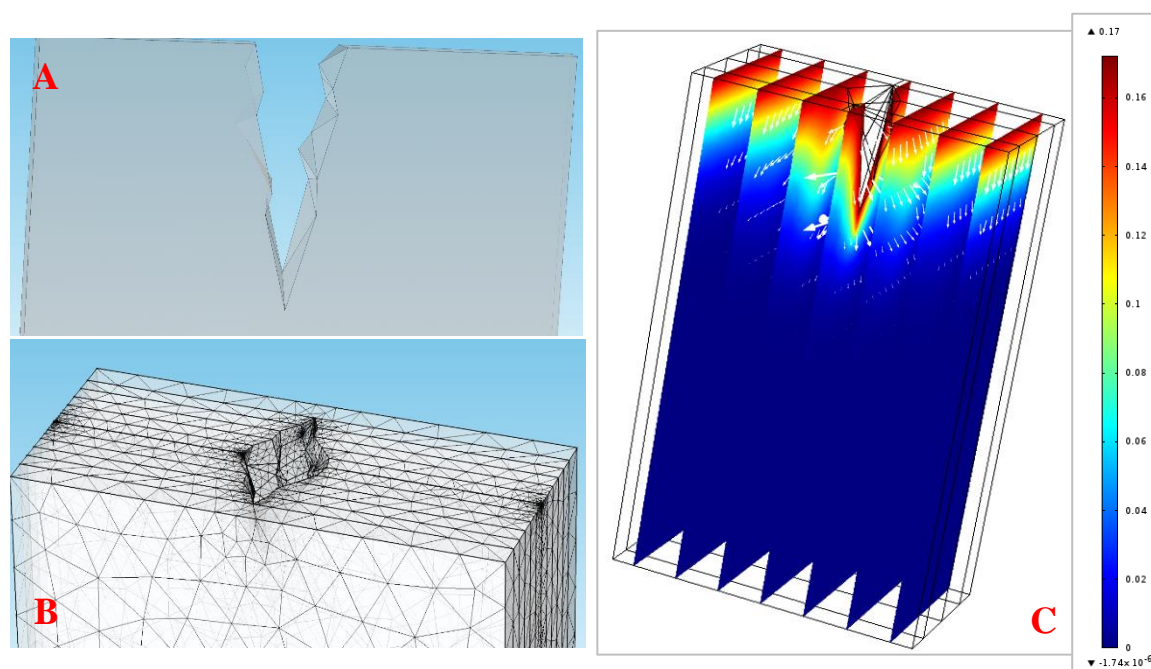
516 4.2.4. Numerical simulation of insulin permeation in 3D

517 The last case is an extension from the first scenario where we attempted to demonstrate
518 simulation of 2D structured MNs. There are plenty of previous studies which have used 3D MNs
519 model to simulate diffusion in TDD [38]. However, our 3D model is constructed from the pores
520 created by MNs instead of building a model using the shape of MNs. Different slices of
521 histological images from one MN cavity are combined to form a 3D model of the MN cavity and
522 the accuracy of the reconstructed MN cavity will increase when more slices are involved. In this
523 case, we choose the sample shape from Fig. 14 as the standard to maintain the consistency and
524 illustrate the process by including another 8 slices to construct the 3D model. The profile of each
525 sample slice is acquired using previous method and then all slices are imported to COMSOL as
526 individual surfaces which are shown in Fig. 21. After all sample slices are imported into COMSOL,
527 triangular and quadrilateral surface elements are created to connect one slice to its adjacent
528 slices (Fig. 22A). These connected slices are then knitted into one complete solid computational
529 domain and meshed using FEM, so the 3D boundary conditions from equation (5) and (6) can be
530 applied accordingly (Fig. 22B). The same concentration (1000 ppm of insulin solution) is applied
531 on the top surface of the model and the cumulative concentrations at the bottom surface are
532 recorded for 48h with a 4h interval (Fig. 22C).

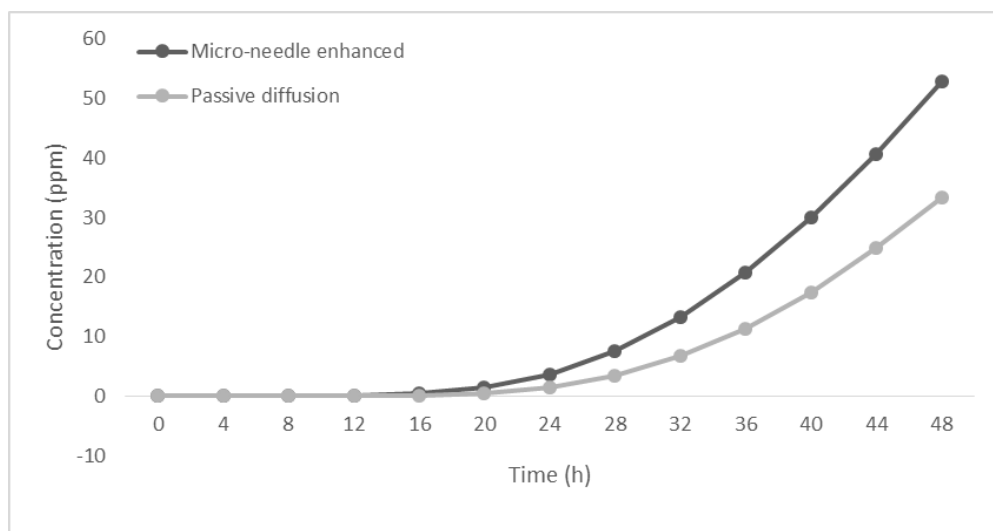
533



534
535 Fig. 21 The sample slices have been acquired individually and then imported into COMSOL. A)
536 The profile of the sample slice from Fig. 14 which is located in the middle of all slices; B) Another
537 sample slice located next to the standard; C) All 9 slices are imported into COMSOL for further
538 study.



539
540 Fig. 22 The process of 3D modelling using sample image slices. A) Two adjacent slices are
541 connected by surface elements; B) All slices are knitted to solid and meshed; C) The diffusion
542 profile when insulin solution is mounted on the top surface of the model.



543

544 Fig. 23 The diffusion profile of the passive diffusion and MNs enhanced diffusion based on the
545 model of Fig. 22. In both cases, only permeation in viable epidermis is considered

546 The numerical results for passive and MNs enhanced diffusion in VE are shown in Fig. 23. The
547 cumulative concentrations of passive diffusion in the Fig. 22 are identical to the 2D results from
548 Fig. 15 which indicates good consistency of the simulation. However, the concentrations of MNs
549 enhanced diffusion of the 3D model are decreased due to the greater flux term in both horizontal
550 and vertical directions. Based on this method, high quality 3D model of MNs treated skin can be
551 achieved in the future if the acquired histological images are consistent and are of good quality.
552 This paper aims to report on the development of the methodology and, therefore experimental
553 results of 3D structured MNs will not be discussed.

554 5. Conclusion

555 Numerical simulation based on histological image using an new MATLAB program and COMSOL
556 have been carried out which shows a great potential for accurate numerical modelling of MN
557 enhanced drug delivery. The histological images provide the image of MNs created holes in the
558 skin. This is hypothesised to be more accurate than simply assuming that the MN holes in the
559 skin have the same shape and size as that of the of MNs' geometry. The histological images
560 indicate an accurate depth of the hole which is required for the numerical simulation. The
561 developed algorithm converts the real images to simulation required coordinates. After importing
562 these data into a numerical simulator (e.g., COMSOL), the diffusion analysis can be easily
563 carried out. It is expected that the developed paradigm for numerical simulation of MN based
564 delivery would help the researches to design more efficient MNs systems.

565

566 **6. References**

567

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